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OM nucleic - protein search using frame_plus_n2p model

Run on: March 11, 2006, 01:37:47 ; Search time 37.2 Seconds
(without alignments)
2289.022 Million cell updates/sec

Title: US-09-905-083a-30
Perfect score: 1780
Sequence: 1 9gattccgggtccatggc.....aagaacacacaaacccctcag 969

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/abes/ABSSWEB spool/US0905083/runat_10032006_152452_29654/app_query.fasta_1
-DB=A_Geneseq -DEFT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blowum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=prc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes02p
-USER=US0905083 @CGN 1.1 348 @runat_10032006_152452_29654 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1 | 1364 | 76.6 | 253 | 2 AAR67888 | Human str |
| 2 | 1364 | 76.6 | 253 | 2 AAW05383 | Human amy |
| 3 | 1364 | 76.6 | 253 | 5 ABB84421 | Human SCC |
| 4 | 1364 | 76.6 | 253 | 5 ABB84406 | Human SCC |
| 5 | 1364 | 76.6 | 253 | 5 ABB84406 | Amino aci |
| 6 | 1364 | 76.6 | 253 | 6 ABU07440 | Protein d |
| 7 | 1364 | 76.6 | 253 | 6 ABU07471 | Protein d |
| 8 | 1364 | 76.6 | 253 | 6 ABR58471 | Human str |
| 9 | 1364 | 76.6 | 253 | 7 ADB80484 | Ovarian c |

| | | | | | |
|----|--------|------|-----|------------|-----------|
| 10 | 1364 | 76.6 | 253 | 7 ADJ68833 | Human hea |
| 11 | 1364 | 76.6 | 253 | 7 ADN39180 | Cancer/an |
| 12 | 1364 | 76.6 | 253 | 8 ADL06515 | Human tum |
| 13 | 1364 | 76.6 | 253 | 8 ADN04182 | Antipgori |
| 14 | 1364 | 76.6 | 253 | 8 ADR72880 | Human ova |
| 15 | 1364 | 76.6 | 253 | 9 ADY67588 | Human kal |
| 16 | 1364 | 76.6 | 253 | 9 AEC00353 | Human kal |
| 17 | 1350 | 75.8 | 250 | 6 ADA05732 | Human NOV |
| 18 | 1344 | 75.1 | 250 | 8 ADN62896 | Human NOV |
| 19 | 1337 | 75.1 | 257 | 3 AAB21326 | Human HSC |
| 20 | 1252 | 70.3 | 247 | 6 ADA05742 | Human NOV |
| 21 | 1252 | 70.3 | 247 | 8 ADN62906 | Human NOV |
| 22 | 1252 | 70.3 | 252 | 6 ADA05734 | Human NOV |
| 23 | 1252 | 70.3 | 252 | 8 ADN62898 | Human NOV |
| 24 | 1235 | 69.4 | 225 | 4 AAB98502 | Human str |
| 25 | 1230 | 69.1 | 224 | 9 ADV21100 | Human str |
| 26 | 1119 | 62.9 | 224 | 6 ADA05744 | Human NOV |
| 27 | 1119 | 62.9 | 224 | 8 ADN62908 | Human NOV |
| 28 | 1085.5 | 61.0 | 249 | 5 ABB84420 | Porcine S |
| 29 | 1035.5 | 58.2 | 198 | 6 ADA05736 | Human NOV |
| 30 | 1035.5 | 58.2 | 198 | 8 ADN62900 | Human NOV |
| 31 | 1011.5 | 56.8 | 249 | 5 ABB84423 | Murine SC |
| 32 | 996.5 | 56.0 | 243 | 5 ABB84419 | Bovine SC |
| 33 | 940.5 | 52.8 | 226 | 5 ABB84422 | Rat SCCE |
| 34 | 937.5 | 52.7 | 181 | 6 ABA05738 | Human NOV |
| 35 | 937.5 | 52.7 | 181 | 8 ADN62902 | Human NOV |
| 36 | 773 | 43.4 | 144 | 8 ADI39727 | Stratum c |
| 37 | 773 | 43.4 | 144 | 8 ADI37151 | Stratum c |
| 38 | 641.5 | 36.0 | 136 | 4 ABG23378 | Novel hum |
| 39 | 614 | 34.5 | 260 | 2 AAW10694 | Human rec |
| 40 | 614 | 34.5 | 260 | 2 AAW12393 | Mouse neu |
| 41 | 614 | 34.5 | 260 | 5 ABB57219 | Mouse isc |
| 42 | 614 | 34.5 | 260 | 5 ADI17073 | Murine NO |
| 43 | 614 | 34.5 | 260 | 8 ADI39731 | Mouse neu |
| 44 | 614 | 34.5 | 260 | 8 ADI37155 | Mouse neu |
| 45 | 612.5 | 34.4 | 293 | 2 AAY16777 | Human ker |

ALIGNMENTS

RESULT 1

AAR67888
ID AAR67888 standard; protein; 253 AA.

XX
AC AAR67888;
XX
DT 25-MAR-2003 (revised)
DT 09-AUG-1995 (first entry)
XX
DE Human stratum corneum chymotrophic recombinant enzyme (SCCS).
XX
DE Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX
OS Homo sapiens.

XX
PN W09500651-A1.
XX
PD 05-JAN-1995.
XX
PF 20-JUN-1994; 94WO-IB000166.
XX
PR 18-JUN-1993; 93DK-00000725.
XX
(SYMB-) SYMBICOM AB.

XX
PI Egelrud T, Hansson L;
XX
DR WPI; 1995-052088/07.
XX
DR N-PSDB; AAQ81203.

XX
PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating

PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.

PS Disclosure; Page 97; 137pp; English.

XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callosities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammal, insect, plant, or microorganism
CC transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x AAR67888 (1-253)

| | | | |
|----|-----|--|-----|
| QY | 16 | ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAACT | 75 |
| DB | 1 | MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr | 20 |
| QY | 76 | GCAGGAGAAGAGCCAGCGTGACAAAGATTATTGATGGCGCCCATGTGCAAGAGCTCC | 135 |
| DB | 21 | AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer | 40 |
| QY | 136 | CACCCATGGCAGGTGCGCTGCTCATGTGCAATCAGCTCACTGCGGAGCGCTCTGGTC | 195 |
| DB | 41 | HieProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHieCysGlyGlyValLeuVal | 60 |
| QY | 196 | AATGAGCGTGGGTGCTCACTGCGCCCACTGCAAGATGAATGAGTACACCGTGACCTG | 255 |
| DB | 61 | AsnGluArgTrpValLeuThrAlaAlaHieCysLysMetAsnGluTrpThrValHieLeu | 80 |
| QY | 256 | GGCAGTGATACGCTGGCGCAGAGAGCTCAGAGATCAAGGCTTCGAAGTCATTCCGC | 315 |
| DB | 81 | GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg | 100 |
| QY | 316 | CACCCGGCTACTCCACAGACCCCATGTATGACCTCATGCTCTGTGAAGCTCAATAGC | 375 |
| DB | 101 | HieProGlyTySerThrGlnThrHieValAsnAspLeuMetLeuValLysLeuAsnSer | 120 |
| QY | 376 | CAGCCAGGCTGTCATCCATGGTGAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT | 435 |
| DB | 121 | GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro | 140 |
| QY | 436 | GGAAACACCTGTACTGCTCCGCTGGGCACTTACCAGGCGCCAGATGTGACCTTTCC | 495 |
| DB | 141 | GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro | 160 |
| QY | 496 | TCTGACCTCATGTGCTGATGTCAGCTCATCTCTCCCGCAGACTGCGACGAGGTTTAC | 555 |
| DB | 161 | SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTy | 180 |
| QY | 556 | AGGACTTACTGGAAATTCATGCTGTGGCTGGCATCCCGATCCCGACCAAGAAACGCC | 615 |
| DB | 181 | LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla | 200 |
| QY | 616 | TGCAATGTGTGACTCAGCGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCTGGTGCC | 675 |
| DB | 201 | CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer | 220 |
| QY | 676 | TGGGGAACCTTCCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG | 735 |
| DB | 221 | TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys | 240 |

| | | | |
|----|-----|---|-----|
| QY | 736 | TTCCACCAAGTGATAAATGACACCATGAAAAAGCATCGC | 774 |
| DB | 241 | PheThrLysTrpIleAsnAspThrMetLysLysHieArg | 253 |

RESULT 2

AAW05383
ID AAW05383 standard; protein; 253 AA.

XX AAW05383;

XX 31-DEC-1996 (first entry)

XX Human amyloid precursor protein protease.

XX Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
KW therapy.

XX Homo sapiens.

XX WO9631122-A1.

XX 10-OCT-1996.

XX 02-APR-1996; 96WO-US004294.

XX 04-APR-1995; 95US-00416257.

XX (ELIL) LILLY & CO ELI.

XX Dixon EP, Johnstone EM, Little SP;

XX WPI: 1996-464694/46.

XX N-PSDB; AAT39783.

XX New isolated human amyloid precursor protein protease - used to develop
PT prods. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.

XX Claim 1; Page 44-45; 55pp; English.

CC Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obtd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells. It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease

XX Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x AAW05383 (1-253)

| | | | |
|----|----|---|----|
| QY | 16 | ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAACT | 75 |
|----|----|---|----|

| | | | |
|----|---|---|----|
| DB | 1 | MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr | 20 |
|----|---|---|----|

| | | | |
|----|----|---|-----|
| QY | 76 | GCAGGAGAAGAGCCAGCGTGACAAAGATTATTGATGGCGCCCATGTGCAAGAGCTCC | 135 |
|----|----|---|-----|

| | | | |
|----|----|--|----|
| DB | 21 | AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer | 40 |
|----|----|--|----|

| | | | |
|----|-----|--|-----|
| QY | 136 | CACCCATGGCAGGTGCGCTGCTCAGTGCATCAGCTCCACTGCGGAGCGCTCTGGTC | 195 |
|----|-----|--|-----|

| | | | |
|----|----|--|----|
| DB | 41 | HieProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHieCysGlyGlyValLeuVal | 60 |
|----|----|--|----|

141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
496 TCTGACCTCATGTGCTGATGTCAGCTCATCTCCCCCAGGACTGCGCAGAGGTTTAC 555
161 SerAspLeuMetCysValAspValValLeuLeuSerProGlnAspCysThrLysValTyr 180
556 AAGGACTTACTGGAATTCATGCTGCTGGCTGGCATCCCGACTCCCAAGAAAAACGCC 615
181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
616 TGCATATGCTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTTCTGGTCTC 675
201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCCAG 735
221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
736 TTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
241 PheThrLysIrpIleAsnAspThrMetLysLysHisArg 253

RESULT 4
ABB84406
ID ABB84406 standard; protein; 253 AA.
XX ABB84406;
AC ABB84406;
XX ABB84406;
DT 08-NOV-2002 (first entry)
XX Human SCE protein.
DE
XX
XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
XX
PN WO200262135-A2.
XX
XX 15-AUG-2002.
PD
XX
XX 08-FEB-2002; 2002WO-1B001300.
PF
XX
XX 09-FEB-2001; 2001CA-02332655.
PR
XX 09-FEB-2001; 2001DK-00000218.
XX
XX (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
XX
PI Egelrud T, Hansson L;
XX
XX WPI; 2002-643380/69.
DR N-PSDB; ABQ76226.
DR
XX
XX Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
XX
PS Claim 10; Page 58-59; 74pp; English.
XX
XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a

compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the human stratum
CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
CC with human kallikrein 7 (KLK7) and is used in the development of the
CC transgenic mammals described in the invention
XX
SQ Sequence 253 AA;
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0
US-09-905-083A-30 (1-969) x ABB84406 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGTCTATCTTACGCTTGGAACCT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAAAGATTATTGATGGCGCCCATGTGTCAAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCCCTGCTCAGTGCGCAATCAGCTCCATCGCGAGGCGTCTGGTTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 ANTGAGCCCTGGTGTCTCAGTCCGCCCTCAGAGATGAATGAGTACACCGTGCACCTG 255
DB 61 AsnGluArgTrpValIleuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGTATACCTGCGGCGACAGAGAGCTCAGAGGATCAAGGCTTCGAAGTCATTCGCC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACTCATGCTGTGTAAGCTCAATAGC 375
DB 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGCTGTCTATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCAACCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCTCCGCTGGGCGACTACACAGAGCCAGAGTGTACCTTTCCTCC 495
DB 141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAGGCTCATCTCTCCCGGAGGCTGACAGAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTCATGCTGCTGGCTGGCATCCCGACTCCCAAGAAAAACGCC 615
DB 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGCATATGCTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTTCTGGTCTC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCCAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240

QY 736 TTCCACCAAGTGGATTAATGACACCATGAAAAGCATCGC 774
 Db 241 PheThrIysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 5
 AAU82740
 ID AAU82740 standard; protein; 253 AA.
 AC AAU82740;
 XX
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Amino acid sequence of novel human protease #39.
 XX
 KW Human; protease; cancer; immune-related disorder; cardiovascular disease;
 KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 KW ocular disease; cytostatic; enzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO200200860-A2;
 PN
 XX 03-JAN-2002.
 PD
 XX 26-JUN-2001; 2001WO-US020171.
 PF
 XX 26-JUN-2000; 2000US-0214047P.
 PR
 XX (SUGS-) SUGEN INC.
 PA
 XX Plowman G, Whyte D, Sudareanum S, Manning G, Caenepeel S;
 PI Charyczak G;
 XX
 XX WPI; 2002-139913/18.
 DR N-PSDB; ABK31782.
 DR
 XX Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related diseases
 PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 PT disorders.
 XX
 XX Claim 6; Fig 2N; 313pp; English.
 PS
 XX The present invention relates to the isolation of novel human proteases,
 CC and the nucleic acids encoding them. The sequences of the invention are
 CC useful for treating diseases and disorders such as cancers (e.g. breast,
 CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
 CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
 CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
 CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
 CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
 CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
 CC disorders, cognitive disorders, hypotension, hypertension, psychotic
 CC disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease) and dyskinesias. The nucleic acids and polypeptides are also
 CC useful for treating viral infections caused by human immunodeficiency
 CC virus (HIV), and non-viral infections such as ocular disease (e.g.
 CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
 CC human proteases of the invention
 XX
 XX Sequence 253 AA;
 SQ

Alignment Scores:
 Pred. No.: 1.16e-134 Length: 253
 Score: 1364.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 76.6% Indels: 0
 DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x AAU82740 (1-253)
 QY 16 ATGGCAAGATCCCTTCTCTGCCCCCTGCAGATCTTACTGTATCCTTAGCCTTGGAAACT 75
 Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
 QY 76 GCAGGAGAAGAGCCAGGGGTGCAAGATTATTGATGGCGCCCCCATGTGGAAGGGTCC 135
 Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
 QY 136 CACCCATGCGAGGTGGCCCTGCTCAGTGGCAATCAGCTCCAGCTGCGAGCGCTCTCGTC 195
 Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
 QY 196 AATGAGCGTGGGTGCTCACTGCGGCCCATGTCGAAGATGAATGAGTACACCGTGCACCTG 255
 Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
 QY 256 GGCAAGTATACGCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGC 315
 Db 81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
 QY 316 CACCCCGGTACTCCACAGAGCCCATGTTAATGACTCATGCTCGTGAAGCTCAATAGC 375
 Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
 QY 376 CAGGCCAGGCTGTCACTCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTCGCAACCCCT 435
 Db 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
 QY 436 GGAACCACTGTACTGTCTCCGCTGGGGCAGTACCAAGAGCCAGATGACCTTTCCC 495
 Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
 QY 496 TCTGACCTCATGTGCGTGGATGTCAGCTCATCTCCCGCCAGACTGCACGAAGTTTAC 555
 Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTr 180
 QY 556 AAGGACTTACTGGAATAATTCATGCTGTGGCTGGCATCCCGACTCCCAAGAAAAGCC 615
 Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
 QY 616 TGCAATGGTGACTCAGGGGACCGTTGGTGTGAGAGGTACCTCTGCAAGGTCTGGTGTCC 675
 Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
 QY 676 TGGGGAACTTCCCTTGGCGCCCAACCAATGACCCAGAGTCTTACACTCAAGTGTGCAAG 735
 Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240
 QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAGCATCGC 774
 Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 6
 ABU07440
 ID ABU07440 standard; protein; 253 AA.
 XX
 AC ABU07440;
 XX
 XX 28-JAN-2003 (first entry)
 DT
 XX Protein differentially regulated in prostate cancer #43.
 DE
 XX
 XX Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 OS Homo sapiens.
 XX
 XX WO200281638-A2.
 PN
 XX

PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
XX Sun Z, Jay G;
XX
XX WPI; 2003-058520/05.
DR N-PSDB; AEX10343.
XX
XX Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
XX Claim 1; Page 293-294; 416pp; English.
XX
XX The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer
XX
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0

US-09-905-083A-30 (1-969) x ABU07440 (1-253)

QY 16 ATGGCAAGATCCCTTCTCGCCCTGACAGATCTTACTGCTATCTTACCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGCTGACAAAGATTATTGATGGCCCCCAATGTGCAAGAGCTCC 135
|||||

Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCAGTGGAGGCGCTGCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGGTGCTCAGTCCGCCCTCAGTCCCAAGATGAATGAGTACACCGTGACCTG 255
Db 61 AenGluAArgTrpValLeuThrAlaAlaHisCysLysMetAenGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGGGCAGCAGGAGAGCTCAGAGATCAAGGCTCGAAGTCATTCCTCCG 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACACAGACCCATGTTATGACCTCATCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAenAspLeuMetLeuValLysLeuAenSer 120
QY 376 CAGGCCAGGCTGCTCATCTCCATGTTGAAGAAAGTCAGGCTGCCCTCCCGCTCGAACCCTCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGGCTGGGGCACTACACAGAGCCAGATGTGACCTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGGTGGATGTCAGCTCATCTCCGCCAGGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValThr 180
QY 556 AAGGACTTACTGGAAATTTCCATGCTGTGCGCTGGCATCCCGACTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGluAenSerMetLeuCysAlaGlyIleProAspSerLysLysAenAla 200
QY 616 TCATATGTGTACTAGGGGACCGTGTGTGTCAGAGTACCTGCAAGGTCTGGTGTC 675
Db 201 CysAenGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGNACTTTCCCTTGGGCCCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAenAspProGlyValThrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAGAGCATCGC 774
Db 241 PheThrLysTrpIleAenAspThrMetLysLysHisArg 253

RESULT 7
ABU07471
ID ABU07471 standard; protein; 253 AA.
XX
AC ABU07471;
XX
DT 28-JAN-2003 (first entry)
XX
DE Protein differentially regulated in prostate cancer #74.
XX
KW Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX
OS Homo sapiens.
XX
PN WO200281638-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
PA
XX

PI Sun Z, Jay G;
XX WPI; 2003-058520/05.
DR N-PSDB; ABX10375.
XX
PT Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
PS Claim 1; Page 351; 416pp; English.
XX
XX The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer
XX
XX Sequence 253 AA;
SQ
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0
US-09-905-083A-30 (1-969) x ABU07471 (1-253)
QY 16 GTGGAGAGATCCCTTCTCCCTGCGCCCTGAGATCTTACTGCTATCTTACCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAG 135
DB 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGTGCGCCCTGCTCAGTGGCAATCAGCTCCACCTGCGGAGGCGTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGGCGTGGGTGCTACTGCGCCCTGCTGAGAGTGAATGAGTACACCGTGACCTGG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

QY 256 GGCAGTGATACGCTGGGCGACAGAGAGCTCAGAGGATCAAGCCCTCGAAGTCAATTCGCG 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTAAATGACCTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTTCATCCATGGTGAAGAGATCAGGCTGCCCTCCCGCTGCGAAGCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGCTGGGCGACTACACAGAGCCAGATGTGACTTTCCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGGTGTGTCAGCTCATCTCCCGCCAGGACTGCAGAAAGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATTCATGCTGTGCTGGCATCCCGACTCCCAAGAAAAAGCC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGTGTGACTCAGGGGAGCCGTTGGTGTGCGAGAGTACCTGCAAGTCTGGTGTCC 675
DB 201 CysAsnGlyAspSerGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAGACTTTCCTTGGCGCCCAATGAGTACCCAGGAGTCTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGATTAATGACACCATGAAAGAGCATCGC 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 8
ABR58471
ID ABR58471 standard; protein; 253 AA.
XX
AC ABR58471;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX
KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX
OS Homo sapiens.
XX
PN WO2003029468-A1.
XX
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031467.
XX
PR 02-OCT-2001; 2001US-0327135P.
XX
PR 30-MAY-2002; 2002US-0384531P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Mannion J;
XX
DR WPI; 2003-372001/35.
XX
PT New polynucleotide and polypeptide useful for diagnosing and/or treating
PT cancer, particularly ovarian cancer, and as a vaccine.
XX
PS Claim 2; Page 157-158; 169pp; English.
XX
CC The invention relates to a novel isolated polynucleotide. The
CC polynucleotides of the invention have cytostatic activity, and may have a

CC use in gene therapy, and in a vaccine. The composition and methods are
CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
CC The composition may also be used as a vaccine to prevent cancer. The
CC present sequence is used in the exemplification of the invention
XX

| | |
|--|---|
| AC | ADB80484; |
| XX | |
| DT | 04-DEC-2003 (first entry) |
| XX | |
| DE | Ovarian cancer-associated protein #24. |
| XX | |
| KW | cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; |
| KW | post-operative chemotherapy; radiation therapy; tumour prognosis; |
| KW | pre-cancerous lesion detection. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO2002102235-A2. |
| XX | |
| PD | 27-DEC-2002. |
| XX | |
| PF | 18-JUN-2002; 2002WO-US019297. |
| XX | |
| PR | 18-JUN-2001; 2001US-0299234P. |
| PR | 27-AUG-2001; 2001US-0315287P. |
| PR | 05-SEP-2001; 2001US-0317544P. |
| PR | 13-NOV-2001; 2001US-0350666P. |
| PR | 12-APR-2002; 2002US-0372246P. |
| XX | |
| PA | (EOSB-) EOS BIOTECHNOLOGY INC. |
| XX | |
| PI | Mack DH, Gish KC; |
| XX | |
| DR | WPI; 2003-167431/16. |
| DR | N-PSTB; ADB80483. |
| XX | |
| PT | Detecting an ovarian cancer-associated transcript in a cell from a |
| PT | patient, comprises contacting a biological sample from the patient with a |
| PT | polynucleotide that hybridizes to an ovarian cancer gene. |
| XX | |
| PS | Claim 13; Page 291; 332pp; English. |
| XX | |
| CC | The invention relates to a method of detecting an ovarian cancer- |
| CC | associated transcript in a cell from a patient, by contacting a |
| CC | biological sample from the patient with a polynucleotide that selectively |
| CC | hybridizes to a sequence at least 80% identical to any one of 80 |
| CC | nucleic acid sequences given in the specification. The method is useful |
| CC | in diagnosing ovarian cancer and in identifying and using agents and/or |
| CC | targets that inhibit ovarian cancer. The nucleic acid molecule, |
| CC | polypeptide and the antibody may also be used in detecting ovarian |
| CC | cancers, monitoring and early detection of relapse following treatment, |
| CC | monitoring response to therapy, selecting patients for post-operative |
| CC | chemotherapy or radiation therapy, in selecting mode of therapy, |
| CC | determining tumour prognosis, early detection of pre-cancerous lesions, |
| CC | and as vaccines. This sequence corresponds to one of the proteins used |
| XX | for the detection method of the invention. |
| SQ | Sequence 253 AA; |
| | |
| | Alignment Scores: |
| Pred. No.: | 1.16e-134 Length: 253 |
| Score: | 1364.00 Matches: 253 |
| Percent Similarity: | 100.0% Conservative: 0 |
| Best Local Similarity: | 100.0% Mismatches: 0 |
| Query Match: | 76.6% Indels: 0 |
| DB: | 7 Gaps: 0 |
| | |
| US-09-905-083A-30 (1-969) x ADB80484 (1-253) | |
| Qy | 16 ATGGCAAGATCCCTTCTCCTGCCCTCGAGACTTACTGCTATCCTTAGCCTTGGAAC T 75 |
| | |
| Db | 1 MetaLaArgSerLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20 |
| | |
| Qy | 76 GCAGGAGGAAGCCAGGGTGACAAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC 135 |
| | |
| Db | 21 AlaGlyGluGluAlaGlnGlyAspPhysIleleapGlyAlaProCyAlaIaArgGlySer 40 |
| | |
| Qy | 136 CACCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTTCCA CTCGGAGGCTCTGGTC 195 |

Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
Qy 196 AATGAGCGCTGGTGTCTCACTGCGCCACTGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
Qy 256 GGCAGTGTATCGCTGGCGGACAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
Qy 316 CACCCCGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
Qy 376 CAGCGCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCGACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
Qy 436 GGAACACCTGTACTGTCTCGGCTGGGGCACTACACGAGCCAGATGTGACTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
Qy 496 TCTGACCTCATGTGCGGTGATGCAAGCTCATCTCTCCCGCAGGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTyr 180
Qy 556 AAGGACTTACTGGAATAATTCATGCTGTGGCTGGCATCCCGACTCCAGAAAAAGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
Qy 616 TGAATGCTGACTCAGGGGACCGTTGGTGTGAGAGTACCTCGCAAGCTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
Qy 676 TGGGGAACTTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTGAAGTGTCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
Qy 736 TTCACCAAGTGGATMAATGACACCATGAAAAAGCATGCC 774
Db 241 PheThrLysTrpLeuAsnAspThrMetLysLysHisArg 253

RESULT 10
ID ADJ68833
XX AC ADJ68833; standard; protein; 253 AA.
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID639.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KW Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX

PA (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX Claim 1; SEQ ID NO 639; 180pp; English.
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nontropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX SQ Sequence 253 AA;
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 7 Gaps: 0
US-09-905-083A-30 (1-969) x ADJ68833 (1-253)
Qy 16 ATGGCAAGATCCCTTCTCTGCCCCCTGCAGATCTTACTGCTATCTTAGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
Qy 76 GCAGGAGAGAGAGAGAGAGAGAGATTTATGATGGCGCCCGCCATGTCGCAAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
Qy 136 CACCCATGCGAGTGGCGCCCTGCTCAGTGGCAATCAGCTCCACATGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
Qy 196 AATGAGCGCTGGTGTCTCACTGCGCCCGCTCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
Qy 256 GGCAGTGTATCGCTGGCGGACAGAGAGCTCAGAGGATCAGGCTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
Qy 316 CACCCCGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
Qy 376 CAGCGCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCGACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
Qy 436 GGAACACCTGTACTGTCTCGGCTGGGGCACTACACGAGCCAGATGTGACTTTCC 495

Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGGACTGCGACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTCATGCTGTGCGCTGGCATCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TCGAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCGTGGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACTTCCCTTGGCGCCNACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAATGACACCATGAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 11
ID ADN39180
XX ADN39180 standard; protein; 253 AA.
AC ADN39180;
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
DE
XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularization syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnary; gene therapy; vaccine.
XX Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX
XX 21-NOV-2001; 2001US-0332464P.
XX
XX 29-NOV-2001; 2001US-0334393P.
XX
XX 03-DEC-2001; 2001US-0335394P.
XX
XX 14-DEC-2001; 2001US-0340376P.
XX
XX 08-JAN-2002; 2002US-0347211P.
XX
XX 10-JAN-2002; 2002US-0347349P.
XX
XX 08-FEB-2002; 2002US-0355250P.
XX
XX 13-FEB-2002; 2002US-0356714P.
XX
XX 20-FEB-2002; 2002US-0359077P.
XX
XX 29-MAR-2002; 2002US-0368809P.
XX
XX 04-APR-2002; 2002US-0370110P.
XX
XX 12-APR-2002; 2002US-0372246P.
XX
XX 05-JUN-2002; 2002US-0386614P.
XX
XX 16-JUL-2002; 2002US-0396839P.
XX
XX 22-JUL-2002; 2002US-0397775P.
XX
XX 22-JUL-2002; 2002US-0397845P.
XX
XX 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
XX

DR N-PSDB; ADN39179.
XX
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO 498; 1385pp; English.
PS
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 253 AA;
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 7 Gaps: 0
US-09-905-083A-30 (1-969) x ADN39180 (1-253)
QY 16 ATGCGAAGATCCCTCTCTGCGCCCTGCAGATCTTACTGTCTAGCTTGGAACCT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuThr 20
QY 76 GCAGGAGAAGAGCCAGGCGTGCAGAGATTATTGATGGCGCCCATGTGCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGCGCCCTGCTCAGTGCATCAGCTCCATCGCGAGGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGTGTCTCACTGCGCCCTGCAGAGATGAATGATGATACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGATAGCTGGCGCAGGAGAGCTCAGAGGATCAAGGCGCTCGAAGTCATTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATAGCTCATCTGCTGTAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGCTGTCACTCCATGTTGAGAAAGTCAGGCTGCGCCCTCCCGCTGCGAACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAAACCACTGTACTGTCTCCGGCTGGGCGCACTACACAGAGCCAGATGTACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGGACTGCGACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180

| | | | |
|-------------------|-------------------------------------|---|-----|
| QY | 556 | ARGACTTACTCGAAATTCATGCTGTGCGCTGGCATFCCCGACTCCAGAAAAACGCC | 615 |
| Db | 181 | LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla | 200 |
| QY | 616 | TGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCGTGCAAGGCTCTGGTGTCC | 675 |
| Db | 201 | CysAsnGlyAspSerGlyGlyProLeuValCysargGlyThrLeuGlnGlyLeuValSer | 220 |
| QY | 676 | TGGGGAACCTTTCCCTTGGGGCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG | 735 |
| Db | 221 | TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys | 240 |
| QY | 736 | TTCCACCAAGTGGATTAATGACACCATGAAAAAGCATCGC | 774 |
| Db | 241 | PheThrLysTrpIleAsnAspThrMetLysLysHisarg | 253 |
| RESULT 12 | | | |
| ADL06515 | ADL06515 standard; protein; 253 AA. | | |
| XX | AC | ADL06515; | |
| XX | AC | | |
| XX | DT | 20-MAY-2004 (first entry) | |
| XX | XX | Human tumour-associated antigenic target (TAT) polypeptide #14. | |
| XX | DE | | |
| XX | KW | Human; tumour-associated antigenic target; TAT; cell death; tumour; | |
| XX | KM | cancer; cytostatic. | |
| XX | XX | | |
| OS | OS | Homo sapiens. | |
| XX | XX | | |
| XX | PN | WO2004016225-A2. | |
| XX | XX | | |
| XX | PD | 26-FEB-2004. | |
| XX | PF | 19-AUG-2003; 2003WO-US025892. | |
| XX | XX | | |
| XX | PR | 19-AUG-2002; 2002US-0404809P. | |
| XX | PR | 21-AUG-2002; 2002US-0405645P. | |
| XX | PR | 23-SEP-2002; 2002US-0413192P. | |
| XX | PR | 15-OCT-2002; 2002US-0413008P. | |
| XX | PR | 15-NOV-2002; 2002US-0426847P. | |
| XX | PR | 02-JUL-2003; 2003US-0484959P. | |
| XX | PA | (GETH) GENENTECH INC. | |
| XX | XX | | |
| XX | PI | Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V; | |
| XX | PT | Spencer SD, Wu TD, Zhang Z; | |
| XX | XX | | |
| XX | DR | WPI; 2004-257144/24. | |
| XX | DR | N-PSDB; ADL06435. | |
| XX | XX | | |
| XX | PT | New antibody that binds to a tumor-associated antigenic target (TAT) | |
| XX | PT | polypeptide, useful for preparing a composition for diagnosing or | |
| XX | PT | treating cancer. | |
| XX | XX | | |
| XX | PS | Claim 2; SEQ ID NO 95; 319pp; English. | |
| XX | XX | | |
| XX | CC | The present invention relates to the isolation of human tumour-associated | |
| XX | CC | antigenic target (TAT) polynucleotide and polypeptide sequences. Also | |
| XX | CC | disclosed is an antibody that binds to a TAT polypeptide. The antibody is | |
| XX | CC | a monoclonal antibody, an antibody fragment, a chimeric antibody or a | |
| XX | CC | humanised antibody. It is conjugated to a growth inhibitory agent. It is | |
| XX | CC | produced in bacteria or in CHO cells and induces death of a cell to which | |
| XX | CC | it binds. The antibody is useful for preparing a composition for | |
| XX | CC | diagnosing or treating tumours and cancer. The present sequence | |
| XX | CC | represents a human TAT polypeptide of the invention. | |
| XX | XX | | |
| XX | XX | Sequence 253 AA; | |
| Alignment Scores: | | | |
| Pred. No.: | 1.16e-134 | Length: | 253 |

| Score: | 1364.00 | Matches: | 253 |
|---|--|--|-----|
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 76.6% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |
| US-09-905-083A-30 (1-1969) x ADL06515 (1-253) | | | |
| Qy | 16 | ATGCCAAGATCCCTCTCTCTCCCTCGAGATCTTACTGCTATCTTACGCTTGGAAACT | 75 |
| Db | 1 | MetAlaArgSerLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr | 20 |
| Qy | 76 | GCAGGAGAGNAGCCAGGCTGACAGATTATTGATGGGCCCCATGTGCAGAGAGCTCC | 135 |
| Db | 21 | AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer | 40 |
| Qy | 136 | CACCACATGGCAGTGGCCCTCCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCCTGGTC | 195 |
| Db | 41 | HisProThrGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal | 60 |
| Qy | 196 | AATCAGCGCTGGGCTGCTCCTCAGTGGCCCACTGCAAGATGAATAGCTACACCGTGCACCTG | 255 |
| Db | 61 | AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu | 80 |
| Qy | 256 | GGCAGTGAATACCTGGGGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCATCTCCGC | 315 |
| Db | 81 | GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg | 100 |
| Qy | 316 | CACCCCGCTACTCCACACAGACCCTGTTAATGACCTCAGCTCGTGAAGCTCAATAGC | 375 |
| Db | 101 | HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer | 120 |
| Qy | 376 | CAGGCCAGGCTGTTCATCATGGTCAAGAAATCAAGCTGCGCTCCCGCTGCCAACCCTCT | 435 |
| Db | 121 | GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro | 140 |
| Qy | 436 | GGAAACCACTGTACTGTCTCCGGCTGGGGCACTACACAGAGCCAGATGTGACCTTTCCC | 495 |
| Db | 141 | GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro | 160 |
| Qy | 496 | TCTGACCTCATGTGGTGGATGTCAGCTCATCTCCCCCAGGACTGCACGAAGGTTTAC | 555 |
| Db | 161 | SerAspLeuMetCysValAspValLysLeuLysSerProGlnAspCysThrLysValTyr | 180 |
| Qy | 556 | AAGACTTACTTGGAAATTCATGCTGTGCGCTGGCATCCCGACTCCAAGAAAAACGCC | 615 |
| Db | 181 | LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla | 200 |
| Qy | 616 | TGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGTACCTCCAGAGGCTGTGTC | 675 |
| Db | 201 | CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer | 220 |
| Qy | 676 | TGGGGAACTTTCCTTGGGGCAACCCCATGACCAGGAGTCTACACTCAAGTGTGCAG | 735 |
| Db | 221 | TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys | 240 |
| Qy | 736 | TTCAACCAAGTGGATAAATGCACCATGAAAAAGCATCGC | 774 |
| Db | 241 | PheThrLysTrpIleAsnAspThrMetLysLysHisArg | 253 |
| RESULT 13 | | | |
| ID | ADN04182 | | |
| XX | ADN04182 standard; protein; 253 AA. | | |
| AC | ADN04182; | | |
| XX | XX | | |
| DT | 01-JUL-2004 (first entry) | | |
| XX | XX | | |
| DE | Antipsoriatic protein sequence #286. | | |
| XX | antipsoriatic; gene therapy; psoriasis; diagnosis. | | |
| OS | Homo sapiens. | | |

XX WO2004028479-A2.
XX
XX PD 08-APR-2004.
XX
XX PF 25-SEP-2003; 2003WO-US030907.
XX
XX PR 25-SEP-2002; 2002US-0414006P.
XX
XX (GETH) GENENTECH INC.
XX
XX PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI; 2004-305105/28.
DR N-PSDB; ADN04181.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 9; SEQ ID NO 576; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
XX SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1,16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 8 Gaps: 0

US-09-905-083A-30 (1-969) x ADN04182 (1-253)

QY 16 ATGGCAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACCTTGGAACCT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAGAGCCAGGGTGACAGATATTATGATGGCGCCCATGTGCAAGAGCTCC 135
DB 21 AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

QY 136 CACCCATGCGAGTGGCCCTGCTCAGTGGCAATCAGCTCCAGTGGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60

QY 196 AATGAGCGTGGGTGCTCACTGCGGCCCTGCAAGATGAATGAGTACACCGTCGACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

QY 256 GGCAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGCCCTCGAAGTCATCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100

QY 316 CACCCCGGTACTCCACACAGACCCCATGTTATGACCTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120

QY 376 CAGGCGAGGCTGTATCCATCGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAAACCCCTC 435
DB 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140

QY 436 GGAACCACTGTACTGTCTCCGGCTGGGGCAGCTACACAGAGCCGAGATGTGACCTTTCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160

QY 496 TCTGACCTCATGTGCGTGGATGTCAGGCTCATCTCCCTCCAGGACTGCACGAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180

QY 556 AAGGACTTACTGGAATAATTCATGCTGTGCGCTGGCATCCCGGACTCCAGAAACGCGC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200

QY 616 TGCATATGCTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCCTCAAGGCTCTGGTGTC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220

QY 676 TGGGGAACCTTCCCTTGGCGGCCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240

QY 736 TTCACCAAGTGATAAATGACACCATGAAAGCATCGC 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 14
ADR72880
ID ADR72880 standard; protein; 253 AA.
XX
AC ADR72880;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human ovarian cancer-related tumour marker kallikrein 7 (hk7) protein.
XX
KW kallikrein 7; tumour marker; ovarian cancer;
KW epithelial ovarian carcinoma; human; serine protease; enzyme; KLK7.
XX
OS Homo sapiens.
XX
PN WO2004075713-A2.
XX
PD 10-SEP-2004.
XX
PF 26-FEB-2004; 2004WO-CA000281.
XX
PR 26-FEB-2003; 2003US-0450406P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Diamandis BP;
XX
DR WPI; 2004-661815/64.
DR N-PSDB; ADR72881, ADR72882.
XX
XX Kallikrein markers detection method for detecting ovarian cancer in
PT patient, involves detecting kallikrein markers and CA125 in sample
PT obtained from patient, and comparing detected amounts with standard
PT amounts.
XX
PS Example 2; SEQ ID NO 10; 102pp; English.
XX
CC The invention relates to a novel method for detecting a plurality of
CC kallikrein markers associated with ovarian cancer. The method comprises
CC obtaining a sample from a patient and detecting in the sample a plurality
CC of kallikrein markers, and optionally carbohydrate antigen CA125, wherein
CC the kallikrein markers are selected from the group consisting of
CC kallikrein 5, kallikrein 6, kallikrein 7, kallikrein 8, kallikrein 10 and
CC kallikrein 11. The detected amounts of the kallikrein markers are
CC compared with standard amounts. The method of the invention may be useful
CC for detecting kallikrein markers associated with ovarian cancer in a
CC patient and thus for detecting ovarian cancer, particularly epithelial
CC ovarian carcinoma. The current sequence is that of the human ovarian
CC cancer-related tumour marker kallikrein 7 (hk7) protein of the invention
CC which is a secreted serine protease and is encoded by DNA located at
CC chromosome 19q13.4.
XX
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 8 Gaps: 0

US-09-905-083A-30 (1-969) x ADR72880 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCCCTGCAGATCTTACTGCTATCTTAGCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCTGTCAGAGGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspLysIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGTGCGCCCTGCTCAGTGGCAATCAGCTCCACTGGCGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGACGCTGGTGTCTCACTGCCGCCCTGCAAGATGAATGATACACCGTGCACTCG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGCACAGAGAGCTCAGAGGATCAAGGCTCGAAGTCATTCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCGGCTACTCCACAGACCCATGTTAATGACTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGCCAGGCTGTCATCCATGGTGAGAAAGTCAGGCTGCCCTCCGCTCGGAACCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGCTCCGCTGGGCACTACACAGAGCCAGATGTGACCTTTCC 495
DB 141 GlyThrCysThrValSerGlyTrpGlyThrThrThrSerProaspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGGATGCAAGCTCATCTCCCCCAGAGCTGCAAGAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGAAAATTCCATGCTGTGGCTGGCATCCCGACTCCCAAGAAAACGCC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeProAspSerLysLysAsnAla 200
QY 616 TGAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCGCAAGGTCTGGTGTC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTTCCCTTTCGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCANTCGC 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 15
ADY67588
ID ADY67588 standard; protein; 253 AA.
XX
AC ADY67588;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human kallikrein 7 protein SEQ ID NO:1.
XX

KW kallikrein; serine protease; neurodegenerative disease;
KW neurological disease; nootropic; neuroprotective; Alzheimer's disease;
XX dementia.
OS Homo sapiens.
XX
PN CA2468651-A1.
XX
PD 13-DEC-2004.
XX
XX 14-JUN-2004; 2004CA-02468651.
PF
XX 13-JUN-2003; 2003US-0478486P.
PR
XX (MOUN) MOUNT SINAI HOSPITAL.
PA
XX Diamandis EP;
XX
XX WPI; 2005-092436/11.
DR N-PSDB; ADY67589, ADY67590.
DR GENBANK; L33404, AF166330.
XX
PT Detecting kallikrein polypeptides or their polynucleotides, associated
PT with neurodegenerative disease in patient, by identifying kallikrein
PT polypeptides or polynucleotides, in patient's sample, comparing detected
PT amount with standard.
XX
PS Disclosure; SEQ ID NO 1; 71pp; English.
XX
XX The invention describes a method for detecting kallikrein polypeptides or
CC their encoding polynucleotides, associated with neurodegenerative disease
CC in a patient, by taking a sample from a patient, detecting/identifying
CC one or more kallikrein polypeptides or polynucleotides encoding
CC kallikrein polypeptides, in the sample, and comparing the detected amount
CC with an amount detected for a standard, where kallikrein polypeptides are
CC chosen from kallikrein 7 and kallikrein 10. Nootropic; Neuroprotective;
CC Cerebroprotective; Antiparkinsonian. The method is useful for diagnosing,
CC detecting and monitoring a neurodegenerative disease in a subject. The
CC method is also useful for assessing whether a patient is afflicted with
CC or has a pre-disposition for Alzheimer's disease or frontotemporal
CC dementia. The present sequence represents human kallikrein 7. Human
CC tissue kallikreins are secreted serine proteases encoded by genes that
CC are tandemly localized on chromosome 19, more specifically to region
CC 19q13.4.
XX
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 9 Gaps: 0

US-09-905-083A-30 (1-969) x ADY67588 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCCCTGCAGATCTTACTGCTATCTTAGCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCTGTCAGAGGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspLysIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGTGCGCCCTGCTCAGTGGCAATCAGCTCCACTGGCGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGACGCTGGTGTCTCACTGCCGCCCTGCAAGATGAATGATACACCGTGCACTCG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

| | | | |
|----|-----|---|-----|
| QY | 256 | GGCAGTGATACGCTGGGGCACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC | 315 |
| Db | 81 | GlySerAspThrLeuGlyAspArgAlaGlnArgIleuAlaSerLysSerPheArg | 100 |
| QY | 316 | CACCCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC | 375 |
| Db | 101 | HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer | 120 |
| QY | 376 | CAGGCCAGGCTGTATCCATGCTGAAGAAAGTCAGGTCGCCCTCCCGCTGCCAACCCCT | 435 |
| Db | 121 | GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro | 140 |
| QY | 436 | GGAACCCACCTGTACTCTCCGGCTGGGGCAGCTTACACAGAGCCAGATGTGACCTTTGCC | 495 |
| Db | 141 | GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProaspValThrPhePro | 160 |
| QY | 496 | TCTGACCTCATGTGGTGGATGTCAAGCTCATCTCCCCCAGGACTGCACGAAGGTTTAC | 555 |
| Db | 161 | SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr | 180 |
| QY | 556 | AAGGACTTACTGGAAATTCATGCTGTGGCTGGCATCCCGACTCCCAAGAAAACGCC | 615 |
| Db | 181 | LysAspLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla | 200 |
| QY | 616 | TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCCAAGTCTGGTGCC | 675 |
| Db | 201 | CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer | 220 |
| QY | 676 | TGGGGAACCTTTCCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG | 735 |
| Db | 221 | TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys | 240 |
| QY | 736 | TTCACCAAGTGATAAATGACACCATGAAAAAGCATCGC | 774 |
| Db | 241 | PheThrLysTrpIleAsnAspThrMetLysLysHisArg | 253 |

Search completed: March 11, 2006, 01:45:01
Job time : 191 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 01:45:18 ; Search time 9 Seconds
(without alignments)
2071.868 Million cell updates/sec

Title: US-09-905-083A-30
Perfect score: 1780
Sequence: 1 GGatttcgggtccatggc.....aagaacacacaaacccctcsg 969

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp
-O=/abs/ABSSWEB_spool/US0905083/runat_10032006_152455_29708/app_query.fasta_1
-DB=PIR -QFMT=fasta -SUFFIX=n2p.rpr -MINMATCH=0_1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US0905083 @CGN 1 1 63 @runat_10032006_152455_29708 -NCPV=6 -ICPV=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----------|--------------------|
| 1 | 1364 | 76.6 | 253 | 2 A53968 | serine proteinase |
| 2 | 614 | 34.5 | 260 | 2 I56559 | neuropilin - mouse |
| 3 | 582 | 32.7 | 261 | 2 A29745 | tissue kallikrein |
| 4 | 568 | 31.9 | 261 | 2 S01971 | tissue kallikrein |
| 5 | 563 | 31.6 | 261 | 1 NGMSG | 7S nerve growth fa |
| 6 | 563 | 31.6 | 261 | 2 A34079 | tissue kallikrein |
| 7 | 561 | 31.5 | 246 | 1 TRRT1 | trypsin (EC 3.4.21 |
| 8 | 552 | 31.0 | 261 | 1 QKMS1 | tissue kallikrein |
| 9 | 552 | 31.0 | 261 | 2 A31136 | tissue kallikrein |
| 10 | 551 | 31.0 | 261 | 2 A25606 | tissue kallikrein |
| 11 | 547.5 | 30.8 | 260 | 2 A37938 | tissue kallikrein |
| 12 | 541.5 | 30.4 | 246 | 1 TRRT2 | trypsin (EC 3.4.21 |
| 13 | 536 | 30.1 | 248 | 2 S55067 | trypsin (EC 3.4.21 |
| 14 | 535 | 30.1 | 229 | 1 TRBOTR | trypsin (EC 3.4.21 |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 15 | 535 | 30.1 | 265 | 1 KQRTP | tissue kallikrein |
| 16 | 534 | 30.0 | 261 | 1 TRMSM5 | tissue kallikrein |
| 17 | 533.5 | 30.0 | 244 | 2 A44284 | tissue kallikrein |
| 18 | 533.5 | 30.0 | 247 | 2 A27547 | trypsin (EC 3.4.21 |
| 19 | 533 | 29.9 | 246 | 2 B25528 | trypsin (EC 3.4.21 |
| 20 | 533 | 29.9 | 259 | 1 KQRTTN | tonin (EC 3.4.21.- |
| 21 | 533 | 29.9 | 259 | 2 A29746 | tissue kallikrein |
| 22 | 533 | 29.9 | 259 | 2 B31136 | tissue kallikrein |
| 23 | 532.5 | 29.9 | 231 | 2 S31778 | trypsin (EC 3.4.21 |
| 24 | 532 | 29.9 | 242 | 2 S31776 | trypsin (EC 3.4.21 |
| 25 | 532 | 29.9 | 242 | 2 S31775 | trypsin (EC 3.4.21 |
| 26 | 531 | 29.8 | 261 | 2 A41020 | tissue kallikrein |
| 27 | 527.5 | 29.6 | 247 | 1 TRDG | trypsin (EC 3.4.21 |
| 28 | 527 | 29.6 | 261 | 2 JE0236 | tissue kallikrein |
| 29 | 526.5 | 29.6 | 242 | 2 S49489 | trypsin (EC 3.4.21 |
| 30 | 526.5 | 29.6 | 247 | 2 S13813 | trypsin (EC 3.4.21 |
| 31 | 524 | 29.4 | 231 | 1 TRPGTR | trypsin (EC 3.4.21 |
| 32 | 521 | 29.3 | 261 | 2 A24378 | tissue kallikrein |
| 33 | 519 | 29.2 | 261 | 1 EGMSB | tissue kallikrein |
| 34 | 518.5 | 29.1 | 243 | 2 A35871 | trypsin (EC 3.4.21 |
| 35 | 518.5 | 29.1 | 262 | 1 KQHU | tissue kallikrein |
| 36 | 516.5 | 29.0 | 256 | 1 NGMSA | 7S nerve growth fa |
| 37 | 516 | 29.0 | 257 | 2 S33772 | tissue kallikrein |
| 38 | 514 | 28.9 | 232 | 1 KQPG | tissue kallikrein |
| 39 | 513 | 28.8 | 261 | 2 A29586 | tissue kallikrein |
| 40 | 511 | 28.7 | 238 | 2 S31779 | trypsin (EC 3.4.21 |
| 41 | 510.5 | 28.7 | 247 | 1 A25852 | trypsin (EC 3.4.21 |
| 42 | 509 | 28.6 | 263 | 2 S15686 | tissue kallikrein |
| 43 | 508 | 28.5 | 246 | 1 TRDGC | trypsin (EC 3.4.21 |
| 44 | 506 | 28.4 | 261 | 2 S45303 | tissue kallikrein |
| 45 | 503 | 28.3 | 248 | 2 S55066 | trypsin (EC 3.4.21 |

ALIGNMENTS

RESULT 1

A53968

serine proteinase SCCE precursor - human

N;Alternate names: stratum corneum chymotryptic enzyme

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

R;Accession: A53968

R;Hansson, L.; Stromqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.

J. Biol. Chem. 269, 19420-19426, 1994

A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme

A;Reference number: A53968; MUID:94308225; PMID:8034709

A;Accession: A53968

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-253 <HAN>

A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:g521214; PIDN:f

C;Genetics:

A;Gene: GDB:PRSS6; SCCE

A;Cross-references: GDB:377730

A;Map position: 7q35-7q35

C;Superfamily: trypsin; trypsin homology

F;30-245/Domain: trypsin homology <TRY>

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1,49e-109 | Length: | 253 |
| Score: | 1364.00 | Matches: | 253 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 76.6% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-905-083A-30 (1-969) x A53968 (1-253)

QY 16 ATGGCAAGATCCCTTCTCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGAACCT 75

Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAGAAGACCACCGGTGCAAGATTATTGTGGCGCCCCCATGTGTCAAGAGGCTCC 135

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Db      21 AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY      136 CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCAGCTGCGGAGCGCTCTGGTC 195
Db      41 HisProTrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyValLeuVal 60
QY      196 AATGACGCTGGTGTCTACTGCGCCGCTCAAGATCAATGAGTACACCGTGACACCTG 255
Db      61 AenGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY      256 GGCAGTGAATACGCTGGCGGCACGAGAGCTCAGAGGATCAAGGCTTCGAAGTCATTCGCG 315
Db      81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY      316 CACCCCGGTACTCCACAGACCCCATGTTAATGACCTCATGCTGCTGAAGCTCAATAGC 375
Db      101 HisProGlyTy-SerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY      376 CAGGCCAGGCTGCATCCATGTTGAAGAAGTCAGGCTGCCCTCCCGCTGCCGAACCCCT 435
Db      121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY      436 GGAACACCTGTACTGCTCCGCTGGGCGCTACCTACCAGGAGCCAGATGTGACCTTTCC 495
Db      141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY      496 TCTGACCTCATGTGCTGATGTCAGATCATCTCCCGCCAGGACTGCGACGAGGTTTAC 555
Db      161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTy 180
QY      556 AAGGACTTACTGGAATTCATGCTGCTGCTGGCTGAGAGTACCCGACCTCCAGAAACGCC 615
Db      181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY      616 TGCATATGGTGACTCAGGGGACCGTTGGTGTGAGAGTACCCGACCTCCAGAAACGCC 675
Db      201 CysAenGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY      676 TGGGGAACCTTTCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db      221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY      736 TTCACCAAGTGAATAATGACACCATGAAAGCAATCGC 774
Db      241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 2
I56559
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishin
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease gen
A:Reference number: I56559; MUID:95348817; PMID:7623137
A:Accession: I56559
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: UNIPROT:Q61955; UNIPARC:UPI00000292C5; GB:D30785; NID:g1648847; PIDN
A:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRI>

Alignment Scores:
Pred. No.: 7, 4e-45 Length: 260
Score: 614.00 Matches: 114
Percent Similarity: 61.9% Conservative: 39
Best Local Similarity: 46.2% Mismatches: 88
Query Match: 34.5% Indels: 6
DB: 2 Gaps: 3
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US-09-905-083A-30 (1-969) x I56559 (1-260)
QY      37 CCCCTGCAGATCTTACTGCTATCTTAGCTTGGAAACTGCAGGAGAAGAGCCAGGCT 96
Db      11 ProTrpIleLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGly 30
QY      97 GACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCCCATGGCAGGTGGCCCTG 156
Db      31 SerLysIleLeuGluGlyArgGluCysIleProHisSerGlnProTrpGlnAlaLeu 50
QY      157 CTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTCAATGAGCGCTGGGTGCTCACT 216
Db      51 PheGlnGlyGluArgLeuIleCysGlyValLeuValGlyAspArgTrpValLeuThr 70
QY      217 GCGGCCCATCTGCAAGTGAATGAGTACACCGTGACCTGGCGAGTGCAGTGCAGTGTG 270
Db      71 AlaAlaHisCysLysGlnLysTyrservAlaArgLeuGlyAspHisserLeuGlnSer 90
QY      271 GCGCAGCAGGAGAGCTCAGAGGATCAAGGCTCGGAGTCAATCCCGCCACCCCGCTACTCC 330
Db      91 ArgAspGlnProGluGlnGluIleGlnValAlaGlnSerIleGlnHisProCysTyAsn 110
QY      331 ACA-----CAGACCCATGTTAATGACCTCATGCTGCTGAAGCTCAATAGCCAGGCC 381
Db      111 AsnSerAsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAla 130
QY      382 AGGCTGTCAATCCATGCTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAAACCCCTCGAACC 441
Db      131 AsnLeuGlyAspLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlyGln 150
QY      442 ACCTGTACTCTCTCGGCTGGGCGCACTACCAGAGCCAGATGTGACCTTTCCCTCTGAC 501
Db      151 LysCysIleIleSerGlyTrpGlyThrValThrSerProGlnGluAsnPheProAsnThr 170
QY      502 CTCATGTGCTGGATGTCAAGCTCATCTCCCGCCAGGACTGACAGAGTTTACAGGAC 561
Db      171 LeuAsnCysAlaGluValLysIleTyrservGlnAsnLysCysGluAlaTyPrGly 190
QY      562 TTACTGGAAATTCATGCTGCTGGCATCCCGCTCCCAAGAAACCGCTGCAAT 621
Db      191 LysIleThrGluGlyMetValCysAlaGly----SerSerAsnGlyAlaAspThrCysGln 209
QY      622 GGTGACTCAGGGGACCGTTGGTGTGCGAGAGTACCTCCGAAGGCTGGTCTCTGGGGA 681
Db      210 GlyAspSerGlyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTrpGly 229
QY      682 ACTTTCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCCAC 741
Db      230 SerAspProCysGlyLysProGluLysProGlyValTyThrLysIleCysArgTyThr 249
QY      742 AAGTGGATAAATGACACCATG 762
Db      250 ThrTrpIleLysLysThrMet 256

RESULT 3
A29745
tissue kallikrein (EC 3.4.21.35) mgk-9 precursor, submandibular - mouse
N:Alternate names: glandular kallikrein MGK-9; major epidermal growth factor-binding prot
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: C29746; A29745; A2120; I70015
R:Drinkwater, C.C.; Evans, B.A.; Richards, R.I.
Biochemistry 26, 6750-6756, 1987
A:Title: Mouse glandular kallikrein genes: identification and characterization of the ge
A:Reference number: A90522; MUID:88107594; PMID:3322387
A:Accession: C29746
A:Molecule type: DNA
A:Residues: 1-261 <DRI>
A:Cross-references: UNIPROT:P15949; UNIPARC:UPI00000019EA; GB:M17985; NID:g193476; PIDN:
A:Experimental source: strain BALB/c, salivary gland
R:Blaber, M.; Isackson, P.J.; Bradshaw, R.A.
Biochemistry 26, 6742-6749, 1987
A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein ;
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QY 160 AGTGGCAATCAGCTCCACTGCGAGGCGTCCGTGAATGAGCGCTGGTCTCACTGCC 219
Db 44 ArgTyrAsnLysTyrIleCysGlyGlyValLeuLeuAspArgAsnTrpValLeuThrAla 63
QY 220 GCCCACTGCAAGATGAATGAGTACACCGCTGCACCTGGCAGTGATACGCTGGCGCACAGG 279
Db 64 AlaHisCysHisValSerGlnTyrAsnValTrpLeuGlyThrLysLeuPheGlnArg 83
QY 280 AGA-----GCTCAGAGGATCAAGGCTCGAAGTCAATTCGGCACCCCGGCTACTCCACA 333
Db 84 GluProSerAlaGlnHisArgMetValSerLysSerPheProHisProAspTyrAsnMet 103
QY 334 CAGACCCATGTT-----AATGACCTCATGCTC 360
Db 104 SerLeuLeuIleHisAsnProGluProGluAspGluSerAsnAspLeuMetLeu 123
QY 361 GTGAAGCTCAATAGCCAGCCAGGCTGTCATCTCCATGGTGAAGAAAGTCAAGGCTGCCCTCC 420
Db 124 LeuArgLeuSerGluProAlaAspIleThrAspAlaValLysProIleAlaLeuProThr 143
QY 421 CGCTGCGAACCCTCGAACCCTGACTGCTCCGCTGGGCACTACCTACCGAGCCCA 480
Db 144 GluGluProLysLeuGlySerThrCysLeuValSerGlyTrpGlySerIleThrProThr 163
QY 481 GATGTGACCTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCGAGGAC 540
Db 164 LysPheGlnThrProAspAspLeuGlnCysValSerIleLysLeuLeuProAsnGluVal 183
QY 541 TGCACGAAGGTTTACAGGACTTACTTGGAAATTCATGCTGCTGCGCTGGCATCCCCGAC 600
Db 184 CysValLysAsnHisAsnGlnLysValThrAspValMetLeuCysAlaGlyGluMetGly 203
QY 601 TCCAGAAACCCCTGCAATGTGTACTCAGGGGACCGTTGGTGTGTCAGAGTACCTCG 660
Db 204 GlyGlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeu 223
QY 661 CAAGGTCTGGTGCCTCGGGGAATTCCTTCCCTGCGGCAACCCCAATGACACGAGGTCTAC 720
Db 224 HisGlyIleThrAlaTrpGlyProIleProCysGlyLysProAsnThrProGlyValTyr 243
QY 721 ACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAGCAT 771
Db 244 ThrLysLeuIleLysPheThrAsnTrpIleLysAspThrMetAlaLysAsn 260
RESULT 5
NGMSG
7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence revision 17-May-1985 #text change 09-Jul-2004
C:Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705
R:Evans, B.A.; Richards, R.I.
EMBO J. 4, 133-138, 1985
A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contiguous
A:Reference number: A91005; MUID:85257431; PMID:3848399
A:Accession: A91005
A:Molecule type: DNA
A:Residues: 1-261 <EVA>
A:Cross-references: UNIPROT:P00756; UNIPARC:UPI0000020EFS
R:Ullrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.
DNA 3, 387-392, 1984
A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth factor
A:Reference number: A90949; MUID:85076169; PMID:6548955
A:Accession: A90949
A:Molecule type: mRNA
A:Residues: 1-261 <ULL>
A:Cross-references: UNIPARC:UPI000020EFS; GB:X01389; NID:G53373; PIDN:CAA25645.1; PID:G
R:Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W.
Nucleic Acids Res. 12, 2791-2805, 1984
A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to
A:Reference number: A93510; MUID:84169573; PMID:6200835
A:Accession: A93510
A:Molecule type: mRNA

A:Residues: 127-202, 'E', 204-261 <HOW>
A:Cross-references: UNIPARC:UPI00000E6698; GB:X00472; NID:G54260; PIDN:CAA25154.1; PID:G
A:Experimental source: inbred strain DBA/2J
R:Thomas, K.A.; Baglan, N.C.; Bradshaw, R.A.
J. Biol. Chem. 256, 9156-9166, 1981
A:Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S neu
A:Reference number: A92341; MUID:81264363; PMID:7263706
A:Accession: A92341
A:Molecule type: protein
A:Residues: 25-107, 112-261 <THO>
A:Cross-references: UNIPARC:UPI0000112CC7
A:Experimental source: outbred strain Swiss Webster
C:Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer composed
C:Comment: The active form of the gamma chain occurs naturally as combinations of either
C:Genetics:
A:Map position: 7
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular glar
F:1-18/Domain: signal sequence #status predicted <SIG>
F:25-253/Domain: trypsin homology <TRY>
F:25-107/Domain: segment B1 <GB1>
F:112-261/Domain: segment A <GAA>
F:112-164/Domain: segment C <GCC>
F:165-261/Domain: segment B2 <GB2>
F:31-173, 50-66, 152-219, 184-198, 209-234/Disulfide bonds: #status predicted
F:65, 120, 213/Active site: His, Asp, Ser #status predicted
F:102/Binding site: carbohydrate (Asn) (covalent) #status experimental
Alignment Scores:
Pred. No.: 1, 866-40 Length: 261
Score: 563.00 Matches: 112
Percent Similarity: 59.9% Conservative: 42
Best Local Similarity: 43.6% Mismatches: 87
Query Match: 31.6% Indels: 16
DB: 1 Gaps: 4
US-09-905-083a-30 (1-969) x NGMSG (1-261)
QY 49 TTACTGTATCTTACCTTAGCCTTGGAAACTGCAGAGAGAACGCCAG-----GGTGAC 99
Db 4 LeuIleLeuPheLeuAlaLeuSerLeuGlyGlyIleAspAlaProValGlnSer 23
QY 100 AGATATTATGTCGCGCCCAATGTCACAGAGCTCCACCCATGCGAGTGCCTGCTC 159
Db 24 ArgIleValGlyGlyPheLysCysGluLysAsnSerGlnProTrpHisValAlaValTyr 43
QY 160 AGTGGCAATCAGCTCCACTGCGAGGCGTCTCTGGTCAATGAGCGCTGGTGTCTCACTGCC 219
Db 44 ArgTyrThrGlnTyrLeuCysGlyGlyValLeuLeuAspProAsnTrpValLeuThrAla 63
QY 220 GCCCACTGCAAGATGAATGAGTACACCGTGCACCTGGCAGTGAATACGCTG-----GGC 273
Db 64 AlaHisCysTyrAspAspAsnTyrLysValTrpLeuGlyLysAsnLeuPheLysAsp 83
QY 274 GACAGAGAGCTCAGAGGATCAAGCCCTCGAAGTCATTCGCGCACCCCGGCTACTCC--- 330
Db 84 GluProSerAlaGlnHisArgPheValSerLysAlaIleProHisProGlyPheAsnMet 103
QY 331 -----ACACAGACCCATGTT-----AATGACCTCATGCTC 360
Db 104 SerLeuMetArgLysPheHisIleArgPheLeuGluTyrAspTyrSerAsnAspLeuMetLeu 123
QY 361 GTGAAGCTCAATAGCCAGCCAGGCTGTCATCCATGGTGAAGAAAGTCAAGGCTGCCCTCC 420
Db 124 LeuArgLeuSerLysProAlaAspIleThrAspThrValLysProIleThrLeuProThr 143
QY 421 CGCTGCGAACCCTCGGAACCACTGTACTGCTCCGCTGGGCACTACCTACCGAGCCCA 480
Db 144 GluGluProLysLeuGlySerThrCysLeuAlaSerGlyTrpGlySerIleThrProThr 163
QY 481 GATGTGACCTTTCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCGAGGAC 540

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Db 164 LysPheGlnPheThrAspAspLeuTyrCysValAsnLeuLysLeuLeuProAsnGluAsp 183
QY 541 TGCACGAAGCTTTACAGGACTTACTGGAATAATTCATGCTGCGCTGGCATCCCGAC 600
Db 184 CysAlaLysAlaHisIleGluLysValThrAspAlaMetLeuCysAlaGlyGluMetAsp 203
QY 601 TCCAGAAAACCCCTGCATGTGACTCAGGGGACCGTGTGTGTGCAGAGGTACCTG 660
Db 204 GlyGlyLysAspThrCysLysGlyAspSerGlyProLeuIleCysAspGlyValLeu 223
QY 661 CAAAGTCTGTGCTCTGGGAACTTTCTCTGGGCAACCAATGACCCAGAGGTCTAC 720
Db 224 GlnGlyIleThrSerTrpGlyHisThrProCysGlyGluProAspMetProGlyValTyr 243
QY 721 ACTCAAGTGCAGTTCACCAAGTGGATAAATGACACCACTGAAAAGCAT 771
Db 244 ThrLysLeuAsnLysPheThrSerTrpIleLysAspThrMetAlaLysAsn 260

RESULT 6
A34079 tissue kallikrein (BC 3.4.21.35) P1 precursor - rat
N;Alternate names: kallikrein-related proteinase k8
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A34079; S10700
R;Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28, 5203-5210, 1989
A;Title: Expression of two kallikrein gene family members in the rat prostate.
A;Reference number: A34079; PMID:89352606; PMID:2165531
A;Accession: A34079
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-261 <BRA>
A;Cross-references: UNIPROT:P36374; UNIPARC:UPI000012DEE7; GB:M27215; GB:M27216; GB:M272
A;Experimental source: prostate
R;Elmoujaned, A.; Gutman, N.; Brillard, M.; Gauthier, P.
FEBS Lett. 265, 137-140, 1990
A;Title: Substrate specificity of two kallikrein family gene products isolated from the
F;112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
A;Reference number: S10698; PMID:90306305; PMID:2194829
A;Accession: S10700
A;Molecule type: protein
A;Residues: 25-43;112-138 <ELM>
A;Cross-references: UNIPARC:UPI0000175BEB; UNIPARC:UPI0000175BEC
A;Experimental source: submaxillary gland
A;Note: 125-Lys was also found
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;25-253/Domain: trypsin homology <TRY>
F;25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>
F;112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
F;65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 1.86e-40 Length: 261
Score: 563.00 Matches: 112
Percent Similarity: 58.3% Conservative: 39
Best Local Similarity: 43.2% Mismatches: 94
Query Match: 31.6% Indels: 14
DB: 2 Gaps: 3

US-09-905-083A-30 (1-969) x A34079 (1-261)
QY 34 CTGCCCTCCAGACTTACTGCTATCTCTAGCCTTGGAACCTGCAGGAGAAGACCCAG 93
Db 3 LeuLeuLeuPheLeuIleLeuSerLeuGlyTrpAsnAspAlaProProGlyGln 22
QY 94 GGTGACAAGATTATGATGCGCGCCCATGTGCAAGAGGCTCCACCCATGCGAGGTGCC 153
Db 23 ---SerArgIleIleGlyPheAsnCysGluLysAsnSerGlnProTrpGlnValAla 41
QY 154 CTGCTCAGTGGCAATCAGCTCCACTCGGAGGGCTCTGTGTCATGAGCGCTGGTGCTC 213
DB: 3
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```
Db 42 ValTyrHisPheAsnGluProGlnCysGlyGlyValLeuIleHisProSerTrpValIle 61
QY 214 ACTGCCGCCCACTGCAGAGTGAATAGTACACCGTCACCTGGCAGTGTAGTACGCTG--- 270
Db 62 ThrAlaAlaHisCysTyrSerValAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuLeu 81
QY 271 ---GGCGACAGGAGACTCAGAGGATCAAGGCTTCGAAGTTCATTCGCCACCCCGGCTAC 327
Db 82 GluAspGluProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProGlyPhe 101
QY 328 TCCACA-----CAGACCCACTGTTAATGACCTC 354
Db 102 AsnLeuAspIleIleLysAsnHisThrArgLysProGlyAsnAspTyrSerAsnAspLeu 121
QY 355 ATGCTCGTGAAGCTCAATAGCAGGCGAGGCTGTCTATCCATGTGTGAAGAAAGTCAGGCTG 414
Db 122 MetLeuLeuHisLeuLysThrProAlaAspIleThrAspGlyValLysValIleAspLeu 141
QY 415 CCTCTCCGCTGCGAACCCCTTGGAACCACTGTACTGTCTCCGCTGGGCGACTTACCACG 474
Db 142 ProThrGluGluProLysValGlySerThrCysLeuThrSerGlyTrpGlySerIleThr 161
QY 475 AGCCACAGATGTGACCTTTCCCTCTGACCTCATGTGGTGTGATGTCAAGCTCATCTCCCC 534
Db 162 ProLeuLysTrpGluPheProAspAspLeuGlnCysValAsnIleHisLeuLeuSerAsn 181
QY 535 CAGGACTGCACGAAGCTTTACAAAGACTTACTCGAATAATTCATGTCTCGCTGGCATC 594
Db 182 GluLysCysIleLysAlaTyrAsnAspGluValThrAspValMetLeuCysAlaGlyGlu 201
QY 595 CCGGACTCCAGAAAACCGCTGCATGTGACTCAGGGGACCGTGTGTGTGCAGAGGT 654
Db 202 MetAspGlyGlyLysAspIleCysLysGlyAspSerGlyGlyProLeuIleCysAspGly 221
QY 655 ACCTCCAAAGTCTGTGTCTCTGGGCAACTTTCCCTTGGCGCAACCCCAATGACCCACGGA 714
Db 222 ValLeuGlnGlyIleThrSerTrpGlySerMetProCysGlyGluProAsnLysProSer 241
QY 715 GTCTACACTCAAGTGCAGGTTCCAAAGTGTGATAAATGACACCATGAAAGACAT 771
Db 242 ValTyrThrLysLeuIleLysPheThrSerTrpMetLysLysValMetLysGluAsn 260

RESULT 7
TRYPTI
trypsin (BC 3.4.21.4) I precursor - rat
N;Alternate names: trypsinogen I
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: B22657; A00948
R;Cralk, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; PMID:85054880; PMID:6094547
A;Accession: B22657
A;Molecule type: DNA
A;Residues: 1-246 <CRA>
A;Cross-references: UNIPROT:P00762; UNIPARC:UPI00001376DD; GB:J00778; NID:g206507; PIDN:J
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 170
R;Macdonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
A;Reference number: A00948; PMID:82265624; PMID:6896710
A;Accession: A00948
A;Molecule type: mRNA
A;Residues: 1-246 <MAC>
A;Cross-references: UNIPARC:UPI00001376DD; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:J
C;Genetics:
A;Introns: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-246/Product: trypsin I #status predicted <ENZ>
```

F:24-239/Domain: trypsin homology <TRY>

F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
Pred. No.: 2,75e-40 Length: 246
Score: 561.00 Matches: 113
Percent Similarity: 60.1% Conservative: 39
Best Local Similarity: 44.7% Mismatches: 87
Query Match: 31.5% Indels: 14
DB: 1 Gaps: 5

US-09-905-083A-30 (1-969) x TRRT1 (1-246)

| | | | |
|----|-----|---|-----|
| QY | 16 | ATGGCAAGATCCCTTCTCTGCGCCCTGACAGATCTTACTGCTATCTCTGCTTGGAACT | 75 |
| Db | 1 | MetSerAlaLeuLeuLeuAlaLeuValGlyAlaAlaPheProLeuGlu--- | 19 |
| QY | 76 | GCAGGAGAAGAGCCAGGCGTACAAAGATTATTGATGGCGCCCATGTCGAAGAGGCTCC | 135 |
| Db | 20 | -----AspAspIleValGlyTyrThrCysProGluHisSer | 34 |
| QY | 136 | CACCCATGGCAGTGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGTCTGGTC | 195 |
| Db | 35 | ValProTyrGlnValSerLeuAsnSerGlyTyrHisPhe---CysGlyGlySerLeuIle | 53 |
| QY | 196 | AATGACGCTGGTGTCTACTGCGCCCTGCAAGATCAATGAGTACACCGTGACCTG | 255 |
| Db | 54 | AsnAspGlnTrpValValSerAlaAlaHisCysTyrLysSerArgIleGlnValArgLeu | 73 |
| QY | 256 | GGCAGTGATACGCTG-----GGCAGCAGGAGAGCTCAGAGGATCAAGGCGCTCG | 303 |
| Db | 74 | GlyGluHisAsnIleAsnValLeuGluGlyAspGlu-----GlnPheIleAsnAlaIa | 91 |
| QY | 304 | AGTCAATCCGCCACCCCGCTACTCCACACAGACCCATGTTAATGACCTCATGTCGTG | 363 |
| Db | 92 | LysIleIleLysHisProAsnTyrSerSerTrpThrLeuAsnAsnAspIleMetLeuIle | 111 |
| QY | 364 | AGCTCAATAGCAGGCCAGGCTGTCTCATCTGCTGTAAGAAAGTCAAGGCTGCCCTCCG | 423 |
| Db | 112 | LysLeuSerSerProValLysLeuAsnAlaArgValAlaProValAlaLeuProSerAla | 131 |
| QY | 424 | TGGGAACCCCTGGAAACCACTGTACTGTCTCGGCTGGGGACTACACAGAGCCAGAT | 483 |
| Db | 132 | CysAlaProAlaGlyThrGlnCysLeuIleSerGlyTyrPGLYAsnThrLeuSerAsnGly | 151 |
| QY | 484 | GTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCGAGACTGC | 543 |
| Db | 152 | ValAsnAsnProAspLeuLeuGlnCysValAspAlaProValLeuSerGlnAlaAspCys | 171 |
| QY | 544 | ACGAAGTTTACAGGACTTACTGGAAATTCATGCTGTGCGTGGCATCCCGACTCC | 603 |
| Db | 172 | GluAlaAlaTyrProGlyGluIleThrSerSerMetIleCysValGlyPheLeuGluGly | 191 |
| QY | 604 | AAGAAAACGCTGCAATGTGCTCAGGGGACCGTGTGTGTCAGAGGTACCCCTGCAA | 663 |
| Db | 192 | GlyLysAspSerCysGlnGlyAspSerGlyGlyProValValCysAsnGlyGlnLeuGln | 211 |
| QY | 664 | GGTCTGGTGTCTGGGGAATTTCCCTTGGCGGCAACCCCAATGACCCAGGAGTCTACACT | 723 |
| Db | 212 | GlyIleValSerTrpGly--TyrGlyCysAlaLeuProAspAsnProGlyValTyrThr | 230 |
| QY | 724 | CAAGTGTGCAAGTTTACCAAGTGGATAAATGACACCATG | 762 |
| Db | 231 | LysValCysAsnPheValGlyTrpIleGlnAspThrIle | 243 |

RESULT 8

QKMS1

tissue kallikrein (BC 3.4.21.35) mGK-1 precursor, submandibular - mouse

N:Alternate names: glandular kallikrein; kininogenin

C:Species: Mus musculus (house mouse)

C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

C:Accession: A00941

R:Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.

Nature 303, 300-307, 1983

A:Title: Structure of mouse kallikrein gene family suggests a role in specific processing

A:Reference number: A00941; MUID:83219214; PMID:602295

A:Accession: A00941

A:Molecule type: DNA

A:Residues: 1-261 <MAS>

A:Cross-references: UNIPROT:P00755; UNIPARC:UPI0000001AOC; GB:V00829; NID:G52775; PIDN:CU

A:Experimental source: Quakenbush inbred strain

C:Comment: mGK-1 belongs to a family of 25 to 30 homologous kallikrein genes.

C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release 1

C:Genetics:

A:Gene: mGK-1

A:Map position: 7

A:Introns: 16/1; 69/2; 165/1; 210/3

C:Superfamily: trypsin; trypsin homology

C:Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland; zym

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-24/Domain: activation peptide #status predicted <APT>

F:25-261/Product: tissue kallikrein, submandibular #status predicted <MPT>

F:25-253/Domain: trypsin homology <TRY>

F:31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted

F:65,120,213/Active site: His, Asp, Ser #status predicted

F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1,65e-39 | Length: | 261 |
| Score: | 552.00 | Matches: | 109 |
| Percent Similarity: | 57.6% | Conservative: | 39 |
| Best Local Similarity: | 42.4% | Mismatches: | 93 |
| Query Match: | 31.0% | Indels: | 16 |
| DB: | 1 | Gaps: | 3 |

US-09-905-083A-30 (1-969) x QKMS1 (1-261)

| | | | |
|----|-----|--|-----|
| QY | 49 | TTACTGCTATCTTACCTTGGAAACTGCAGGAGAAGACCCAG-----GGTGAC | 99 |
| Db | 4 | LeuIleLeuPheLeuAlaLeuSerLeuGlyIleAspAlaProValGlnSer | 23 |
| QY | 100 | AGATTATGTATGGCGCCCATGTGCAGAGAGCTCCACCATGGCAGGTGCCCTGCTC | 159 |
| Db | 24 | ArgIleValGlyGlyPheLysCysGluLysAsnSerGlnProTrpHisValAlaValTyr | 43 |
| QY | 160 | AGTGGCAATCACTCCACTGCGGAGCGTCTGTGTCATAGCGCTGGGTGCTCACTGCC | 219 |
| Db | 44 | ArgTyrLysGluTyrIleCysGlyValLeuLeuAspAlaAsnTrpValLeuThrAla | 63 |
| QY | 220 | GCCCACTGCAAGATGAATGATACCGGTGCACCTGGGCGAGTATACGCTG-----GGC | 273 |
| Db | 64 | AlaHisCysTyrTyrGluLysAsnAsnValTrpLeuGlyLysAsnLeuTyrGlnAsp | 83 |
| QY | 274 | GACAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGCCACCCCGCTACTCCACA | 333 |
| Db | 84 | GluProSerAlaGlnHisArgLeuValSerLysSerPheLeuHisProCysTyrAsnMet | 103 |
| QY | 334 | CAGACCCATGTTAAT-----GACCTCATGCTC | 360 |
| Db | 104 | SerLeuHisArgAsnArgIleGlnAsnProGlnAspAspTyrSerTyrAspLeuMetLeu | 123 |
| QY | 361 | GTGAAGCTCAATPAGCCAGCCAGGCTGTCATCCATGGTGAAGAAAGTCAAGGTGCCCTCC | 420 |
| Db | 124 | LeuArgLeuSerLysProAlaAspIleThrAspValValLysProIleAlaLeuProThr | 143 |
| QY | 421 | CGCTGGAAACCCCTGGAAACCACTGTACTGCTCGGCTGGGCACTACCAAGAGCCCA | 480 |
| Db | 144 | GluGluProLysLeuGlySerThrCysLeuAlaSerGlyTrpGlySerIleIleProVal | 163 |
| QY | 481 | GATGTGACCTTTCCCTCTGACCTCATGTGCTGGAGTGTCAAGCTCATCTCCCCCAGGAC | 540 |
| Db | 164 | LysPheGlnTyrAlaLysAspLeuGlnCysValAsnLeuLysLeuLeuProAsnGluAsp | 183 |
| QY | 541 | TGCACGAAGGTTTACAAGGACTTACTGGAAATTCATGCTGTGCGCTGGCATCCCCGAC | 600 |

Db 184 CyAspLysAlaTyrValGlnLysValThrAspValMetLeuCysAlaGlyValLysGly 203
QY 601 TCAAGAGAAACCCCTGCAATGCTACTCAGGGGGGACCGTGTGGTGTGCAGAGGTACCCCTG 660
Db 204 GlyGlyLysAspThrCysLysGlyAspSerGlyGlyProLeuLeuCysAspGlyValLeu 223
QY 661 CAAGGTCTGTGCTCTGGGGAACCTTCCCTTGGGGGCAACCCCAATGACCCAGGAGTCTAC 720
Db 224 GlnGlyLeuThrSerTrpGlyTyrAsnProCysGlyGluProLysLysProGlyValTyr 243
QY 721 ACTCAAGTGTGCAAGTTCACCAAGTGTGATAAATGACACCATGAAAGCAT 771
Db 244 ThrLysLeuLeuLysPheThrSerTrpLysAspThrLeuAlaGlnAsn 260

RESULT 9
A31136
tissue kallikrein (BC 3.4.21.35) 7 precursor, submandibular - rat
N:Alternate names: glandular prokallikrein 7, submandibular; proteinase A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A31136; S10698; S10699; D41429; B41429; S09315
R:Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A:Reference number: A31136; MUID:89088074; PMID:2849988
A:Accession: A31136
A:Molecule type: DNA
A:Residues: 1-261 <CHE>
A:Cross-references: UNIPROT:P36373; UNIPARC:UPI000012DEB6; GB:M19647; GB:J02837; NID:920
R:Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A:Title: Substrate specificity of two kallikrein family gene products isolated from the
A:Reference number: S10698; MUID:90306305; PMID:2194829
A:Accession: S10698
A:Molecule type: protein
A:Residues: 25-36 <ELM>
A:Cross-references: UNIPARC:UPI0000175BE3
A:Accession: S10699
A:Molecule type: protein
A:Residues: 112-139 <EL2>
A:Cross-references: UNIPARC:UPI0000175BE3
R:Kato, H.; Nakanishi, E.; Enyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi
A:Reference number: A41429; MUID:88198057; PMID:3482210
A:Accession: D41429
A:Molecule type: protein
A:Residues: 112-133 <KAT>
A:Cross-references: UNIPARC:UPI0000175BE5
A:Accession: B41429
A:Molecule type: protein
A:Residues: 25-34, 'D', '36-45', 'S', '47-67', 'X', '69-75' <KA2>
A:Cross-references: UNIPARC:UPI0000175BE5
R:Brady, J.M.; MacDonald, R.J.
Arch. Biochem. Biophys. 278, 342-349, 1990
A:Title: The expression of two kallikrein gene family members in the rat kidney.
A:Reference number: S09315; MUID:90225801; PMID:2183721
A:Accession: S09315
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 43-45, 'S', '47-114', 'A', '116-261' <BRA>
A:Cross-references: UNIPARC:UPI0000175BE7
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores: 1.65e-39 Length: 261
Pred. No.: 552.00 Matches: 110
Score:

Percent Similarity: 57.8% Conservative: 38
Best Local Similarity: 43.0% Mismatches: 94
Query Match: 31.0% Indels: 14
DB: 2 Gaps: 3

US-09-905-083A-30 (1-969) x A31136 (1-261)

QY 46 ATCTTACTGCTATCTCTAGCTTGGAACTGCAAGGAGAGAACCCAGGT---GACAAG 102
Db 5 IleLeuPheLeuAspLeuSerLeuGlyGlnIleAspAlaProGlyGlnSerArg 24
QY 103 ATTATTGATGGCGCCCATGTCACAGAGGTCCACCCATGGCAGGTGGCCCTGCTCAGT 162
Db 25 ValIleGlyGlyTyrLysCysGluLysAsnSerGlnProTrpGlnValAlaLeuTyrSer 44
QY 163 GGCATCAGCTCCACTGCGAGCGCTCTGGTCAATCAGCGCTGGGTGCTCATCTGCCGCC 222
Db 45 PheThrLysTyrLeuCysGlyValLeuLeuAspProSerTrpValIleThrAlaAla 64
QY 223 CACTGCAAGATGAATGATGACCGTGCACCTGGGAGTATACGCTG-----GGCGAC 276
Db 65 HisCysSerSerAsnAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuLeuGluAspGlu 84
QY 277 AGGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCGCACCCCGCTACTCCACA--- 333
Db 85 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProAspTyrLysProPhe 104
QY 334 -----CAGACCCATGTTAATGACCTCATCTGCTCGT 363
Db 105 LeuMetArgAsnHisThrArgLysProGlyAspAspHisSerAsnAspLeuMetLeuLeu 124
QY 364 AAGCTCAATPAGCAGCCAGCGTGTCCATCCATGTTGAAGAAAGTCAAGGTGCCCTCCCGC 423
Db 125 HisLeuSerGlnProAlaAspIleThrAspGlyValLysValIleAspLeuProThrGlu 144
QY 424 TCGGAACCCCTGGACACCACTGACTCTCTCGGCTGGGCACTACCAAGGCTCATCTCC 483
Db 145 GluProLysValGlySerThrCysLeuAlaSerGlyTrpGlySerThrLysProLeuLeu 164
QY 484 GTGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
Db 165 TrpGluPheProAspAspLeuGlnCysValAsnIleHisLeuLeuSerAsnGluLysCys 184
QY 544 ACGAAGTTTCAAGCACTTACTTGGAAATTCATCTGTGCGCTGGCATCCCGACTCC 603
Db 185 IleLysAlaTyrLysGluLysValThrAspLeuMetLeuCysAlaGlyGluLeuGluGly 204
QY 604 AAGAAAACGCTGCAATGCTGACTCAGGGGACCGTGTGGTGTGACAGGTACCTGCAA 663
Db 205 GlyLysAspThrCysThrGlyAspSerGlyProLeuLeuCysAspGlyValLeuGln 224
QY 664 GGTCTGTGCTCTGGGGAACCTTCCCTGCGGCAACCAATGACCCAGGAGTCTACACT 723
Db 225 GlyIleThrSerTrpGlySerValProCysAlaLysThrAsnMetProAlaIleTyrThr 244
QY 724 CAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT 771
Db 245 LysLeuIleLysPheThrSerTrpLysGluValMetLysGluAsn 260

RESULT 10
A25606
tissue kallikrein (BC 3.4.21.35) submandibular precursor - mouse
N:Alternate names: glandular kallikrein; kininogenin
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: A25606; S06661
R:Van Leeuwen, B.H.; Evans, B.A.; Tregear, G.W.; Richards, R.I.
J. Biol. Chem. 261, 5529-5535, 1986
A:Title: Mouse glandular kallikrein genes. Identification, structure, and expression of t
A:Reference number: A25606; MUID:86168299; PMID:3007510
A:Accession: A25606
A:Molecule type: DNA
A:Residues: 1-261 <VAN>


```

Db      46 GlyGluPheAlaCysGlyGlyValLeuValHisProGluTrpValLeuThrAlaAlaHis 65
      226 TGAAGATGAATGATGATACACCGTGCACCTGGCAGTGTATACGCTGGCGCAGCAGG----- 279
      66 CysAlaAsnSerAenCysGluValTrpLeuGlyArgHisAsnLeuSerGluSerGluAsp 85
      280 AGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGGCCACCCCGCTACTCCACA----- 333
      86 GluGlyGlnLeuValGlnValArgLysSerPheIleHisProLeuTyrLysThrLysVal 105
      334 -----CAGACCCATGTTAATGACCTCATGCTCGTGGTGAAGCTC 369
      106 ProArgAlaValIleArgProGlyGluAspArgSerHisAspLeuMetLeuLeuHisLeu 125
      370 AATAGCCAGCCAGGCTGTATCCATCGTGTGAAGAAAGTCAAGGCTGCCCTCCCGCTCGCAA 429
      126 GluGluProAlaLysIleThrLysAlaValArgValMetAspLeuProLysLysGluPro 145
      430 CCCCTGGAAACACCTGTACTGTCTCCGGCTGGGGCACTACCAAGAGCCCGATGTGACC 489
      146 ProLeuGlySerThrCysTyrValSerGlyTrpGlySerThrAspProGluThrIlePhe 165
      490 TTTCCCTCTGACCTCATGTGCGGGATGTCAAGCTCATCTCCCGCAGGACTCACGAAG 549
      166 HisProGlySerLeuGlnCysValAspLeuLysLeuLeuSerAsnAsnGlnCysAlaLys 185
      550 GTTTCAAGGACTTACTGGAATAATTCATGCTGTGGCTGGCACTCCCGCACTCCAAGAAA 609
      186 ValTyrThrGlnLysValThrLysPheMetLeuCysAlaGlyValLeuGluGlyLysLys 205
      610 AAGCCTCGAATGGTGAATGAGGAGACCGTGTGGTGTGAGAGTACCTGCAAGGTCTG 669
      206 AspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyGluLeuValGlyIle 225
      670 GTGTCCTGGGACTTTCCTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTG 729
      226 ThrSerTrpGlyAlaThrProCysGlyLysProGlnMetProSerLeuTyrThrArgVal 245
      730 TGCAAGTTCACCAAGTGGATAATGACACCATGAAA 765
      246 MetProHisLeuMetTrpIleLysAspThrMetLys 257

RESULT 12
TRRT2
trypsin (EC 3.4.21.4) II precursor - rat
N:Alternate names: trypsinogen II
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A22657; A00949
R:Cralk, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A:Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; MUID:85054880; PMID:6094547
A:Accession: A22657
A:Molecule type: DNA
A:Residues: 1-246 <CRA>
A:Cross-references: UNIPROT:P00763; UNIPARC:UPI0000172AAB
R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
A:Reference number: A00948; MUID:82265624; PMID:6896710
A:Accession: A00949
A:Molecule type: mRNA
A:Residues: 9-246 <MAC>
A:Cross-references: UNIPARC:UPI0000172AAC
C:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I mRNA.
C:Genetics:
A:Introns: 14/1; 67/2
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>

```

```

F:24-246/Product: trypsin II #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Diulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
Pred. No.: 1,32e-38 Length: 246
Score: 541.50 Matches: 108
Percent Similarity: 59.8% Conservative: 38
Best Local Similarity: 44.3% Mismatches: 87
Query Match: 30.4% Indels: 11
DB: 1 Gaps: 5

```

US-09-905-083A-30 (1-969) x TRRT2 (1-246)

```

QY 52 CTGCTATCTTACCTTGTG-----GAAACTGCAGGAGAAGAGCCAGGCGTGAACG 102
Db      4 LeuLeuPheLeuAlaLeuValGlyAlaAlaValAlaPheProValAspAspAspLys 23
QY 103 ATTATTGATGGCGCCCATGTGTCAAGAGGCTCCACCCATGGCAGGTGGCCCTGCTCAGT 162
Db 24 ILeValGlyGlyTyrThrCysGlnGluAsnSerValProTyrGlnValSerLeuAsnSer 43
QY 163 GGCATCACTCCACTGCGGAGGCTCTGTGTCAATGAGGCTGGGTGCTCACTGCGGCC 222
Db 44 GlyTyrHisPhe---CysGlyGlySerLeuIleAsnAspGlnTrpValValSerAlaAla 62
QY 223 CACTGCAAGTGAATGAGTACACCGTGCACCTGGGCGAGTGATACGCTG----- 270
Db 63 HisCysTyrLysSerArgIleGlnValArgLeuGlyGluHisAsnIleAsnValLeuGlu 82
QY 271 GCGCAGGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCCACCCCGCTACTCTCC 330
Db 83 GlyAspGlu-----GlnPheIleAsnAlaAlaLysIleIleLysHisProAsnPheAsp 100
QY 331 ACACAGACCATGTTAATGACCTCATGCTGTGTAAGCTCAATAGCCAGGCGGCTGTCTCA 390
Db 101 ArgLysThrLeuAsnAsnAspIleMetLeuIleLysLeuSerSerProValLysLeuAsn 120
QY 391 TCCATGGTGAAGAAAGTCAAGGCTGCCCTCCCGCTGCGAACCCTCGAACCACCTGTACT 450
Db 121 AlaArgValAlaThrValAlaLeuProSerSerCysAlaProAlaGlyThrGlnCysLeu 140
QY 451 GTCTCGGCTGGGCACTACACGAGCCAGATGTCACCTTTCCCTCTGCACCTCATGTGC 510
Db 141 IleSerGlyTrpGlyAsnThrLeuSerSerGlyValAsnGluProAspLeuLeuGlnCys 160
QY 511 GTGGATGTCAGACTCATCTCCCCCAGGACTGCGACGAGGTTTACAGGACTTACTGGAA 570
Db 161 LeuAspAlaProLeuLeuProGlnAlaAspCysGluAlaSerTyrProGlyLysIleThr 180
QY 571 AATTCATGCTGTGGCTGCGATCCCGACTCCAGAAAAAGCCCTGCAATGTGTGACTCA 630
Db 181 AspAsnMetValCysValGlyPheLeuGluGlyLysAspSerCysGlnGlyAspSer 200
QY 631 GGGGGACCGTGTGGTGTGCAAGAGTACCTGCAAGGTCTGTGTCTGGGGAACTTCCCT 690
Db 201 GlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSerTrpGly---TyrGly 219
QY 691 TCGGGCAACCAATGACCCAGGAGTCTATCACTCAAGTGTGCAAGTTCACCAAGTGATGA 750
Db 220 CysAlaLeuProAspAsnProGlyValTyrThrLysValCysAsnTyrValAspTrpIle 239
QY 751 AATGACACCATG 762
Db 240 GlnAspThrIle 243

RESULT 13
S55067
trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
N:Alternate names: trypsinogen I
C:Species: Gallus gallus (chicken)

```


F:58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental
F:131-132/Cleavage site: Lys-Ser (autolytic) #status experimental

Alignment Scores:
Pred. No.: 4,79e-38 Length: 229
Score: 535.00 Matches: 100
Percent Similarity: 60.7% Conservative: 36
Best Local Similarity: 44.6% Mismatches: 84
Query Match: 30.1% Indels: 4
DB: 1 Gaps: 3

US-09-905-083A-30 (1-969) x TRBOTR (1-229)

```
QY 97 GACAAATATTGATGGCGCCCATGTGCAAGAGGTCCACCCATGCGAGGTGGCCCTG 156
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 AspIleValGlyGlyThrCysGlyAlaAsnThrValProGlyGlnValSerLeu 24
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 CTCAGTGGCAATCAGTCCACTCGGAGGCGTCTGTCAATGAGCGCTGGTCACT 216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 AsnSerGlyThrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValSer 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 GCCGCCCATGCAAGATGAATGATACACCGTGCACCTGGGCAGTGTATCGCTGGC 273
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44 AlaAlaHisCysTyrIysSerGlyIleGlnValArgLeuGlyGluAspAsnIleAsnVal 63
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 274 ---GACAGGAGAGCTCAGAGATCAAGCTCGAAGTCATTCGCCACCCCGGCTACTCC 330
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 ValGluGlyAsnGluGlnPheIleSerAlaSerLysSerIleValHisProSerTyrAsn 83
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 ACACAGACCATGTTATGACCTCATGCTCGTGAAGTCAATAGCCAGCCAGCGCTGCA 390
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 SerAsnThrLeuAsnAsnAspIleMetLeuIleLysSerAlaAlaSerLeuAsn 103
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 391 TCCATGTTGAAGAGTCAAGCTGCGCTCCCGTGGCAACCCCTGGAACCACTGTACT 450
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 104 SerArgValAlaSerIleSerLeuProThrSerCysAlaSerAlaGlyThrGlnCysLeu 123
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 GTCTCCGCTGGGCACTACACGAGCCAGATGTGACCTTTCCCTCTGACCTCATGTGC 510
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 IleSerGlyTrpGlyAsnThrLysSerSerGlyThrSerTyrProAspValLeuLysCys 143
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 GTGGATGTCAGTCTATCTCCCGGAGGACTGCACGAGTTTACAGGACTTACTGGAA 570
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 LeuLeuAlaProIleLeuSerAspSerSerCysLysSerAlaTyrProGlyGlnIleThr 163
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 AATTCCATGCTGTGCGTGCATCCCGACTCCCAAGAAACCGCTCAATGTGTGACTCA 630
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 SerAsnMetPheCysAlaGlyTyrLeuGluGlyGlyLysAspSerCysGlnGlyAspSer 183
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 631 GGGGACCGTGTGTGTCAGAGGTACCTGTCAGAGGTCTGTGTCCTGGGGAACCTTCCCT 690
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 GlyGlyProValValCysSerGlyLysLeuGlnGlyIleValSerTrpGlySer---Gly 202
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 691 TGGGCGCAACCCCAATGACCCAGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGATA 750
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 CysAlaGlnLysAsnLysProGlyValTyrThrLysValCysAsnTyrValSerTrpIle 222
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 751 AATGACACCATG 762
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 LysGlnThrIle 226
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 15

KORTP

N;Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence revision 05-Apr-1983 #text change 09-Jul-2004
C;Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R;Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A;Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of
A;Reference number: A00944; MUID:83117659; PMID:6961406
A;Accession: A00944

A;Molecule type: mRNA
A;Residues: 1-265 <SWI>
A;Cross-references: UNIPROT:P00758; UNIPARC:UPI0000167958
A;Experimental source: pancreatic
R;Kato, H.; Nakanishi, E.; Enryoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A;Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi-
A;Reference number: A41429; MUID:88198057; PMID:3482210
A;Accession: A41429
A;Status: preliminary
A;Molecule type: protein
A;Residues: 29-53, X', 55-87 <KAT>
A;Cross-references: UNIPARC:UPI0000172ABF
R;Gerald, W.L.; Chao, J.; Chao, L.
Biochim. Biophys. Acta 866, 1-14, 1986
A;Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A;Reference number: A25137; MUID:86131678; PMID:3004582
A;Accession: A25137
A;Molecule type: mRNA
A;Residues: 115-265 <GER>
A;Cross-references: UNIPARC:UPI0000172AC0
R;Inoue, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A;Title: Identification and structure of the rat true tissue kallikrein gene expressed in
A;Reference number: JX0073; MUID:89327211; PMID:2753879
A;Accession: JX0073
A;Molecule type: DNA
A;Residues: 1-265 <INO>
A;Cross-references: UNIPARC:UPI0000167958; GB:D00448; NID:9220792; PIDN:BAA00346.1; PID:
A;Experimental source: kidney
R;Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A;Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A;Reference number: A23863; MUID:86051477; PMID:2998455
A;Accession: A23863
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-265 <ASH>
A;Cross-references: UNIPARC:UPI0000167958; GB:M11563; NID:g205029; PIDN:AAA41464.1; PID:
A;Experimental source: submaxillary gland
R;Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A;Title: Organization and expression of the rat kallikrein gene family.
A;Reference number: A33359; MUID:89214217; PMID:2708383
A;Accession: A33359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 3-265 <WIN>
A;Cross-references: UNIPARC:UPI000012DEE1; GB:M23874; GB:J04701; GB:M23875; GB:M23876; N
C;Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin
C;Comment: The protein presumably assumes the two-chain form by cleavage between residue
C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release l
C;Genetics: 20/1; 73/2; 169/1; 214/3
A;Introns: 20/1; 73/2; 169/1; 214/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-28/Domain: activation peptide #status predicted <APT>
F;29-265/Product: tissue kallikrein; pancreatic #status predicted <MPT>
F;29-257/Domain: trypsin homology <TRY>
F;35-177,54-70,156-223,188-202,213-238/Disulfide bonds: #status predicted
F;69,124,217/Active site: His, Asp, Ser #status predicted

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 4,84e-38 | Length: | 265 |
| Score: | 535.00 | Matches: | 104 |
| Percent Similarity: | 57.6% | Conservative: | 44 |
| Best Local Similarity: | 40.5% | Mismatches: | 93 |
| Query Match: | 30.1% | Indels: | 16 |
| DB: | 1 | Gaps: | 3 |

US-09-905-083A-30 (1-969) x KORTP (1-265)

| | | | |
|----|-----|---|-----|
| Qy | 49 | TTACTGCTATCCTTAGCCTTGAAACTCGAGAGAAAGACCAG-----GGTGAC | 99 |
| Db | 8 | Leu11LeuPheLeuAlaLeuSerLeuGlyArgAsnAspAlaAaProProValGlnSer | 27 |
| Qy | 100 | AAGATTATTGATGCGCCCATGTGCAAGAGGCTCCCAACCATGACAGTGGGTGCTCTCACTGCC | 159 |
| Db | 28 | ArgValValGlyGlyTyrAsnCysGluMetAsnSerGlnProTrpGlnValAlaValTyr | 47 |
| Qy | 160 | AGTGCGCAATCAGCTCCACTCGGCGAGCGCTCTGGTCAATGAGCGCTGGGTGCTCTCACTGCC | 219 |
| Db | 48 | TyrPheGlyGluTyrLeuCysGlyGlyValLeuIleAspProSerTrpValIleThrAla | 67 |
| Qy | 220 | GCCCACTGCAAGATGAATGATACACCTGTGCACCTGGCGGAGTATACGCTGGCGACAGG | 279 |
| Db | 68 | AlaHisCysAlaThrAspAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuTyrGluAsp | 87 |
| Qy | 280 | AGA-----GCTCAGAGGATCAAGGCCTCGAAGTCATTCGCCACCCCGCTACTCCACA | 333 |
| Db | 88 | GluProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProGlyPheAsnGln | 107 |
| Qy | 334 | -----CAGACCCACTGTAATCACCTCATGCTC | 360 |
| Db | 108 | AspLeuIleTrpAsnHisThrArgGlnProGlyAspAspTyrSerAsnAspLeuMetLeu | 127 |
| Qy | 361 | GTGAAGCTCAATAGCCAGCGCGTGCATCCATGGTGAAGAAAGTCAAGGTGCCTCC | 420 |
| Db | 128 | LeuHisLeuSerGlnProAlaAspIleThrAspGlyValValLeuIleAspLeuProIle | 147 |
| Qy | 421 | CGCTGCGNAACCCCTGGAACCACTGTACTGTCTCCGCTGGGCACTACCAACGAGCCCA | 480 |
| Db | 148 | GluGluProLysValGlySerThrCysLeuAlaSerGlyTrpGlySerIleThrProAsp | 167 |
| Qy | 481 | GATGTGACTCTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCGACAG | 540 |
| Db | 168 | GlyLeuGluLeuSerAspAspLeuGlnCysValAsnIleAspLeuLeuSerAsnGluLys | 187 |
| Qy | 541 | TGCACGAAGGTTTACAGGACTTACTGGAATAATTCATGCTGTGTGGCTGGCATCCCCGAC | 600 |
| Db | 188 | CysValGluAlaHisLysGluGluValThrAspLeuMetLeuCysAlaGlyGluMetAsp | 207 |
| Qy | 601 | TCCAAGAAAAACGCTGCAATGGTGACTCAGGGGACCGTGGTGTGCAGAGGTACCCCTG | 660 |
| Db | 208 | GlyGlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAsnGlyValLeu | 227 |
| Qy | 661 | CAAGCTGTGTGTCCTGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGAGTCTAC | 720 |
| Db | 228 | GlnGlyIleThrSerTrpGlyPheAsnProCysGlyGluProLysIleAspProGlyIleTyr | 247 |
| Qy | 721 | ACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT | 771 |
| Db | 248 | ThrLysValLeuLysPheThrProTrpIleLysGluValMetLysGluAsn | 264 |

Search completed: March 11, 2006, 01:55:32
Job time : 50 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 01:39:02 ; Search time 52.9 Seconds
(without alignments)
2584.714 Million cell updates/sec

Title: US-09-905-083A-30
Perfect score: 1780
Sequence: 1 ggaattccgggtccatggc.....aagaacacaaacccctcag 969

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=klp
-O=/abs/ABSSWEB_spool/US0905083/runat_10032006_152453_29666/app_query.fasta_1
-DB=UniProt -QFWT=fastan -SUFFIX=n2p_rup -MINMATCH=0.1 -LOORCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum2 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=prc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US0905083 @CGN 1.1.466 @runat_10032006_152453_29666 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------|
| 1 | 1364 | 76.6 | 253 | 1 | KLK7 HUMAN |
| 2 | 1028.5 | 57.8 | 249 | 1 | KLK7 MOUSE |
| 3 | 760 | 42.7 | 140 | 2 | QSR567_PONPY |
| 4 | 614 | 34.5 | 260 | 1 | NRPN MOUSE |
| 5 | 612.5 | 34.4 | 293 | 1 | KLK5 HUMAN |
| 6 | 612.5 | 34.4 | 293 | 1 | Q532R3_HUMAN |
| 7 | 611.5 | 34.4 | 260 | 1 | NRPN RAT |
| 8 | 609.5 | 34.2 | 276 | 2 | NRPN MOUSE |
| 9 | 608.5 | 34.2 | 293 | 2 | Q532R3_HUMAN |
| 10 | 604.5 | 34.0 | 246 | 2 | Q6P320_MOUSE |
| 11 | 593.5 | 33.3 | 250 | 2 | Q8CGR5_MOUSE |
| 12 | 589 | 33.1 | 293 | 2 | Q9D140_MOUSE |
| 13 | 586.5 | 32.9 | 242 | 2 | Q80VS4_MOUSE |
| 14 | 583 | 32.8 | 251 | 1 | KLK14_HUMAN |
| 15 | 583 | 32.8 | 251 | 2 | Q6B089_HUMAN |
| 16 | 582.5 | 32.7 | 260 | 1 | NRPN_HUMAN |

| | | | | | |
|----|-------|------|-----|---|--------------|
| 17 | 582 | 32.7 | 261 | 1 | KLK9_MOUSE |
| 18 | 580.5 | 32.6 | 260 | 2 | Q8IW69_HUMAN |
| 19 | 578 | 32.5 | 277 | 1 | KLK13_HUMAN |
| 20 | 576.5 | 32.4 | 239 | 2 | Q63275_RAT |
| 21 | 573.5 | 32.2 | 255 | 1 | KLK15_SAGO |
| 22 | 571.5 | 32.1 | 250 | 1 | KLK11_HUMAN |
| 23 | 568 | 31.9 | 261 | 1 | KLK11_MOUSE |
| 24 | 567.5 | 31.9 | 254 | 1 | KLK4_HUMAN |
| 25 | 567.5 | 31.9 | 254 | 2 | Q4VB16_HUMAN |
| 26 | 563 | 31.6 | 256 | 1 | KLK15_HUMAN |
| 27 | 563 | 31.6 | 261 | 1 | KLK3_MOUSE |
| 28 | 563 | 31.6 | 261 | 1 | KLK8_RAT |
| 29 | 561.5 | 31.5 | 255 | 2 | Q6IS70_HUMAN |
| 30 | 561.5 | 31.5 | 276 | 2 | Q9QIN3_MOUSE |
| 31 | 561 | 31.5 | 246 | 1 | TRY1_RAT |
| 32 | 560 | 31.5 | 263 | 1 | KLK27_MOUSE |
| 33 | 559.5 | 31.4 | 254 | 2 | Q4VB17_HUMAN |
| 34 | 559.5 | 31.4 | 255 | 2 | Q96RQ0_HUMAN |
| 35 | 556 | 31.2 | 275 | 2 | Q8IXD7_HUMAN |
| 36 | 555 | 31.2 | 248 | 1 | KLK12_HUMAN |
| 37 | 555 | 31.2 | 276 | 2 | Q53YL3_HUMAN |
| 38 | 554.5 | 31.2 | 234 | 2 | Q9CV76_MOUSE |
| 39 | 553.5 | 31.1 | 249 | 2 | Q9QYN4_MOUSE |
| 40 | 552.5 | 31.0 | 260 | 1 | ESTA_CANFA |
| 41 | 552 | 31.0 | 261 | 1 | KLK1_MOUSE |
| 42 | 552 | 31.0 | 261 | 1 | KLK6_MOUSE |
| 43 | 552 | 31.0 | 261 | 1 | KLK7_RAT |
| 44 | 551.5 | 31.0 | 246 | 2 | Q6IE66_RAT |
| 45 | 551 | 31.0 | 261 | 2 | Q8C232_MOUSE |

ALIGNMENTS

| | | | | |
|----------|--|-----------------|------|---------|
| RESULT 1 | KLK7_HUMAN | STANDARD; | PRT; | 253 AA. |
| ID | KLK7_HUMAN | Q8W5N9; Q8W5V7; | | |
| AC | P49862; Q8W5N9; Q8W5V7; | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DE | Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum chymotryptic enzyme) (hSCCE). | | | |
| DE | Names=KLK7; Synonyms=PRSS6, SCCE; | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; | | | |
| OC | Homo | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53. | | | |
| RC | TISSUE=Skin; | | | |
| RX | MEDLINE=94308225; PubMed=8034709; | | | |
| RA | Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T., | | | |
| RT | "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; | | | |
| RL | J. Biol. Chem. 269:19420-19426(1994). | | | |
| RN | [2] | | | |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION. | | | |
| RC | TISSUE=keratinocyte; | | | |
| RX | PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8; | | | |
| RA | Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., Diamandis E.P.; | | | |
| RT | "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal regulation."; | | | |
| RL | Gene 254:119-128(2000). | | | |
| RN | [3] | | | |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. | | | |
| RX | PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; | | | |
| RA | Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepel B., Wang K.; | | | |

Db 21 AlaGlyGluGluAlaGlnGlyAspLysLeileAspGlyAlaProCysAlaAaGlySer 40
 QY 136 CACCCATGGAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGAGCGCTCTGGTC 195
 Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
 QY 196 AATGAGCGCTGGGTGCTCACTCGCCGCTGCAAGATGAATGAGTACACCGTGCACCTG 255
 Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
 QY 256 GGCAGTGTATCGCTGGCGCAGCAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
 Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgileLysAlaSerLysSerPheArg 100
 QY 316 CACCCGGCTACTCCACAGACCCATGTAATGACCTCATGCTGCTGTAAGCTCAATAGC 375
 Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
 QY 376 CAGCCAGCGCTGCATCCATGCTGCAAGAGTCAAGGCTGCGCTCCGCTCGCAACCCCT 435
 Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
 QY 436 GGAACACACCTGTACTGCTCCGCTGGCGCACTACACGAGCCAGATGTGACTTTCCTCC 495
 Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
 QY 496 TCTGACCTCATGTGCGTGGTGTCAAGCTCATCTCCCGCCAGGAGTGCACGAAGTTTAC 555
 Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuLysLeuLysLeuLysValThr 180
 QY 556 AAGGACTTACTGAAATTCATGCTGCTGGCTGGCATCCCGCTCCGCTCCAGAAACGCC 615
 Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
 QY 616 TGCATGTGTGACTCAGGGGACCGTGTGTGTGAGAGGTACCTCGCAAGTCTGTGTGTC 675
 Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
 QY 676 TGGGGAATTTCCCTTCGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
 Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValThrThrGlnValCysLys 240
 QY 736 TTCACCAAGTGGTAATGACACATGAAAGCAATCGCTCCG 774
 Db 241 PheThrLysTrpLeuAsnAspThrMetLysLysHisArg 253

RESULT 2
 ID_KLK7_MOUSE STANDARD; PRT; 249 AA.
 AC Q91VE3; Q9R048;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (Thymopain).
 DE Names:Klk7; Synonyms=Prss6, Scce;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP STRAIN=C57BL/6J; TISSUE=Thymus;
 RC MEDLINE=99399282; PubMed=10469296;
 RX DOI=10.1046/j.1523-1747.1999.00662.x;
 RA Baekman A., Strandén P., Bratteand M., Hansson L., Egelrud T.;
 RT "A novel cDNA cloning of mouse serine protease, thymopain.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP STRAIN=129/SvJ;
 RC Hanson L., Baekman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.;
 RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in

RT mice; a model for chronic itchy dermatitis.";
 RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakaki I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis B.D.,
 RA Kanai A., Kawai J., Kawasawa Y., Kedzierzki R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirose-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Waki J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Iotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino K., Sasaki D., Shibata K., Shinagawa A.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RN Nature 420:563-573 (2002).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.S., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP NUCLEOTIDE SEQUENCE OF 1-234, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6J; TISSUE=Tail;
 RX MEDLINE=99399282; PubMed=10469296;
 RX DOI=10.1046/j.1523-1747.1999.00662.x;
 RA Baekman A., Strandén P., Bratteand M., Hansson L., Egelrud T.;
 RT "Molecular cloning and tissue expression of the murine analog to human
 RL stratum corneum chymotryptic enzyme.";
 RL J. Invest. Dermatol. 113:152-155 (1999).
 CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
 CC structures in the cornified layer of the skin in the continuous
 CC shedding of cells from the skin surface. Specific for amino acid
 CC residues with aromatic side chains in the P1 position. SCCE
 CC cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-


```
Pred. No.: 1-23e-56 Length: 140
Score: 760.00 Matches: 138
Percent Similarity: 99.3% Conservative: 1
Best Local Similarity: 98.6% Mismatches: 1
Query Match: 42.7% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x QSR567_PONPY (1-140)

QY 355 ATCTCGTGAAGTCATATACCCAGGCGAGCTGTCTATCCATGTGTGAAGAAAGTCAGCGTG 414
Dy 1 MetLeuValLysLeuAenSerGlnAlaArgLeuSerMetValLysLysValArgLeu 20
QY 415 CCCTCCGCTGCGAACCCTGACACCTGACTGTCTCCGCTGGGCGATACCAAG 474
Dy 21 ProSerArgCysGlyProGlyThrThrCysThrValSerGlyTrpGlyThrThrThr 40
QY 475 AGCCAGATGTGACCTTTCCTCTGACCTCATGTGCGTGTGATGTCAAGCTCATCTCCCC 534
Dy 41 SerProAspValThrPheProSerAspLeuMetCysValAspValLysLeuLleSerPro 60
QY 535 CAGGACTGCACGAAGTTTACAAGGACTTACTGGAATAATTCATGCTGTGCGTGGCATC 594
Dy 61 GlnAspCysThrLysValLysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIle 80
QY 595 CCGACTCCAGAAAAACGCTGCAATGTGACTCAGGGGACCGTGTGTGTCAGAGGT 654
Dy 81 ProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyProLeuValCysArgGly 100
QY 655 ACCCTGCAGGTCTGTGTCTCGGGAACCTTCCCTTGGCGGCAACCCCAATGACCCAGGA 714
Dy 101 ThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnProAsnAspProGly 120
QY 715 GTCTACACTCAAGTGTGCAAGTTCACCAAGTGTGATAATGACACCATGAAAAAGCATCGC 774
Dy 121 ValTyThrGlnValCysLysPheThrLysTrpLleAsnAspThrLysLysLysHisArg 140

RESULT 4
NRPN MOUSE
ID NRPN MOUSE STANDARD; PRT; 260 AA.
AC O6195;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Neuropein precursor (SC 3.4.21.-) (NP) (Kallikrein 8).
GN Names=Klk8; Synonyms=Nrpn; Prss19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimo S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus.";
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neuropein gene, Prss19 to chromosome
RT 7B4.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS
RP SPECTROMETRY.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neuropein, a plasticity-
RT related serine protease.";
RL J. Biol. Chem. 273:11189-11196(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neuropein, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224(1999).
CC -I- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin.
CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -I- ENZYME REGULATION: Strongly inhibited by diisopropyl
CC fluorophosphate, leupeptin and (4-aminophenyl)methanesulfonyl 1-
CC fluoride.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
CC mouse brain and is localized at highest concentration in pyramidal
CC neurons of the hippocampal CA1-3 subfields.
CC -I- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
CC NOTE=Ref.4.
CC -I- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
CC NOTE=Ref.4.
CC -I- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -I- SIMILARITY: Contains 1 peptidase S1 domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D30785; BAA06451.1; -; mRNA.
CC EMBL; AB032202; BAA92435.1; -; Genomic_DNA.
CC EMBL; BC055895; AAH55895.1; -; mRNA.
CC PIR; I56559; I56559.
CC PDB; 1NPM; X-ray; A/B=33-257.
CC MEROPS; S01.244; -.
CC Ensembl; ENSMUSG00000064023; Mus musculus.
CC MGI; MGI:892018; Klk8.
CC InterPro; IPR001254; Peptidase S1_S6.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
```


RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4";
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepier B., Wang X.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Genes 257:119-130(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in desquamation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF168768; AAF03101.1; -; mRNA.
CC EMBL; AF135028; AAD26429.1; -; Genomic DNA.
CC EMBL; AF243527; AAG33358.1; -; Genomic DNA.
CC EMBL; AY359010; AAO89369.1; -; mRNA.

DR EMBL; BC008036; AAH08036.1; -; mRNA.
DR HSSP; P00760; IEZX.
DR MEROPS; S01.017; -.
DR Ensembl; ENSG00000167754; Homo sapiens.
DR HGNC; HGNC:6366; KLK5.
DR MIM; 605643; -; C:extracellular space; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 293 Kallikrein 5.
FT DOMAIN 67 290 Peptidase S1.
FT ACT_SITE 108 108 Charge relay system (By similarity).
FT ACT_SITE 153 153 Charge relay system (By similarity).
FT ACT_SITE 245 245 Charge relay system (By similarity).
FT CARBOHYD 69 69 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 208 208 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).
FT DISULFID 73 205 By similarity.
FT DISULFID 93 109 By similarity.
FT DISULFID 178 279 By similarity.
FT DISULFID 185 251 By similarity.
FT DISULFID 217 231 By similarity.
FT DISULFID 241 266 By similarity.
FT CONFLICT 25 56 Missing (in Ref. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C2F5609E5946 CRC64;

Alignment Scores:
Pred. No.: 7,32e-44 Length: 293
Score: 612.50 Matches: 114
Percent Similarity: 66.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 9
DB: 1 Gaps: 4

US-09-905-083a-30 (1-969) x KLK5_HUMAN (1-293)

QY 76 GCAGGAGAGAGAGCCAGGTCAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAspAlaArgSerSerSerArgIleAsnGlySerAspCys 73
QY 124 GCAAGAGAGTCCCAACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaLeuLeuLeuArgProAsnGlnLeuTyrCys 93
QY 181 GGAGGCGTCTCGTCAATGAGCGCTGGTCTCCTCAGTCCGCCCATCTCAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysVal 113
QY 241 TACACCGTCACCTGGCGAGTATACGCTGGGC-----GACAGGAGAGCTCAGAGG 291
Db 114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMet 133
QY 292 ATCAAGCGCTCGAAGTCATTCCGCCACCCCGGCTACTCCACACAGACCCCATGTTAATGAC 351
Db 134 PheGlnGlyValIysSerIleProHisProGlyTyrSerHisProGlyHisSerAsnAsp 153
QY 352 CTCATGCTCGTGAAGCTCAATAGCCAGCCAGCGCTGTCTATCCATGCTGTAAGAAGTCAGG 411
Db 154 LeuMetLeuIleLysLeuAsnArgAlaGlyProThrLysAspValArgProIleAsn 173
QY 412 CTGCCCCCTCCGCTCGAAGCCCTGTAACACCTGTACTGTCTCCGGCTGGGCGACTACC 471
Db 412 CTGCCCCCTCCGCTCGAAGCCCTGTAACACCTGTACTGTCTCCGGCTGGGCGACTACC 471

RT, "Serine proteases in rodent hippocampus.";
 RL, J. Biol. Chem. 273:23004-23011(1998).;
 CC -I- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity. Has a strong proteolytic activity against
 CC fibronectin (By similarity).
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -I- TISSUE SPECIFICITY: Restricted to hippocampus.
 CC -I- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -I- SIMILARITY: Contains 1 peptidase S1 domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AJ005641; CRA06643.1; -; mRNA.
 DR HSSP: Q61955; INPM.
 DR SMR: O88780; 33-256.
 DR MEROPS: S01.244; -.
 DR Ensembl: ENSRNOG0000018580; Rattus norvegicus.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00134; TRYPSIN_DOM; 1.
 DR PROSITE: PS00135; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Glycoprotein; Hydrolyase; Protease; Serine protease; Signal; Zymogen.
 KW SIGNAL 1 28 Potential.
 FT PROPEP 29 32 By similarity.
 FT CHAIN 33 260 Neuropein.
 FT DOMAIN 33 257 Peptidase S1.
 FT ACT_SITE 73 73 Charge relay system (By similarity).
 FT ACT_SITE 120 120 Charge relay system (By similarity).
 FT ACT_SITE 212 212 Charge relay system (By similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT DISULFID 39 173 By similarity.
 FT DISULFID 58 74 By similarity.
 FT DISULFID 145 246 By similarity.
 FT DISULFID 152 218 By similarity.
 FT DISULFID 184 198 By similarity.
 FT DISULFID 208 233 By similarity.
 SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;
 Alignment Scores:
 Pred. No.: 8,71e-44 Length: 260
 Score: 611.50 Matches: 114
 Percent Similarity: 62.3% Conservative: 40
 Best Local Similarity: 46.2% Mismatches: 86
 Query Match: 34.4% Indels: 7
 DB: 1 Gaps: 4
 US-09-905-083a-30 (1-969) x NRPN_RAT (1-260)
 QY 46 ATCTTACTGTCATCTTGGAACTGCAGGA---GAAGAAGCCAGGCTGACAG 102
 Db 13 IleLeuLeuPheLeuLeuMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGlySerLys 32
 QY 103 ATTATTGATGGCCCCCATGTGCAAGAGGCTCCACCCATGGCAGGTGGCCCTGTCAGT 162
 Db 33 IleLeuGluGlnGluCysLysProHisSerGlnProTrpGlnThrAlaLeuPheGln 52
 QY 163 GCAATCACTCCACTCGGAGCGGCTCTGTCGAATGAGCGTGGTGTCTCACTGCGGCC 222
 Db 53 GlyGluArgLeuValCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72
 QY 223 CACTGCAAGATGAATGAGTACACCGTGCACCTGGCAGTCATACGCTG-----GGCGAC 276
 Db 73 HisCysLysLysAspLysTrpSerValArgLeuGlyAspHisSerLeuGlnLysArgAsp 92

QY 277 AGGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCGCACCCGGCTACTCCACA--- 333
 Db 93 GluProGluGlnGluIleGlnValAlaArgSerIleGlnHisProCysPheAsnSerSer 112
 QY 334 -----CAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGCCAGGCTG 387
 Db 113 AsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsnLeu 132
 QY 388 TCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCTCGAACCACCTGT 447
 Db 133 GlyAspLysValLysProIleGluLeuAlaAsnLeuCysProLysValGlyGlnLysCys 152
 QY 448 ACTGTCTCCGCTGGGCGACTACAGAGCCAGAGTGTACCTTCCCTCTGACCTCATG 507
 Db 153 IleIleSerGlyTrpGlyThrValThrSerProGlnGluAsnPheProAsnThrLeuAsn 172
 QY 508 TGGCTGGATGTCAGGCTCATCTCCCGCCAGGACTGCACGAGGTTTACAGGACTTACTG 567
 Db 173 CysAlaGluValLysIleTrpSerGlnAsnLysCysGluArgAlaTrpProGlyLysIle 192
 QY 568 GAAATTCATGCTGTGCGTGGCTGCCGACTCCAGGATCCCAAGAAAAACGCTCAATGGTGAC 627
 Db 193 ThrGluGlyMetValCysAlaGly---SerSerAsnGlyAlaAspThrCysGlnGlyAsp 211
 QY 628 TCAGGGGACCGTGTGTGTCGAGAGTACCTCCAGAGTGTGTGTCTGCTGGGAACTTTC 687
 Db 212 SerGlyGlyProLeuValCysAsnGlyValLeuGlnGlyIleThrThrTrpGlySerAsp 231
 QY 688 CCTTGGCGCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGG 747
 Db 232 ProCysGlyLysProGluLysProGlyValThrLysIleCysArgTrpThrAsnTrp 251
 QY 748 ATAAATGACACCATGAAAAAG 768
 Db 252 IleLysLysThrMetGlyLys 258
 RESULT 8
 Q8CGR6 MOUSE PRELIMINARY; PRT; 276 AA.
 AC Q8CGR6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
 DE Glandular kallikrein KLK13.
 GN Name=KLK13;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
 RA Olsson A.Y.; Lundwall A.;
 RT "Organization and evolution of the glandular kallikrein locus in Mus
 RT musculus.";
 RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Adams M.; Mural R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY152432; AAN78420.1; -; Genomic_DNA.
 DR HSSP; P00760; 1EZX.
 DR MEROPS; S01.306; -.
 DR Ensembl; ENSMUSG00000054046; Mus musculus.
 DR MGI; MGI:95292; Klkl3.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.

DR PROSITE; PS02440; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin H1S; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_Ser; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDCA CRC64;

Alignment Scores:
Pred. No.: 1 31e-43 Length: 276
Score: 609.50 Matches: 120
Percent Similarity: 63.2% Conservative: 43
Best Local Similarity: 46.5% Mismatches: 76
Query Match: 34.2% Indels: 19
DB: 2 Gaps: 6

US-09-905-083A-30 (1-969) x Q8CGR6_MOUSE (1-276)

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QY 46 ATCTTACTCTATCCCTTACCTTGGAACTGCAGGAGAGAGCCAGGGTGACAGATT 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 IleAlaCysLeuThrLeuAlaLeu---SerGluGlyIleSerArgAspTyrProLysIle 26
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 106 ATGTATGGCGCC-----CCATGTGCAGAGGC 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 LeuAsnGlyThrAsnGlyThrSerGlyPheLeuProGlyTyrThrCysLeuProHis 46
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 133 TCCACCCCATGGCAGGTGGCCCTCTCAGTGGCAATCAGCTCCACCTGCGGAGCGCTCTG 192
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 47 SerGlnProTrpGlnAlaLeuLeuIleArgGlyArgLeuLeuCysGlyGlyValLeu 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 193 GTCATATGAGCGTGGTGTCTACTGCCGCCCACTGCAAGATGAATGAGTACACCGTGAC 252
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 67 ValHisProLysTrpValLeuThrAlaHisCysArgLysAspGlyTyrThrValHis 86
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 253 CTGGGCAGTGTACGTCTGGC-----GACAGGAGAGCTCAGAGNATCAAGSCCTCGAG 306
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 LeuGlyLysHisAlaLeuGlyArgValGluAsnGlyGluAlaMetGluValValArg 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 307 TCATTCGCCACCCCGCTACTCC---ACACAGACCCATGTTAAT-----GACCTC 354
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 107 SerIleProHisProGluTyrGlnValThrProThrHisLeuAsnHisAspHisAspIle 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 355 ATGCTCTGTAAGCTCAATAGCCAGGCGCTGTCTATCCATGGTGAAGAAATGTCAGGCTG 414
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 MetLeuLeuGluLeuLysSerProValGlnLeuSerSerHisValArgThrLeuLysLeu 146
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 415 CCTCC--CGTGGCAACCCCTGCAACCACTGTACTCTCCGGCTGGGGCACTACC 471
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 SerAlaAspAspCysLeuProThrGlyThrCysCysArgValSerGlyTrpGlyThrThr 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 472 ACAGGCCAGATGTGACCTTCCCTCTGACCTCATGTGGTGATGTCAAGCTCATCTCC 531
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 167 ThrSerProGlnValAsnTyrProLysThrLeuGlnCysAlaAsnIleGluLeuArgSer 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 532 CCCCAGGACTGCAGAGGTTTACAAAGGACTTACTGGAAATTTCCATGTGTGCGCTGCG 591
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 AspGluGluCysArgGlnValTyrProGlyLysIleThrAlaAsnMetLeuCysAlaGly 206
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 592 ATCCCGACTCCNAGNAAAACGCTCCATGTGACTCAGGGGACCGTGTGTGTGCAGA 651
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 207 ThrLysGluGlyLysAspSerCysGluGlyAspSerGlyGlyProLeuIleCysAsn 226
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 652 GTTACCCTGCAGAGTCTGTGTCTGGGAACCTTCCCTTGGCGGCAACCCCAATGACCCA 711
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 227 GlyLysLeuTyrGlyIleSerTrpGlyAspPheProCysGlyGlnProAsnArgPro 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 712 GGAGTCTACCACTGAGTGTGCAAGTTTACCACCAATGGATGAATGACACCACTGAAA 765
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 247 GlyValTyrThrArgValSerLysTyrLeuArgTrpIleArgGluIleIleArg 264
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 9

Q53F68 HUMAN
ID Q53F68_HUMAN PRELIMINARY; PRT; 293 AA.
AC Q53F68;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)

```
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Kallikrein 5 preproprotein variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1) NUCLEOTIDE SEQUENCE.
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN (2) NUCLEOTIDE SEQUENCE.
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN (3) NUCLEOTIDE SEQUENCE.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK223421; BAD97141.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 293 AA; 32034 MW; B24E30C4PDCAS1DF CRC64;
```

Alignment Scores:
Pred. No.: 1 62e-43 Length: 293
Score: 608.50 Matches: 113
Percent Similarity: 65.8% Conservative: 43
Best Local Similarity: 47.7% Mismatches: 72
Query Match: 34.2% Indels: 9
DB: 2 Gaps: 4

US-09-905-083A-30 (1-969) x Q53F68_HUMAN (1-293)

```
QY 79 GGAGAGAAGCCCGGGTGAC-----AAGATTATTGATGGCGCCCATGTGCA 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 55 GlyGluAspAlaArgSerAspAspSerSerArgIleIleAsnGlySerAspCysAsp 74
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 127 AGAGGCTCCCACTGCGAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACCTGCGGA 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 MetHisThrGlnProTrpGlnAlaProLeuLeuAcgProAsnGlnLeuTyrCysGly 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 184 GCGCTCTGTCAATGAGCGGTGGTGTCTACTGCGGCCCATGCAAGATGAATGAGTAC 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 AlaValLeuValHisProGlnTrpLeuLeuThrAlaHisCysArgLysLysValPhe 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 244 ACCGTGCACCTGGGCGAGTACGCTGGGC-----GACAGGAGAGCTCAGAGGATC 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 ArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnMetPhe 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 295 AAGGCTCGAAGTCAATCCGCGCCCTACTCCACAGACCCCATGTTAATGACCTC 354
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 GlnGlyValLysSerIleProHisProGlyTyrSerHisProGlyHisSerAsnAspLeu 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 355 ATGCTCTGTAAGCTCAATAGCCAGGCGGTGTCTATCCATGCTGAAGAAATCAGGCTG 414
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 155 MetLeuIleLysLeuAsnArgIleArgProThrLysAspValArgProIleAsnVal 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 415 CCTCCCGCTCGAACCCTGGACCACTGTACTGTCTCCGGTGGGGCACTACCAG 474
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 SerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLys 194
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 475 AGCCCATGATGTGACCTTTCCCTCTCATCTCATGTGCTGGATGTCAGCTCATCTCCCC 534
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 SerProGlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSerGln 214
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 535 CAGGACTGCAGCAAGGTTTACAAAGGACTTACGGAATAATTCATGTCGCTGCGCATC 594
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 215 LysArgCysGluAspAlaTyrProArgGlnIleAspAspThrPheCysAlaGly--- 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```


RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";
 RN Genome Res. 10:1617-1630(2000).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shino K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishimi T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RN Genome Res. 10:1757-1771(2000).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK003996; BAB23113.1; -, mRNA.
 DR HSSP; P00760; 1EZX.
 DR MEROPS; S01.418; -.
 DR MGI; MGI:1915918; 1110030019rik.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 293 AA; 31908 MW; ED145D08226FE911 CRC64;
 Alignment Scores:
 Pred. No.: 7,75e-42 Length: 293
 Score: 589.00 Matches: 108
 Percent Similarity: 63.6% Conservative: 44
 Best Local Similarity: 45.2% Mismatches: 79
 Query Match: 33.1% Indels: 8
 DB: 2 Gaps: 4
 US-09-905-083a-30 (1-969) x Q9D140_MOUSE (1-293)
 QY 76 GCAGGAGNAGAACCCAGGTGAC-----AAGATTATTGATGGCGCCCATGTGCA 126
 Db 56 SerGlycluaSpThrArgSerAspSerSerArgIleValAsnGlySerAspCysGln 75
 QY 127 AGAGGCTCCACCCAGGTGGCCCTGCTCAGTGGC---AATCAGCTCCACTGGCGA 183
 Db 76 LysAspAlaGlnProIrrpGlnGlyAlaLeuLeuGlyProAsnLysLeuTyfCysGly 95
 QY 184 GCGGTCTGTGTCATGAGCGCTGGGTCTCAGTGGCCGCCCATGTGCAAGATGAGTAC 243

Db 96 AlaValLeuIleSerProGlnTrpLeuLeuThrAlaAlaHisCysArgLysProValPhe 115
 QY 244 ACCTGTCACCTGGGCAAGTATGATCGTGGG-----GACAGGAGAGCTCAGAGGATC 294
 Db 116 ArgIleArgLeuGlyHisHisSerMetSerProValTyrgluSerGlyGlnMetPhe 135
 QY 295 AGGCGCTCGAAGTCAATCCGCCACCCGGCTACTCCACAGACCCATGTTAATGACTC 354
 Db 136 GlnGlyIleLeuSerIleProHisProGlyTySerHisProGlyHisSerAsnAspLeu 155
 QY 355 ATGCTCGTGAAGCTCAATGACGAGGCGAGCTGCTCATCTCCATGCTGGAAGAAGTCAGCTG 414
 Db 156 MetLeuIleLysMetAsnArgLysIleArgAspSerHisSerValLysProValGluIle 175
 QY 415 CCCTCCGCTCGCAACCCCTCGGAACACCTGCTACTGCTCTCCGGCTGGGGCCTACCCAGC 474
 Db 176 AlaCysAspCysAlaThrGluGlyThrArgCysMetValSerGlyTrpGlyThrSer 195
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 Db 196 SerSerHisAsnAsnPheProLysValLeuGlnCysLeuAsnIleThrValLeuSerGlu 215
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 Db 255 LysLeuGlnGlyLeuValSerTrpGlyAspPheProCysAlaGlnArgAsnArgProGly 274
 QY 715 GCTACACTCAAGTGTGCAAGTTCACCAAGTGTGTAATACACACCATGAAAGCAT 771
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 Q80VS4_MOUSE
 ID Q80VS4_MOUSE PRELIMINARY; PRT; 242 AA.
 AC Q80VS4; 24, Created
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE K1k14 protein (Fragment).
 GN Name=K1k14;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinska M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Director MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC074905; AAH74905.1; -; mRNA.
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 DR Ensemble; ENSG00000129437; Homo sapiens.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
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 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
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US-09-905-083A-30 (1-969) x Q6B089_HUMAN (1-251)
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 QY 148 GTGGCCCTGCTCAGTGGC-----AATCAGTCCACTCGGAGGGCTCCTGCTCAATGAG 201
 Db 40 AlaAlaLeuLeuAlaGlyProArgArgPheLeuGlyGlyGlyAlaLeuLeuSerGly 59
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 Db 60 GlnTrpValIleThrAlaAlaHisCysGlyArgProIleLeuGlnValAlaLeuGlyLys 79
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Search completed: March 11, 2006, 01:53:58
 Job time : 272.5 secs

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| Db | 140 | GlyThrSerCysArgValSerGlyTrpGlyThrIleSerSerProIleAlaArgTyrPro | 159 |
| QY | 496 | TCTGACCTCATGTGGTGGATGTCAAGTCTATCTCCCCCAGGACTGCACGAAAGGTTTAC | 555 |
| Db | 160 | AlaSerLeuGlnCysValAsnIleAsnIleSerProAspGluValCysGlnLysAlaTyr | 179 |
| QY | 556 | AAGGACTTACTGGAATAATTCATGTGTGGCTGCATCCCGACTCCCAAGAAAAACGCC | 615 |
| Db | 180 | ProArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyGlyLysAspSer | 199 |
| QY | 616 | TGCAATGGTGACTCAGGGGACCGTTGGTGCAGAGGTACCTGCAGGCTGCTGGTGCTCC | 675 |
| Db | 200 | CysGlnGlyAspSerGlyGlyProLeuValCysArgGlyGlnLeuGlnGlyLeuValSer | 219 |
| QY | 676 | TGGGGAACCTTTCCCTTGGGGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG | 735 |
| Db | 220 | TrpGlyMetGluArgCysAlaLeuProGlyTyrProGlyValTyrThrAsnLeuCysLys | 239 |
| QY | 736 | TTCCACCAAGTGAATAATGACACCATGAAA 765 | |
| Db | 240 | TyrArgSerTrpIleGluGluThrMetArg 249 | |

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 01:54:13 ; Search time 8.5 Seconds
(without alignments)
1885.005 Million cell updates/sec

Title: US-09-905-083A-30

Perfect score: 1780

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/6 COMB.pcp:*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1371 | 77.0 | 265 | 2 | US-09-949-016-7716 Sequence 7716, Ap |
| 2 | 1364 | 76.6 | 253 | 1 | US-08-557-146-2 Sequence 2, Appli |
| 3 | 1364 | 76.6 | 253 | 1 | US-08-824-874-3 Sequence 3, Appli |
| 4 | 1364 | 76.6 | 253 | 1 | US-09-154-344-2 Sequence 2, Appli |
| 5 | 1364 | 76.6 | 253 | 2 | US-08-930-188-2 Sequence 2, Appli |
| 6 | 1364 | 76.6 | 253 | 2 | US-09-210-084-3 Sequence 3, Appli |
| 7 | 1364 | 76.6 | 253 | 2 | US-09-764-762-3 Sequence 3, Appli |
| 8 | 1364 | 76.6 | 253 | 4 | PCT-US96-04294-2 Sequence 4, Appli |
| 9 | 1235 | 69.4 | 225 | 1 | US-09-027-337-4 Sequence 2, Appli |
| 10 | 1235 | 69.4 | 225 | 2 | US-09-644-600-4 Sequence 4, Appli |
| 11 | 1235 | 69.4 | 224 | 2 | US-09-654-600A-4 Sequence 4, Appli |
| 12 | 1230 | 69.1 | 224 | 2 | US-08-944-483-33 Sequence 33, Appli |

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|----|--------|------|-----|---|--------------------|--------------------|
| 13 | 1215.5 | 68.3 | 225 | 1 | US-08-557-146-12 | Sequence 12, Appli |
| 14 | 1215.5 | 68.3 | 225 | 1 | US-09-154-344-12 | Sequence 12, Appli |
| 15 | 829 | 46.6 | 154 | 2 | US-09-261-416-7 | Sequence 7, Appli |
| 16 | 773 | 43.4 | 144 | 2 | US-09-618-259-4 | Sequence 4, Appli |
| 17 | 614 | 34.5 | 260 | 2 | US-09-025-059-3 | Sequence 3, Appli |
| 18 | 614 | 34.5 | 260 | 2 | US-09-618-259-8 | Sequence 8, Appli |
| 19 | 612.5 | 34.4 | 270 | 2 | US-09-949-016-7712 | Sequence 7712, Ap |
| 20 | 612.5 | 34.4 | 293 | 2 | US-09-509-908-2 | Sequence 2, Appli |
| 21 | 612.5 | 34.4 | 293 | 2 | US-09-991-181-309 | Sequence 309, App |
| 22 | 612.5 | 34.4 | 293 | 2 | US-09-990-444-309 | Sequence 309, App |
| 23 | 612.5 | 34.4 | 293 | 2 | US-09-997-333-309 | Sequence 309, App |
| 24 | 612.5 | 34.4 | 293 | 2 | US-09-992-598-309 | Sequence 309, App |
| 25 | 582.5 | 32.7 | 260 | 2 | US-09-070-526-2 | Sequence 2, Appli |
| 26 | 582.5 | 32.7 | 260 | 2 | US-09-618-259-7 | Sequence 7, Appli |
| 27 | 582.5 | 32.7 | 260 | 2 | US-09-999-833A-395 | Sequence 395, App |
| 28 | 582.5 | 32.7 | 260 | 2 | US-10-020-445A-395 | Sequence 395, App |
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| 32 | 573.5 | 32.2 | 282 | 2 | US-09-025-059-1 | Sequence 1, Appli |
| 33 | 573.5 | 32.2 | 282 | 2 | US-09-856-320A-2 | Sequence 2, Appli |
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| 35 | 571.5 | 32.1 | 250 | 2 | US-10-004-860-427 | Sequence 427, App |
| 36 | 571.5 | 32.1 | 250 | 2 | US-10-012-231A-170 | Sequence 170, App |
| 37 | 571.5 | 32.1 | 250 | 2 | US-10-015-389A-170 | Sequence 170, App |
| 38 | 571.5 | 32.1 | 250 | 2 | US-10-006-768A-170 | Sequence 170, App |
| 39 | 571.5 | 32.1 | 250 | 2 | US-10-015-671A-170 | Sequence 170, App |
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| 43 | 571.5 | 32.1 | 250 | 2 | US-10-012-064A-170 | Sequence 170, App |
| 44 | 568.5 | 31.9 | 288 | 2 | US-09-386-642-13 | Sequence 13, Appli |
| 45 | 567.5 | 31.9 | 254 | 2 | US-09-439-313-525 | Sequence 525, App |

ALIGNMENTS

RESULT 1

US-09-949-016-7716
; Sequence 7716, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7716
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7716

Alignment Scores:
Pred. No.: 2,33e-131 Length: 265
Score: 1371.00 Matches: 254
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 77.0% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-949-016-7716 (1-265)

QY

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QY 370 AATAGCCAGCCCGCTGCTCATCCATGCTGGAAGAAAGTCAAGGCTGCCCTCCGCTCGAA 429
Db 131 AsnSerGlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGlu 150
QY 430 CCCCCTGGAAACCACTGTACTGCTCGCGGTGGGGCACTACACAGCCCGCATGTGAC 489
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Db 231 ValSerTrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnVal 250
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RESULT 2

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US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hanson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-146-2

Alignment Scores:
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Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0
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QY 736 TTCAACAAAGTGAATAATGACACCATGAAAAAGCATGCG 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 3
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; US-08-824-874-3

Alignment Scores:
Pred. No.: 1.19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x US-08-824-874-3 (1-253)

QY 16 ATGGCAGATCCCTTCTCCCTGCCCCGACATCTTACTGCTATCTGCTATGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAACAGCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluIleAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTTGCTCAGTGGCAATCAGCTCCAGGAGCGCTCTGGTC 195

Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGGTGGGTGCTCACTGCGGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTCCATCCATGGTGAAGAAAGTCAAGGCTGCCCTCCCGCTCGAAGCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGCTGGGGGACCTACACAGAGCCAGATGTGACCTTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCGCCAGGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATCCATGCTGTGGCTGGCATCCCGCTCCCGCTCCAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCGAAGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATCACACCATGAAAAAGCATGCG 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 4
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egeirud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Alignment Scores:
Pred. No.: 1,19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-154-344-2 (1-253)

QY 16 ATGGCAAGATCCCTCTCTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAACCT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspGlyAlaLeuSerLeuAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGTGTCTCACTCGCGCCCACTGCAAGATGAATGAGTACACCGTGACACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGTATACGTGGCGCAGAGGAGCTCAGAGGATCAAGGCTTCGAAGTCATTCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACAGACCCATGTTATGACCTCATGCTGTGTAAGCTCAATAGC 375
DB 101 HisProGlyTyrrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGCCAGGCTGTCAATCATGTGTGAAGAAGTCAGGCTGCCCTCGCCCTGCGAACCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGCTGGGCACTTACCACGAGCCCGAGATGTGACCTTTCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGGATGTCAAGTCATCTCCCCCAGGACTGACGACGAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAAATTCATGCTGTGCTGGCATCCCGACTCCCAAGAAAACGCC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAla 200
QY 616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCCTGCAAGGTCTGGTGCC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACTTTCCTTGGCGCCACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240

QY 736 TTCACCAAGTGGATTAATGACACCACTGAAAGGATCGC 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 5
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2
Alignment Scores:
Pred. No.: 1,19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0
US-09-905-083A-30 (1-969) x US-08-930-188-2 (1-253)
QY 16 ATGGCAAGATCCCTCTCTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAACCT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspGlyAlaLeuSerLeuAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGTGTCTCACTCGCGCCCACTGCAAGATGAATGAGTACACCGTGACACCTG 255

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Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAAGTACGCTGGCGGACAGAGAGCTCAGAGGATCAAGCCCTCGAAGTCAATTCGCG 315
Db 81 GlySerAspThrLeuGlyAspArgAgaGalaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACAGACCCATGTAATGACCTCATGCTGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCAGAGCTGCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTCTCCGCTGGGCGGACCTACACAGCCAGAGCTGTGACCTTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGATGTCAGGTCATCTCCCGCCAGACTGCGACGAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuSerProGlnAspCysThrLysValTy 180
QY 556 AGGACTTACTGAAATTCATGCTGTGCTGGCGGATCCCGGATCCCGGATCCGAAAGACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATATGGTACCTGCTGCTGGCGGACCGTTGGTGTGAGAGTCTGAGCTCAATAGC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAACTTTCCCTTGGCGGACCAACCAATGACCCAGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY 736 TTCACCAAGTGAATAATGACACCATGAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 6

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US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
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; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; US-09-210-084-3
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Alignment Scores: 1.19e-130 Length: 253
Pred. No.: 1364.00 Matches: 253
Score: 1364.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0
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US-09-905-083A-30 (1-969) x US-09-210-084-3 (1-253)

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QY 16 ATGGCAAGATCCCTTCTCTGCCCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaAaGlySer 40
QY 136 CACCCATGACAGGTGGCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGACGCTGGGTGCTCACTGCGGCCCTGCAAGATGAATCAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGACAGAGAGCTCAGAGGATCAAGCCCTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAgaGalaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACAGACCCATGTAATGACCTCATGCTGCTGAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCAGAGCTGTCAATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTCGCAACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGCTCTCCGCTGGGCGACCTACCAAGAGCTGAGCTGTGACCTTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGATGTCAGGTCATCTCCCGCCAGACTGCGACGAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuSerProGlnAspCysThrLysValTy 180
QY 556 AAGGACTTACTGAAATTCATGCTGTGCTGGCGATCCCGGATCCCGGATCCGAAAGACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATATGGTACCTGCTGCTGGCGGACCGTTGGTGTGAGAGTACCTCGCAAGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAACTTTCCCTTGGCGGACCAACCAATGACCCAGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY 736 TTCACCAAGTGAATAATGACACCATGAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 7
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatsEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Alignment Scores:
Pred. No.: 1.19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-764-762-3 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCGAGATCTTACTGCTATCTCTAGCCTTGGAACCT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGCCAGAGTGCACAGATTATGATGGGCCCCCATGTCAGAGGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspIleLeuAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCTGCTGCTGAGTGCATCTCAGTCCACTGCGGAGGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 ATGAGCGTGGGTGCTACTGCGCCGCCCTGCAAGATGAATGAGTACCGTGACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

QY 256 GGCAGTGATACGCTGGCGACAGAGAGCTCAGAGGATCAAGGCTTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLeuAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTAATACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTTCATCCATGCTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACACTGTACTGTCTCCGCGCTGGGCGACTACACAGAGCCAGATGTGACCTTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGGATGTCAAGTCTATCTCCCCCAGGACTGCCAAGAGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAAAATTCATGCTGTGCGCTGGCATCCCGACTCCCAAGAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTTGCAAGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAACCTTCCCTTGGCGGCAACCAATGACACCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAGAGCATCCG 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 8
PCT-US96-04294-2
; Sequence 2, Application PC/TUS9604294
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04294
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-04294-2

Alignment Scores:
Pred. No.: 1.19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x PCT-US96-04294-2 (1-253)

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QY 16 ATGCGAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGTATCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAACAGCCAGGCTGCAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGlnAlaGlnGlyAspGlyAlaProCysAlaAspGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGTGTCTACTCGGCCCTGCAAGATGATGATGATGATGATGATGATGATG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCTATCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGCGCAGCTGTCTATCCATGTTGAAGAAAGTCAAGGCTGCCCTCCCGCTCGCAACCCCT 435
DB 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGTCTCGGCTGGGCACTTACCAGAGCCAGATGTGACCTTTCCC 495
DB 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCAGGACTGCACGAAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValThr 180
QY 556 AAGGACTTACTGAAATTCATGCTGTGCTGGCATCCCGCTCCCAAGAAACAGCC 615
DB 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGCATGCTGCTACTCAGGGGACCGTGGTGTGAGAGGTACCTGCAAGGCTGTGGTCC 675
DB 201 CysAsnGlyAspSerGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTGGCGCCCAACCAATGACCCAGAGCTTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValThrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACCAATGACCAATGACCAATGACCAATGACCAATGACCA 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 9

US-09-027-337-4

; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
; OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Alignment Scores:
Pred. No.: 1.69e-117 Length: 225
Score: 1235.00 Matches: 225
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 69.4% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-027-337-4 (1-225)

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QY 100 AAGATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCCATGGCAGGTGGCCCTGCTC 159
DB 1 LysIleIleAspGlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuLeu 20
QY 160 AGTGGCAATCAGCTCCACTCGCGAGCGCTCCTGCTCAATGAGCGCTGGGTGCTCAGTCC 219
DB 21 SerGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrpValLeuThrAla 40
QY 220 GCCACTGCAAGATGAATGAGTACACCGTGCACCTGGCGAGTGAATACGCTGGCGCAGG 279
DB 41 AlaHisCysLysMetAsnGluTrpValHisLeuGlySerAspThrLeuGlyAspArg 60
QY 280 AAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGGCCACCCCGCTACTCCACAGACCC 339
DB 61 ArgAlaGlnArgIleLysAlaSerLysSerPheArgHisProGlyTrpSerThrGlnThr 80
QY 340 CATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGGCTGTCTCATCTCGTGTG 399
DB 81 HisValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerMetVal 100
QY 400 AGAAAGTCAGGCTGCCCTCCCGCTCGGAAACCCCTGGAAACCCCTGTACTGTCTCCGGC 459
DB 101 LysLysValArgLeuProSerArgCysGluProGlyThrThrCysThrValSerGly 120
QY 460 TGGGGCACTACCAAGAGCCAGATGTGACCTTTCCCTCTGACCTCATGTGCTGGTGGATGTC 519
DB 121 TrpGlyThrThrSerProAspValThrPheProSerAspLeuMetCysValAspVal 140
QY 520 AAGCTCATCTCCCCCAGGACTGCACGAGGTTTACAAGGACTTACTTGGAAATTTCCATG 579
DB 141 LysLeuIleSerProGlnAspCysThrLysValTrpLysAspLeuLeuGlnAsnSerMet 160
QY 580 CTGTGGCTGGCACTCCCGCACTCCAAAGAAAAACCCCTGCAATGGTGAATCAGGCGGCG 639
DB 161 LeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyPro 180
QY 640 TTGGTGTGAGAGGTACCTGCAAGGCTGTGGTGTCTCTGGGAACTTCCCTTCGCGGCGCAA 699
DB 181 LeuValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGln 200
QY 700 CCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACCC 759
DB 201 ProAsnAspProGlyValThrThrGlnValCysLysPheThrLysTrpIleAsnAspThr 220
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Qy      760  ATGAAAGCATCGC 774
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Db      221  MetLysLysHisArg 225

RESULT 10
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4

Alignment Scores:
Pred. No.: 1,69e-117 Length: 225
Score: 1235.00 MatChes: 225
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 69.4% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-644-600-4 (1-225)

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QY 460 TGGGGCACTACACGAGCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTC 519
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QY 520 AAGCTCATCTCCCCCAGGACTCGACGAAAGTTTACAAGGACTTACTGGAAATTCATG 579
Db 141 LysLeuIleSerProGlnAspCysThrLysValThrLysAspLeuLeuGluAsnSerMet 160
QY 580 CTGTGCGCTGGCACTCCCGCACTCCAAAGAAAGCCCTGCAATGGTGACTCAGGGGACCG 639
Db 161 LeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyPro 180
QY 640 TTGGTGTGACAGAGTACCTGCAAGTCTGGTGTCTCTGGGAACTTTCCCTTGGCGCCAA 699
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QY 700 CCCAATGACCCAGGACTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATTAATGACACC 759
Db 201 ProAsnAspProGlyValThrThrGlnValCysLysPheThrLysTrpIleAsnAspThr 220
QY 760 ATGAAAAGCATCGC 774
Db 221 MetLysLysHisArg 225

RESULT 12
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Alignment Scores:
Pred. No.: 5,48e-117 Length: 224
Score: 1230.00 Matches: 224
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 69.1% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-08-944-483-33 (1-224)
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Db 1 IleIleAspGlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuSer 20
QY 163 GGCATTCAGCTCCACTGCGAGGCGTCTGGTCAATGAGCGCTGGGTGCTCAGTCCGCGCC 222
Db 21 GlyAsnGlnLeuHisCysGlyValLeuValAsnGluArgTrpValLeuThrAlaAla 40
QY 223 CACTGCAAGATGAATGAGTACACCGGTGACCTGGGCGAGTGATACGCTGGCGCAGAGAGA 282
Db 41 HisCysLysMetAsnGluTyrThrValHisLeuGlySerAspThrLeuGlyAspArg 60
QY 283 GCTCAGAGGATCAAGGCTCGAAGTCATTCGCGCACCCCGGCTACTCCACACAGACCCAT 342
Db 61 AlaGlnArgIleLysAlaSerLysSerPheArgHisProGlyTyrSerThrGlnThrHis 80
QY 343 GTTAATGACCTCATGCTCGTGAAGTCAATAGCAGCGCAGGCTGCATCATGGTGAAG 402
Db 81 ValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLys 100
QY 403 AAAGTCAGGCTGCCCTCCGCTCGGAAACCCCTGGAAACCACTGTACTGTCTCGGCTGG 462
Db 101 LysValArgLeuProSerArgCysGluProGlyThrThrCysThrValSerGlyTrp 120
QY 463 GGCACCTACCACAGCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAG 522
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QY 523 CTCATCTCCCCCAGGACTCGACGAAAGTTTACAAGACTTACTGAAAATTCATGCTG 582
Db 141 LeuIleSerProGlnAspCysThrLysValTyrLysAspLeuLeuGluAsnSerMetLeu 160
QY 583 TGGGCTGGCATCCCCGACTCCAGAAAAAGCGCTGCAATGCTGACTCAGGGGACCGTTG 642
Db 161 CysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeu 180
QY 643 GTGTGACAGAGTACCTCGAAGTCTGGTGTCTCTGGGAACTTCTCCCTTGGCGCCAAACC 702
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QY 763 AAAAGCATCGC 774
Db 221 LysLysHisArg 224

RESULT 13
US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
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/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
/
/ US-08-557-146-12
/
/ Alignment Scores:
/ Pred. No.: 1,666-115 Length: 225
/ Score: 1215.50 Matches: 223
/ Percent Similarity: 99.6% Conservative: 1
/ Best Local Similarity: 99.1% Mismatches: 0
/ Query Match: 68.3% Indels: 1
/ DB: 1 Gaps: 1
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/ US-09-905-083A-30 (1-969) x US-08-557-146-12 (1-225)
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/ Db 1 LLeleAspGlyAlaProCysAlaArgGlySerHisProTrrpGlnValAlaLeuSer 20
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/ QY 163 GCAATCAGTC---CACTGCGAGAGCGTCTGGTCAATGAGCGTGGGTCTCACTGCC 219
/ Db 21 GlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrrpValLeuThrAla 40
/
/ QY 220 GCCCACTGCAAGTGAATGATGATACACCGTGCACCTGGCGAGTGATACGCTGGCGACAGG 279
/ Db 41 AlaHisCysLeuMetAsnGluTrrpValHisLeuValAsnGluArgTrrpValLeuGlyAspArg 60
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/ QY 280 AGAGCTCAGAGATCAAGCGCTCGAAGTCATTCCCGCACCCCGGCTACTCCACACAGACC 339
/ Db 61 ArgAlaGlnArgLleLeuYsAlaSerYsSerPheArgHisProGlyTrrpSerThrGlnThr 80
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/ QY 340 CATGTTAATGACTCATGCTCGTGAAGTCAATAGCCAGCGCAGGCTGTCATCCATGGTG 399
/ Db 81 HisValAsnAspLeuMetLeuValYsLeuAsnSerGlnAlaArgLeuSerMetVal 100
/
/ QY 400 AGAAGTCAGCTGCCCTCCGCTCGGACCCCTGGACCCCTGGAACCACTGTACTCTCCGCG 459
/ Db 101 LysYsValArgLeuProSerArgCysGluProProGlyThrCysThrValSerGly 120
/
/ QY 460 TGGGGCACTACACAGCCAGATGAGCTTTCCCTCTGACTCATGTCGCTGGATGTC 519
/ Db 121 TrpGlyThrThrSerProAspValThrPheProSerAspLeuMetCysValAspVal 140
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/ QY 520 AAGCTCATCTCCCCCAGAGCTGCACGAAGTTTACAAGACTTACTGGAAATTCATG 579
/ Db 141 LysLeuIleSerProGlnAspCysThrGluValTyrYsAspLeuLeuGluAsnSerMet 160
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/ QY 580 CTGTGCGTGGCATCCCGACTCCAGAAACCGCTGCAATGGTGACTCAGGGGACCG 639
/ Db 161 LeuCysAlaGlyIleProAspSerYsYsAsnAlaCysAsnGlyAspSerGlyGlyPro 180
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/ QY 640 TTGGTGTGCAGAGGTACCCCTGCAAGGTCTGGTGTCTCTGGGAACTTTCCCTTTCGCGCCAA 699
/ Db 181 LeuValCysArgGlyThrLeuGlnGlyLeuValSerTrrpGlyThrPheProCysGlyGln 200
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/ QY 700 CCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCCACCAAGTGGATAATGACACC 759
/ Db 201 ProAsnAspProGlyValTrrpGlnValCysYsPheThrLysTrrpIleAsnAspThr 220
/
/ QY 760 ATGAAAAAGCATCGC 774
/ Db 221 MetLysLysHisArg 225
/
/ RESULT 14
/ US-09-154-344-12
/ Sequence 12, Application US/09154344
/ Patent No 5981256
/ GENERAL INFORMATION:
/ APPLICANT: Egelrud, Torbjorn
/ APPLICANT: Hansson, Lennart
/ TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
/ TITLE OF INVENTION: Enzyme (SCCE)
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/154,344
/ FILING DATE: 16-SEP-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
/
/ US-09-154-344-12
/
/ Alignment Scores:
/ Pred. No.: 1,666-115 Length: 225
/ Score: 1215.50 Matches: 223
/ Percent Similarity: 99.6% Conservative: 1
/ Best Local Similarity: 99.1% Mismatches: 0
/ Query Match: 68.3% Indels: 1
/ DB: 1 Gaps: 1
/
/ US-09-905-083A-30 (1-969) x US-09-154-344-12 (1-225)
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Db 1 IleileAspGlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuLeuSer 20
QY 163 GGCAATCAGCTC---CACTCGGAGGCGTCTGTGTCATGAGCGCTGGGTGCTCACTGCC 219
Db 21 GlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrpValLeuThrAla 40
QY 220 GCCCACTGCAAGATGAATAGTACACCGTCACCTGGCGAGTGATACGCTGGCGCAGAG 279
Db 41 AlaHisCysIysMetAsnGluTyThrValHisLeuGlySerAspThrLeuGlyAspArg 60
QY 280 AGAGCTCAGAGGATCAAGGCTCGAGTCAATTCGGCACCCCGCTACTTCCACACAGCC 339
Db 61 ArgAlaGlnArgIleIysAlaSerLysSerPheArgHisProGlyTyThrSerThrGlnThr 80
QY 340 CATGTTAATACCTCATGCTCGTGAAGCTCAATAGCCAGGCTGTCTATCCATGGTG 399
Db 81 HisValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetVal 100
QY 400 AAGAAAGTCAGGTGCGCTCCCGCTGCGAACCCCTGGAAACCACTGTACTGTCTCCGGC 459
Db 101 LysLysValArgLeuProSerArgCysGluProProGlyThrThrCysThrValSerGly 120
QY 460 TGGGGCACTACACAGAGCCAGATGTGACCTTTCCTCTGACCTCATGTCGCTGGATGTC 519
Db 121 TrpGlyThrThrSerProAspValThrPheProSerAspLeuMetCysValAspVal 140
QY 520 AAGCTCATCTCCCCCAGGACTCAGAGAGTTTACAGGACTTACTTGGAAATTCCTCATG 579
Db 141 LysLeuIleSerProGlnAspCysThrGluValTyrlsAspLeuLeuGluAsnSerMet 160
QY 580 CTGTGCGTGGCATCCCGCACTCCAGAAACCGCTTGCATATGGTGACTCAGGGGGACCG 639
Db 161 LeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyPro 180
QY 640 TTGGTGTGACAGGTACCCCTGCAAGTCTGCTGCTCTGCGGAACTTTCCTTCCGCGCAA 699
Db 181 LeuValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGln 200
QY 700 CCCAATGACCAGGAGTCTACACTCAAGTGTGCAAGTTACCAAGTGGATATATGACACC 759
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QY 760 ATGAAAAAGCATCGC 774
Db 221 MetLysLysHisArg 225
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RESULT 15
US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: Chymotryptic enzyme (Scce) homologous to similar
; OTHER INFORMATION: domain in TADG-12
US-09-261-416-7
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Alignment Scores: 4.24e-76 Length: 154
Pred. No.:

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Score: 829.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 46.6% Indels: 0
DB: 2 Gaps: 0
US-09-905-083A-30 (1-969) x US-09-261-416-7 (1-154)
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QY 238 GAGTACACCGTGCACCTGGCGAGTGATACGCTGGCGCAGGAGAGCTCAGAGGATCAAG 297
Db 21 GluTyThrValHisLeuGlySerAspThrLeuGlyAspArgAlaGlnArgIleLys 40
QY 298 GCCTCGAAGTCATTCCCGCACCCCGCTACTCCACACAGACCCCATGTTAATGACCTCATG 357
Db 41 AlaSerLysSerPheArgHisProGlyTyThrSerThrGlnThrHisValAsnAspLeuMet 60
QY 358 CTCGTCAAGCTCAATAGCCAGGCTGTCTATCCATGGTGAAAGTCAAGTCACTCCCCCCC 417
Db 61 LeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArgLeuPro 80
QY 418 TCCCGCTGCGAACCCCTGGAACCACTGTACTGTCTCCGGCTGGGGCACTACACAGAGC 477
Db 81 SerArgCysGluProProGlyThrThrCysThrValSerGlyTrpGlyThrThrSer 100
QY 478 CCAGATGTGACCTTTCCCTCTGACCTCATGTCGCTGGATGTCAGGCTCATCTCCCCCAG 537
Db 101 ProAspValThrPheProSerAspLeuMetCysValAspValLysLeuIleSerProGln 120
QY 538 GACTGCACGAAGGTTTACAAAGGACTTACTTGGAAAATTCATGTGCTGCGCTGGCATCCCC 597
Db 121 AspCysThrLysValTyrlsAspLeuLeuGluAsnSerMetLeuCysAlaGlyIlePro 140
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Job time : 48.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: March 11, 2006, 02:13:49 ; Search time 35.4 Seconds
(without alignments)
2287.439 Million cell updates/sec

Title: US-09-905-083A-30

Perfect score: 1780

Sequence: 1 ggaattccgggtccatggc.....aagaacacacaaacccctcag 969

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abes/ABSSWEB.spool/US0905083/runat.10032006.152504.29930/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US0905083 @CCN 1.1 307 @runat.10032006.152504.29930 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA Main.*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pcp.*
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- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1364 | 76.6 | 253 | 3 | US-09-888-615-98 |
| 2 | 1364 | 76.6 | 253 | 3 | US-09-764-762-3 |
| 3 | 1364 | 76.6 | 253 | 4 | US-10-071-214-2 |
| 4 | 1364 | 76.6 | 253 | 4 | US-10-071-214-48 |
| 5 | 1364 | 76.6 | 253 | 4 | US-10-264-283-90 |
| 6 | 1364 | 76.6 | 253 | 4 | US-10-295-027-498 |
| 7 | 1364 | 76.6 | 253 | 4 | US-10-173-999-48 |
| 8 | 1364 | 76.6 | 253 | 4 | US-10-408-765A-639 |
| 9 | 1364 | 76.6 | 253 | 5 | US-10-643-795A-95 |
| 10 | 1364 | 76.6 | 253 | 5 | US-10-948-518-95 |
| 11 | 1364 | 76.6 | 253 | 5 | US-10-868-490A-1 |

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| 12 | 1350 | 75.8 | 250 | 4 | US-10-262-511-92 | Sequence 92, Appl |
| 13 | 1337 | 75.1 | 257 | 4 | US-10-344-394-38 | Sequence 38, Appl |
| 14 | 1252 | 70.3 | 247 | 4 | US-10-262-511-102 | Sequence 102, App |
| 15 | 1252 | 70.3 | 252 | 4 | US-10-262-511-94 | Sequence 94, Appl |
| 16 | 1235 | 69.4 | 225 | 4 | US-10-600-187-4 | Sequence 4, Appli |
| 17 | 1230 | 69.1 | 224 | 3 | US-09-789-210-33 | Sequence 33, Appl |
| 18 | 1119 | 62.9 | 224 | 4 | US-10-262-511-104 | Sequence 104, App |
| 19 | 1085.5 | 61.0 | 249 | 4 | US-10-071-214-47 | Sequence 47, Appl |
| 20 | 1035.5 | 58.2 | 198 | 4 | US-10-262-511-96 | Sequence 96, Appl |
| 21 | 1011.5 | 56.8 | 249 | 4 | US-10-071-214-50 | Sequence 50, Appl |
| 22 | 996.5 | 56.0 | 243 | 4 | US-10-071-214-46 | Sequence 46, Appl |
| 23 | 940.5 | 52.8 | 226 | 4 | US-10-071-214-49 | Sequence 49, Appl |
| 24 | 937.5 | 52.7 | 181 | 4 | US-10-262-511-98 | Sequence 98, Appl |
| 25 | 773 | 43.4 | 144 | 3 | US-09-796-294-4 | Sequence 4, Appli |
| 26 | 773 | 43.4 | 144 | 4 | US-10-461-787-4 | Sequence 4, Appli |
| 27 | 641.5 | 36.0 | 136 | 5 | US-10-450-763-53737 | Sequence 53737, A |
| 28 | 614 | 34.5 | 260 | 3 | US-09-796-294-8 | Sequence 8, Appli |
| 29 | 614 | 34.5 | 260 | 4 | US-10-461-787-8 | Sequence 8, Appli |
| 30 | 614 | 34.5 | 260 | 4 | US-10-072-012-609 | Sequence 609, App |
| 31 | 612.5 | 34.4 | 293 | 3 | US-09-739-907-82 | Sequence 82, Appl |
| 32 | 612.5 | 34.4 | 293 | 3 | US-09-739-907-97 | Sequence 97, Appl |
| 33 | 612.5 | 34.4 | 293 | 3 | US-09-989-722-309 | Sequence 309, App |
| 34 | 612.5 | 34.4 | 293 | 3 | US-09-989-723-309 | Sequence 309, App |
| 35 | 612.5 | 34.4 | 293 | 3 | US-09-989-279-309 | Sequence 309, App |
| 36 | 612.5 | 34.4 | 293 | 3 | US-09-989-727-309 | Sequence 309, App |
| 37 | 612.5 | 34.4 | 293 | 3 | US-09-989-731-309 | Sequence 309, App |
| 38 | 612.5 | 34.4 | 293 | 3 | US-09-989-732-309 | Sequence 309, App |
| 39 | 612.5 | 34.4 | 293 | 3 | US-09-991-073-309 | Sequence 309, App |
| 40 | 612.5 | 34.4 | 293 | 3 | US-09-990-442-309 | Sequence 309, App |
| 41 | 612.5 | 34.4 | 293 | 3 | US-09-991-163-309 | Sequence 309, App |
| 42 | 612.5 | 34.4 | 293 | 3 | US-09-993-604-309 | Sequence 309, App |
| 43 | 612.5 | 34.4 | 293 | 3 | US-09-990-456-309 | Sequence 309, App |
| 44 | 612.5 | 34.4 | 293 | 3 | US-09-989-721-309 | Sequence 309, App |
| 45 | 612.5 | 34.4 | 293 | 3 | US-09-992-598-309 | Sequence 309, App |

ALIGNMENTS

RESULT 1
US-09-888-615-98
; Sequence 98, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

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| Pred. No.: | 1.26e-118 | Length: | 253 |
| Score: | 1364.00 | Matches: | 253 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 76.6% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-09-905-083A-30 (1-969) x US-09-888-615-98 (1-253)

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Db 21 AlaGlyGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
QY 136 CACCCATGCGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
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Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrValHisLeu 80
QY 256 GGCAGTGATGCTGCGGCGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315
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QY 316 CACCCCGGCTACTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375
Db 101 HisProGlyTyrsThrValSerGlyTrpGlyThrThrHisValAsnAspLeuMetLeuVal 120
QY 376 CAGCCAGGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
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Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrHisValAsnAspLeuMetLeuVal 160
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Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAAATTTCCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
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RESULT 2

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US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764, 762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
Alignment Scores:
Pred. No.: 1,266-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 3 Gaps: 0
US-09-905-083A-30 (1-969) x US-09-764-762-3 (1-253)
QY 16 ATGGCAAGATCCCTCTCTCTGCGCCCTGCAGATCTTACTGTCTCTTAGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
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QY 136 CACCCATGCGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGACGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrValHisLeu 80
QY 256 GGCAGTGATGCTGCGGCGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315
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Db 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
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QY 736 TTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
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RESULT 3
US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-071-214-2 (1-253)
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Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGAGTACAGATTTATTGATGGCGCCCTGTCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTCTCTCAGTGGCAATCAGCTCCACTGCGGAGCGTCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 ATGAGCGTGGTGTCTACTGCGCCGCTCAGCAATGATGATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGATACGTGGCGGACAGGAGCTCAGAGGATCAAGCCCTGCAAGTCAATTCGCG 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACACAGACCCATGTTATGACTCATGCTCGTGAAGTCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCGAAACCCCT 435
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Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
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Db 141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACTCATGTGCTGGATGTCAGGTCATCTCCCTCCAGGACTGTCACAGAGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTTCCATGCTGTGCTGGCATCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAenSerMetLeuCyAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGAGTGTGACTCAGGGGACCGTGTGGTGTGCAGAGGTACCTTGCAGAGGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTCCCTTGGCGGCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGGAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 4
US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-071-214-48 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTCGCCCTGCAGATCTTACTGTATCTCTTAGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGAGTACAGATTTATTGATGGCGCCCTGTCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCCGGTACTCCACACAGACCCATGTTATGACTCATGCTCGTGAAGTCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
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Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyGlyValLeuVal 60
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Db 61 AenGluAArgTrpValLeuThrAlaAlaHisCysLysMetAenGluTrpValHisLeu 80
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Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAenAspLeuMetLeuValLysLeuAenSer 120
QY 376 CAGGCCAGGCTGTCATCCATGTTGAAGAAAGTCAGAGCTCAAGGCCCTCGAAGTCATTCCGC 435
Db 121 GlnAlaAArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
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Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGCTGGATGTCAGCTCATCTCCCCCGAGGATGTCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTCATGCTGTGGCTGGCATCCCGACTCCGAAAGAAACGCC 615
Db 181 LysAspLeuLeuGluAenSerMetLeuCysAlaGlyIleProAspSerLysLysAenAla 200
QY 616 TGCATGTGTGACTCAGGGGACCGTGTGTGTGCAGAGGTACCTCGCAAGGTCTGGTCC 675
Db 201 CysAenGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAenAspProGlyValTyrThrGlnValCysLys 240
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Db 241 PheThrLysTrpIleAenAspThrMetLysLysHisArg 253

RESULT 5

US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US2003014494A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-264-283-90 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTCGCCCTGCAGATCTTACTGCTATCTTAGCCCTTGGAACACT 75

Db 1 MetAlaAArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGAGAGAAGACCCAGGCTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATCGCAGTGGCGCTCTGCTCAGTGCATCAGCTCCACTGCGGAGCGCTCCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGACGCTGGGTCTCTACTCGCCGCCCACTGCAAGATGAATGAGTACACCGTGACCTG 255
Db 61 AenGluAArgTrpValLeuThrAlaAlaHisCysLysMetAenGluTrpValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCACAGGAGCTCAGAGGATCAAGGCCCTCGAAGTCATTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAenAspLeuMetLeuValLysLeuAenSer 120
QY 376 CAGGCCAGGCTGTCATCCATGTTGAAGAAAGTCAGAGCTCAAGGCCCTCGAAGTCATTCCGC 435
Db 121 GlnAlaAArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTCTCCGCTGGGCACCTACCACAGGCCAGATGTGACCTTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGCTGGATGTCAGCTCATCTCCCCCGAGGATGTCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTCATGCTGTGGCTGGCATCCCGACTCCGAAAGAAACGCC 615
Db 181 LysAspLeuLeuGluAenSerMetLeuCysAlaGlyIleProAspSerLysLysAenAla 200
QY 616 TGCATGTGTGACTCAGGGGACCGTGTGTGTGCAGAGGTACCTCGCAAGGTCTGGTCC 675
Db 201 CysAenGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAenAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGATAAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAenAspThrMetLysLysHisArg 253

RESULT 6

US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15

;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/335,394
;; PRIOR FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: US 60/332,464
;; PRIOR FILING DATE: 2001-11-21
;; PRIOR APPLICATION NUMBER: US 60/334,393
;; PRIOR FILING DATE: 2001-11-29
;; PRIOR APPLICATION NUMBER: US 60/340,376
;; PRIOR FILING DATE: 2001-12-14
;; PRIOR APPLICATION NUMBER: US 60/347,211
;; PRIOR FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 60/347,349
;; PRIOR FILING DATE: 2002-01-10
;; PRIOR APPLICATION NUMBER: US 60/355,250
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US 60/356,714
;; PRIOR FILING DATE: 2002-02-13
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1386
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 498
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-295-027-498

Alignment Scores:
Pred. No.: 1,266-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-295-027-498 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAGAGAGCCAGGGTGACAGATATTATGATGGCGCCCATGTGCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleileAspGlyAlaProCysAlaArgGlySer 40

QY 136 CACCCATGCGAGTGGCCCTCTCTGCTGCAATCAGCTCCAGTCCGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60

QY 196 AATGAGCGTGGTGCTCACTGCGCCCTGCAGATGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrValHisLeu 80

QY 256 GCGAGTGATACCTGGCGGACAGAGAGCTCAGAGATCAAGGCTCGAGTATTCCTCCG 315
Db 81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100

QY 316 CACCCCGGTACTCCACACAGACCCATGTTAAGACTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120

QY 376 CAGGCCAGGTGTTCATCCATGGTGAAGAAAGTCAAGCTGCCCTCCCGCTCGCAACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysValLysValArgLeuProSerArgCysGluProPro 140

QY 436 GGNACACCTGTACTGCTCCGCTGGGCGACTACACAGGCCACAGATGACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160

QY 496 TCTGACTCATGTGCGTGGATGTCAGGCTCATCTCCCGCCAGGACTGCAGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValThr 180

QY 556 AAGGACTTACTGGAAAATTCCATGCTGTGGCTGGCATCCCCGACTCCCAAGAAAAGGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200

QY 616 TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCCTGCAAGGTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220

QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTTACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValThrGlnValCysLys 240

QY 736 TTCACCAAGTGGATAAATGACACCAATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 7
US-10-173-999-48
;; Sequence 48, Application US/10173999
;; Publication No. US2004000563A1
;; GENERAL INFORMATION:
;; APPLICANT: Mack, David H.
;; APPLICANT: Gish, Kurt C.
;; APPLICANT: Ros Biotechnology, Inc.
;; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
;; TITLE OF INVENTION: Cancer
;; FILE REFERENCE: 018501-002420US
;; CURRENT APPLICATION NUMBER: US/10/173,999
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: US 60/299,234
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: US 60/315,287
;; PRIOR FILING DATE: 2001-08-27
;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/372,246
;; PRIOR FILING DATE: 2001-04-12
;; NUMBER OF SEQ ID NOS: 163
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 48
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-173-999-48

Alignment Scores:
Pred. No.: 1,266-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-173-999-48 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAGAGAGCCAGGGTGACAGATATTATGATGGCGCCCATGTGCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleileAspGlyAlaProCysAlaArgGlySer 40

QY 136 CACCCATGCGAGTGGCCCTCTCTGCTGCAATCAGCTCCAGTCCGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60

QY 196 AATGAGCGTGGTGCTCACTGCGCCCTGCAGATGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrValHisLeu 80

QY 256 GCGAGTGATACCTGGCGGACAGAGAGCTCAGAGATCAAGGCTCGAGTATTCCTCCG 315

| | | |
|-----|---|-----|
| 81 | GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg | 100 |
| 316 | CACCCGGCTACTCACACAGACCCCATGTTAATGACCTCATCTCGTGAAGCTCAATAGC | 375 |
| 101 | HisProGlyTyrSerThrGlnThrHisValIleAspLeuMetLeuValLysLeuAsnSer | 120 |
| 376 | CAGCCAGGCTGTTCATCATGGTGAAGAAAGTCAGGCTGCCTCCCGCTGCGAACCCCTC | 435 |
| 121 | GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro | 140 |
| 436 | GGACCACTGTACTGTCTCCGGCTGGGGCACTACCAGAGCCAGATGTGACCTTTCCTC | 495 |
| 141 | GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro | 160 |
| 496 | TCTGACCTCATGTGCGTGGATGTCAAGTCTATCTCCCCCAGGATGCACGAAAGGTTTAC | 555 |
| 161 | SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr | 180 |
| 556 | AAGGACTTACTGGAAAAATTCATGTGTGCGCTGGCATCCCGCATCTCCAAGAAAAACGCC | 615 |
| 181 | LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla | 200 |
| 616 | TGCAATGTGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCTCCAGGTCGTGGTCC | 675 |
| 201 | CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer | 220 |
| 676 | TGGGGAACTTTTCCCTTGGGGCCAAACCAATGACCCAGAGGTCTACACTCAAGTGTGCAAG | 735 |
| 221 | TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys | 240 |
| 736 | TTCAACCAAGTCGATAAATGACACCATGAAAAAGCATCGC | 774 |
| 241 | PheThrLysTrpIleAsnAspThrMetLysLysHisArg | 253 |

RESULT 8

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US-10-408-765A-639
? Sequence 639, Application US/10408765A
? Publication No. US20040101874A1
? GENERAL INFORMATION:
? APPLICANT: Ghosh, Soumitra S.
? APPLICANT: Fahy, Eoin D.
? APPLICANT: Zhang, Bing
? APPLICANT: Gibson, Bradford W.
? APPLICANT: Taylor, Steven W.
? APPLICANT: Glenn, Gary W.
? APPLICANT: Watrock, Dale E.
? TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
? FILE NO OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
? FILE REFERENCE: 660088.465
? CURRENT APPLICATION NUMBER: US/10/408,765A
? CURRENT FILING DATE: 2003-04-04
? NUMBER OF SEQ ID NOS: 3077
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 639
? LENGTH: 253
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-408-765A-639

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| | | |
|------------------------|---------------|-----|
| Alignment Scores: | | |
| Pred. No.: | 1,266-118 | 253 |
| Score: | 1364.00 | 253 |
| Percent Similarity: | 100.0% | 0 |
| Best Local Similarity: | 100.0% | 0 |
| Query Match: | 76.6% | 0 |
| DB: | 4 | 0 |
| | Length: | |
| | Matches: | |
| | Conservative: | |
| | Mismatches: | |
| | Indels: | |
| | Gaps: | |

US-09-905-083A-30 (1-969) x US-10-408-765A-639 (1-253)

| QY | 16 | ATGGAAGATCCCTCTCCTGCCCTGCAGATCTTACTGCTATCCTTAGCCCTTGGAAACT | 75 |
|----|----|--|----|
| Dp | 1 | MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr | 20 |

| | | | |
|--|-----|--|-----|
| QY | 76 | GCAGAGAGAAAGCCCGGGTGCACAGATTATTGATGGCGGCCCATATGTGCACAGAGGCTCC | 136 |
| Db | 21 | AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaIaArgGlySer | 40 |
| QY | 136 | CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGCTCCTGGTGC | 195 |
| Db | 41 | HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal | 60 |
| QY | 196 | AATGAGCGCTGGGTGCTCACTGCCGCCCACTGCCAAGATGAATGATACACCTGCACCTG | 255 |
| Db | 61 | AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyThrValHisLeu | 80 |
| QY | 256 | GGCAGTGATAGCTGGCGGACAGAGAGCTCAGAGGATCAGGCGCTCGAAGTCATTCCGC | 315 |
| Db | 81 | GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg | 100 |
| QY | 316 | CACCCCGGCTACTCCACACAGACCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC | 375 |
| Db | 101 | HisProGlyTyThrThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer | 120 |
| QY | 376 | CAGCCGAGGCTGTCATCATCGTGAAGAAATCAGGCTGCCTCCCGCTGCGAAACCCCT | 435 |
| Db | 121 | GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysgluProPro | 140 |
| QY | 436 | GGAAACCCTGTACTGTCTCCGGCTGGCGCACTACCAGAGCCCAAGATGTGACCTTTCC | 495 |
| Db | 141 | GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro | 160 |
| QY | 496 | TCTGACCTCATGTGGTGGATGTCAAGCTCATCTCCCCCAAGGACTGCACGAAGTTTAC | 555 |
| Db | 161 | SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTy | 180 |
| QY | 556 | AAGCACTTACTGGAATAATTCATGCTGTGCGCTGGCATCCCGACTCCAAAGAAAAACGCC | 615 |
| Db | 181 | LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla | 200 |
| QY | 616 | TGCAATGGTGACTCAGGGGACCGTGGTGTGCAGAGGTACCTCCAGGCTCTGGTGTC | 675 |
| Db | 201 | CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer | 220 |
| QY | 676 | TGGGGAACTTTCCCTTGGCGGCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG | 735 |
| Db | 221 | TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys | 240 |
| QY | 736 | TTCAACCAAGTGGATAAATGACACCATGAAAAAGCATCGC | 774 |
| Db | 241 | PheThrLysTrpIleAsnAspThrMetLysLysHisArg | 253 |
| RESULT 9 | | | |
| US-10-643-795A-95 | | | |
| ; Sequence 95, Application US/10643795A | | | |
| ; Publication No. US20040241703A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: FREDERIC J. DESAUVAGE | | | |
| ; APPLICANT: GRETCHEN PRANTZ | | | |
| ; APPLICANT: KENNETH J. HILLAN | | | |
| ; APPLICANT: PAUL POLAKIS | | | |
| ; APPLICANT: ANDREW POLSON | | | |
| ; APPLICANT: VICTORIA SMITH | | | |
| ; APPLICANT: SUSAN D. SPENCER | | | |
| ; APPLICANT: THOMAS D. WU | | | |
| ; APPLICANT: ZEMIN ZHANG | | | |
| ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND | | | |
| ; TITLE OF INVENTION: TREATMENT OF TUMOR | | | |
| ; FILE REFERENCE: P5026R1-US | | | |
| ; CURRENT APPLICATION NUMBER: US/10/643,795A | | | |
| ; CURRENT FILING DATE: 2003-08-19 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/404,809 | | | |
| ; PRIOR FILING DATE: 2002-08-19 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/405,645 | | | |
| ; PRIOR FILING DATE: 2002-08-21 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/413,192 | | | |

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; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-643-795A-95

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-643-795A-95 (1-253)
QY 16 ATGCGAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCTTAGCCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGACCCAGGGTGACAGATTATTGATGGCCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGlnAlaGlnGlyAspIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGCGCCCTGCTCAGTGGCAATCAGCTCCACTGCGAGGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGTGGTGTCTACTGCGGCCCTGCAAGATGAATGATGACACCGTGCACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLeuMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLeuAlaSerIleSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValValLeuAsnSer 120
QY 376 CAGGCGAGGCTGTCATCCATGCTGAGAGAAAGTCAAGGCTGCCCTCCGCTCGAAGCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValValLeuValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGTCCTCGCTGGGCGACTACACAGAGCCAGATGTGACCTTCCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCAGGAGTGCACGAAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValValLeuLeuSerProGlnAspCysThrIleValTyr 180
QY 556 AAGGACTTACTGGAAATTCATGCTGTGGCTGGGATCCCGCTCCAGTCCCAAGAAACGCC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerIleLysAsnAla 200
QY 616 TGCATGCTGACTCAGGGGACCGTGGTGTGAGAGGTACCTGCAAGGCTCTGGTGTCC 675
DB 201 CysAsnGlyAspSerGlyIleProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACCATGAAAAAGCATCGC 774
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Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 10
US-10-948-518-95
; Sequence 95, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN PRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-948-518-95

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-948-518-95 (1-253)
QY 16 ATGCGAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCTTAGCCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGACCCAGGGTGACAGATTATTGATGGCGGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGlnAlaGlnGlyAspIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGCGCCCTGCTCAGTGGCAATCAGCTCCACTGCGAGGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGTGGTGTCTACTGCGGCCCTGCAAGATGAATGATGACACCGTGCACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLeuMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLeuAlaSerIleSerPheArg 100
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QY 316 CACCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTATCCATGTTGTAAGAAGTACAGGCTGCCCTCCCGCTGCGAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTCTCCGGCTGGGCACCTACCACGAGCCAGATGTGACCTTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATTCCATGTGTGCTGGCATCCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAla 200
QY 616 TGCMAATGCTGACTCAGGGGACGTTGTTGTCAGAGGTACCTCTCAAGTCTGGTGCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTTCGCGCCCAACCAATGACCCAGAGGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 11
US-10-868-490A-1
; Sequence 1, Application US/10868490A
; Publication No. US20050106586A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios
; TITLE OF INVENTION: Detection of Neurodegenerative Diseases
; FILE REFERENCE: 11757.96USU1
; CURRENT APPLICATION NUMBER: US/10/868,490A
; PRIOR FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,486
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-490A-1

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-868-490A-1 (1-253)

QY 16 ATGGGAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTCTAGCCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAAGCCAGAGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCCCTGTCTAGTGGCAATAGCTCCACTGCGAGGCGCTCTGGTTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
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QY 196 AATGAGCGCTGGGTGCTCACTGCCCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaIleHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGTATACGCTGGCGACAGAGAGCTCAGAGATCAAGGCTTCGAAGTCATTTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTATCCATGTTGTAAGAAGTACAGGCTGCCCTCCCGCTGCGAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTCTCTCCGGCTGGGCACCTACCACGAGCCAGATGTGACCTTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATTCCATGTGTGCTGGCATCCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAla 200
QY 616 TGCMAATGCTGACTCAGGGGACGTTGTTGTCAGAGGTACCTCTCAAGTCTGGTGCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTTCGCGCCCAACCAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 12
US-10-262-511-92
; Sequence 92, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
```



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QY 241 TACACGCTGCACCTGGCGAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGGCC 300
Db |||||||
81 TyrThrValHisLeuGlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAla 100
QY 301 TCGAAGTCAATCCGCCACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTC 360
Db |||||||
101 SerLysSerPheArgHisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeu 120
QY 361 GTCAGACTCAATAGCCAGGCGAGGCTGTCATCCATGGTGGAAGAAAGTCAGGCTGCCCTCC 420
Db |||||||
121 ValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArgLeuProSer 140
QY 421 CGCTCGGAACCCCTCGAACCACTGTACTGCTCCGGCTGGGCGCACTACCAAGAGCCCA 480
Db |||||||
141 ArgCysGluProProGlyThrThrCysThrValSerGlyTyrGlyThrThrSerPro 160
QY 481 GATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCAGGAC 540
Db |||||||
161 AspValThrPhePro---AspLeuMetCysValAspValLysLeuIleSerProGlnAsp 179
QY 541 TGCACGAAGTTTACNAGCACTTACTGGGAAATTCATGCTGTGCGTGGCATCCCGNC 600
Db |||||||
180 CysThrLysValTyrLysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAsp 199
QY 601 TCCAGAAAACGCTCGCAATGGTGACTCAGGGGACCGTGTGTGTCAGAGGTACCCCTG 660
Db |||||||
200 SerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeu 219
QY 661 CAAGTCTGCTGTCTCTGGGAACTTTTCCCTTGGGCGCAACCAATGACCCAGAGTCTAC 720
Db |||||||
220 GlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyr 239
QY 721 ACTCAAGTGTGCAAGTTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
Db |||||||
240 ThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetLysLysHisArg 257
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RESULT 14

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US-10-262-511-102
; Sequence 102, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elna
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
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; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 102
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-102

Alignment Scores:
Pred. No.: 3,84e-108 Length: 247
Score: 1252.00 Matches: 228
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 70.3% Indels: 0
DB: 4 Gaps: 0

US-09-905-083a-30 (1-969) x US-10-262-511-102 (1-247)
QY 88 GCCCAGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCACCTGGCAG 147
Db |||::|||
11 AlaArgGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySerHisProTrpGln 30
QY 148 GTGGCCCTGCTCAGTGGCAATCAGCTCCACCTCGCGAGGCGTCTCGTCAATCAGCGCTGG 207
Db |||||||
31 ValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrp 50
QY 208 GTGCTCACTGCGCGCCCACTGCAAGATGAATGAGTACACCGTGACCTGGGCGAGTGATAG 267
Db |||||||
51 ValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeuGlySerAspThr 70
QY 268 TTGGGCGACAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCGCCACCCCGGCTAC 327
Db |||||||
71 LeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArgHisProGlyTyr 90
QY 328 TCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGTCAATAGCCAGGCCAGGCTG 387
Db |||||||
91 SerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeu 110
QY 388 TCATCCATGCTGAAGAAAGTCAGGCTGCGCTCCCGCTCGCAACCCCTCGAAACCACTGT 447
Db |||||||
111 SerSerMetValLysValArgLeuProSerArgCysGluProProGlyThrThrCys 130
QY 448 ACTGTCTCCGCTGGGCGACTACACAGAGCCCGAGATGTGACCTTCCCTCTGACCTCATG 507
Db |||||||
131 ThrValSerGlyTrpGlyThrThrThrSerProAspValThrPheProSerAspLeuMet 150
QY 508 TCGGTGATGTCAAGCTCATCTCCCCCAGGACTCAGCGAGGCTTACAGAGGTTTACAAGACTTACTG 567
Db |||||||
151 CysValAspValLysLeuIleSerProGlnAspCysThrLysValTyrLysAspLeuLeu 170
QY 568 GAAATTCATGCTGTGCGCTGGCATCCCGCATCCCGCACTCCAAAGAAAAACCGCTGCAATGGTGC 627
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Db 171 GluAsnSerMetLeuCyAlaGlyIleProAspSerLysLysAsnAlaCyAsnGlyAsp 190
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Db 191 SerGlyGlyProLeuValCyAsArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPhe 210
Qy 688 CTTTGGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGG 747
Db 211 ProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLysPheThrLysTrp 230
Qy 748 ATAAATGACACCATGAAAAAGCATCGC 774
Db 231 IleAsnAspThrMetLysLysHisArg 239

RESULT 15

US-10-262-511-94
; Sequence 94, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 94
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-94
Alignment Scores:
Pred. No.: 3-86e-108 Length: 252
Score: 1252.00 Matches: 228
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 70.3% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-262-511-94 (1-252)

Qy 88 GCCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCCATGGCAG 147
Db 24 AlaArgGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySerHisProTrpGln 43
Qy 148 GTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGTCTGTGTCATGAGCGGTGG 207
Db 44 ValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrp 63
Qy 208 GTGCTCACTGCCGCCCACTGCAAGATTGAATGAGTACACCGTGCACCTGGCGGAGTGATACG 267
Db 64 ValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeuGlySerAspThr 83
Qy 268 CTGGCGCAGAGGAGCTCAGAGGATCAAGCGCTCGAAGTCATTCGCCCAACCCCGGTAC 327
Db 84 LeuGlyAspArgArgAlaGlnArgIleLeuAlaSerLysSerPheArgHisProGlyTrp 103
Qy 328 TCACACAGACCCCATGTTAATGACCTCATGCTGTGAGGCTCAATAGCCAGGCGGAGCGTG 387
Db 104 SerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeu 123
Qy 388 TCATCCATGTGTAAGAAAGTCAGGCTGCCCTGCCGCTGCCAAGCCCTCGAACCACCTGT 447
Db 124 SerSerMetValLysLysValArgLeuProSerArgCysGluProGlyThrThrCys 143
Qy 448 ACTGCTCCGGCTGGGGCACTACACGAGCCCAAGATGTGACCTTTCCTCTGACCTCATG 507
Db 144 ThrValSerGlyTrpGlyThrThrSerProAspValThrPheProSerAspLeuMet 163
Qy 508 TGGGTGGATGTCAAGCTCATCTCCCGGAGGCTGACGAGGCTTTCACAGGCTTACTG 567
Db 164 CysValAspValLysLeuIleSerProGlnAspCysThrLysValTrpLysAspLeuLeu 183
Qy 568 GAAAAATTCATGCTGTGCGCTGGCATCCCGGAGTCCCAAGAAAAACCGCTCAATGGTGAC 627
Db 184 GluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAsp 203
Qy 628 TCAGGGGACCGTGTGTGTGAGAGGTACCTGCAAGGTCTGTGTCTCTGGGAACTTTC 687
Db 204 SerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPhe 223
Qy 688 CTTTGGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGG 747
Db 224 ProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLysPheThrLysTrp 243
Qy 748 ATAAATGACACCATGAAAAAGCATCGC 774
Db 244 IleAsnAspThrMetLysLysHisArg 252

Search completed: March 11, 2006, 02:21:02
Job time : 183 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 02:15:14 ; Search time 3.5 Seconds
(without alignments)
1541.257 Million cell updates/sec

Title: US-09-905-083A-30

Perfect score: 1780

Sequence: 1 ggaattccgggtccatggc.....aagaacacacaaacccctcag 969

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 323334

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/abgs/ABSSWEB.spool/US0905083/runat.10032006.152506.29979/app.query.fasta.1
-DB=Published Applications AA.New -QPMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bts -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abgs02p
-USER=US0905083 @CGN 1.1.17 runat.10032006.152506.29979 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=0.5 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.New:

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pcp.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pcp.*
- 5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pcp.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|--------------------|
| 1 | 1364 | 76.6 | 253 | 6 | US-10-412-748-11 |
| 2 | 1364 | 76.6 | 253 | 6 | US-10-412-748-14 |
| 3 | 1364 | 76.6 | 253 | 6 | US-10-412-748-17 |
| 4 | 988 | 55.5 | 181 | 6 | US-11-037-243-98 |
| 5 | 612.5 | 34.4 | 293 | 6 | US-10-412-748-19 |
| 6 | 612.5 | 34.4 | 293 | 6 | US-10-131-826A-456 |
| 7 | 612.5 | 34.4 | 293 | 6 | US-10-412-748-2 |
| 8 | 612.5 | 34.4 | 293 | 6 | US-10-412-748-7 |
| 9 | 612.5 | 34.4 | 293 | 6 | US-10-973-115B-456 |

| | | | | | | |
|----|-------|------|-----|---|--------------------|-------------------|
| 10 | 583 | 32.8 | 267 | 6 | US-10-995-561-552 | Sequence 552, App |
| 11 | 583 | 32.8 | 267 | 6 | US-10-995-561-553 | Sequence 553, App |
| 12 | 582.5 | 32.7 | 260 | 6 | US-10-131-826A-396 | Sequence 396, App |
| 13 | 582.5 | 32.7 | 260 | 6 | US-10-510-321-2 | Sequence 2, Appli |
| 14 | 582.5 | 32.7 | 260 | 6 | US-10-973-115B-396 | Sequence 396, App |
| 15 | 580.5 | 32.6 | 260 | 7 | US-11-183-914-7 | Sequence 7, Appli |
| 16 | 571.5 | 32.1 | 250 | 6 | US-10-131-826A-506 | Sequence 506, App |
| 17 | 571.5 | 32.1 | 250 | 6 | US-10-973-115B-506 | Sequence 506, App |
| 18 | 571.5 | 32.1 | 250 | 7 | US-11-051-720-1428 | Sequence 1428, Ap |
| 19 | 567.5 | 31.9 | 254 | 7 | US-11-234-786-525 | Sequence 525, App |
| 20 | 564.5 | 31.7 | 320 | 7 | US-11-037-243-90 | Sequence 90, Appl |
| 21 | 559.5 | 31.4 | 449 | 7 | US-11-234-786-617 | Sequence 617, App |
| 22 | 557.5 | 31.3 | 254 | 7 | US-11-234-786-523 | Sequence 523, App |
| 23 | 556 | 31.2 | 275 | 7 | US-11-051-720-1705 | Sequence 1705, Ap |
| 24 | 554.5 | 31.2 | 250 | 5 | US-09-978-360A-657 | Sequence 657, App |
| 25 | 551 | 31.0 | 276 | 7 | US-11-186-284-95 | Sequence 95, Appl |
| 26 | 551 | 31.0 | 276 | 7 | US-11-037-243-87 | Sequence 87, Appl |
| 27 | 546.5 | 30.7 | 220 | 7 | US-11-234-786-327 | Sequence 327, App |
| 28 | 535 | 30.1 | 229 | 7 | US-11-226-788-2 | Sequence 2, Appli |
| 29 | 530.5 | 29.8 | 253 | 7 | US-11-050-857-671 | Sequence 671, App |
| 30 | 530 | 29.8 | 244 | 7 | US-11-186-284-97 | Sequence 97, Appl |
| 31 | 530 | 29.8 | 244 | 7 | US-11-050-857-670 | Sequence 670, App |
| 32 | 517.5 | 29.1 | 262 | 6 | US-10-995-561-849 | Sequence 849, App |
| 33 | 503.5 | 28.3 | 237 | 6 | US-10-401-386B-24 | Sequence 24, Appl |
| 34 | 500.5 | 28.1 | 205 | 7 | US-11-234-786-176 | Sequence 176, App |
| 35 | 482.5 | 27.1 | 261 | 7 | US-11-138-242A-8 | Sequence 8, Appli |
| 36 | 482.5 | 27.1 | 261 | 7 | US-11-150-066-8 | Sequence 8, Appli |
| 37 | 482.5 | 27.1 | 261 | 7 | US-11-033-039-358 | Sequence 358, App |
| 38 | 482.5 | 27.1 | 261 | 7 | US-11-155-288-10 | Sequence 10, Appl |
| 39 | 480.5 | 27.0 | 259 | 6 | US-10-401-386B-2 | Sequence 2, Appli |
| 40 | 478.5 | 26.9 | 230 | 7 | US-11-019-711-135 | Sequence 135, App |
| 41 | 463.5 | 26.0 | 261 | 7 | US-11-138-242A-3 | Sequence 3, Appli |
| 42 | 463.5 | 26.0 | 261 | 7 | US-11-138-242A-10 | Sequence 10, Appl |
| 43 | 463.5 | 26.0 | 261 | 7 | US-11-150-066-3 | Sequence 3, Appli |
| 44 | 463.5 | 26.0 | 261 | 7 | US-11-150-066-10 | Sequence 10, Appl |
| 45 | 461.5 | 25.9 | 237 | 6 | US-10-401-386B-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

| | | | |
|--|-----------|--|-----|
| Alignment Scores: | | | |
| Pred. No.: | 7,13e-116 | Length: | 253 |
| Score: | 1364.00 | Matches: | 253 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 76.6% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |
| US-09-905-083A-30 (1-969) x US-10-412-748-11 (1-253) | | | |
| QY | 16 | ATGCGAAGATCCCTTCTCTGCGCCCTGACAGATCTTACTGCTTACCTTGGAACT | 75 |

Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGAGAGAGAGAGATATTGATGGCGCCCATGTCTCAAGAGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspGlyIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCTCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGACGCTGGGTGCTACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GCGAGTATACCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCAGAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGTGTCATCCATGTGGAAGAGTCAAGCTGCGCTCCGCTCGCAACCCCT 435
Db 121 GlnAlaArgSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGNACCACTGTACTCTCCGCTGGGCACTTACCAGGCGCCAGATGTGACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGTGATGCAAGCTCATCTCCCGCCAGGACTGCACGAGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuSerProGlnAspCysThrLysValTy 180
QY 556 AAGGACTTACTGGAAATTCATGTGTGCGTGGCATCCCGACTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGCTGACTCAGGGGACCGTTGGTGTGCGAGAGTACCTGCAAGTCTGGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACTTTCCCTTTCGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240

RESULT 2

US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Alignment Scores: 7.13e-116 Length: 253
Pred. No.:

Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0
US-09-905-083A-30 (1-969) x US-10-412-748-14 (1-253)
QY 16 ATGSCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGTCTATCTTACGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGAGAGAGGTCACAGATATTGATGGCGCCCATGTGTGCAAGAGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspGlyIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCTCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGACGCTGGGTGCTCAGTGGCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GCGAGTATACCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCAGAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGTGTCATCCATGTGGAAGAGTCAAGCTGCGCTCCGCTCGCAACCCCT 435
Db 121 GlnAlaArgSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGTCTCCGCTGGGCGCACTTACCAGGCGCCAGATGTGACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGTGATGCAAGCTCATCTCCCGCCAGGACTGCACGAGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuSerProGlnAspCysThrLysValTy 180
QY 556 AAGGACTTACTGGAAATTCATGTGTGCGTGGCATCCCGACTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGCTGACTCAGGGGACCGTTGGTGTGCGAGAGTACCTGCAAGTCTGGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACTTTCCCTTTCGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAGAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

QY 616 TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCCTGCAAGGTCTGGGTCC 675
Db 201 CybAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTTCCCTTTCGGGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TTPGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHieArg 253
RESULT 5
US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19
Alignment Scores:
Pred. No.: 7,72e-82 Length: 181
Score: 988.00 Matches: 181
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 55.5% Indels: 0
DB: 6 Gaps: 0
US-09-905-083A-30 (1-969) x US-10-412-748-19 (1-181)
QY 232 ATCAATGAGTACACCTGTGCACCTGGGACGTGATACCTGGGCGACAGGAGCTCAGAGG 291
Db 1 MetAsnGluTyThrValHisLeuGlySerAspThrLeuGlyAspArgAlaGlnArg 20
QY 292 ATCAAGGCTCGAAGTCATTCCGCCACCCCGGCTACTCCACACAGACCCCATGTTAATGAC 351
Db 21 IleLysAlaSerLysSerPheArgHisProGlyTyThrSerThrGlnThrHisValAsnAsp 40
QY 352 CTCATGCTCGTGAAGTCAATAGCCAGGCGCAGCTGTCTATCCATGTGTAAGAAAGTCAGG 411
Db 41 LeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArg 60
QY 412 CTGCCCTCCCGCTCGCAACCCCTCGAACCACTGTACTGTCTCCCGCTGGGGCCTACCC 471
Db 61 LeuProSerArgCysGluProProGlyThrThrCysThrValSerGlyTrpGlyThrThr 80
QY 472 ACAGAGCCAGATGTGACCTTTCCTCTGACCTCATGTGGGTGGATGTCAAGCTCATCTCC 531
Db 81 ThrSerProAspValThrPheProSerAspLeuMetCysValAspValLysLeuIleSer 100
QY 532 CCCAGAGTGCACGAGGTTTACAGGACTTACCTGGAATAATTCATGTGTGCGGTGCG 591
Db 101 ProGlnAspCysThrLysValTyLysAspLeuLeuGluAsnSerMetLeuCysAlaGly 120
QY 592 ATCCCGACTCCAGAAAAACGCTGCATGTGACTCAGGGGACCGTTGGTGTGCAGA 651
Db 121 IleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArg 140
QY 652 GGTACCTGCAAGGTCTGGTGTCTCTGGGGAACCTTCCCTTTCGGGCCAACCAATGACCCA 711

Db 141 GlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnProAsnAspPro 160
QY 712 GGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT 771
Db 161 GlyValTyThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetLysLysHis 180
QY 772 CGC 774
Db 181 Arg 181
RESULT 6
US-10-131-826A-456
; Sequence 456, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 456
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-456
Alignment Scores:
Pred. No.: 8.12e-48 Length: 293
Score: 612.50 Matches: 114
Percent Similarity: 65.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 34
DB: 6 Gaps: 4

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US-09-905-083A-30 (1-969) x US-10-131-826A-456 (1-293)
QY 76 GCAGGAGAAGAGCCAGGGTGAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAspAlaArgSerAspSerSerArgilelleAenGlySerAspCys 73
QY 124 GCAAGAGGCTCCACCCATGGAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyCys 93
QY 181 GGAGGGCTCTGCTCAATGAGCGCTGGTGCTCACTGCCGCCACCTGCACAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysVal 113
QY 241 TACACCGTGCACCTGGGCACTGATACGCTGGGC-----GACAGGAGAGCTCAGAGG 291
Db 114 PheArgValArgLeuGlyHisTySerLeuSerProValTyGluSerGlyGlnMet 133
QY 292 ATCAAGCCCTCGAAGTCATTCGCCACCCCGGCTACTCCACACAGACCCATGTTAATGAC 351
Db 134 PheGlnGlyValLysSerIleProHisProGlyTySerHisProGlyHisSerAsnAsp 153
QY 352 CTATCTCTGCTGAGCTCAATACCCAGGCGGCTGCTCCTCCGCTGGGCACTTACC 471
Db 174 ValSerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThr 193
QY 472 ACAGGCCAGATGTGACTTTCCTCTGACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
Db 194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSer 213
QY 532 CCCAGGAGCTGCAGAGGTTTACAGGACTTACTGGAAATTCATGCTGCTGCTGCTGCTGCT 591
Db 214 GlnLysArgCysGluAspAlaTyProArgGlnIleAspAspThrMetPheCysAlaGly 233
QY 592 ATCCCGAGCTCCAAAGAAAACGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
Db 234 ---AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsn 252
QY 652 GGTACCTCGAAGGTCTGGTGTCTCTGGGAACTTTCCTTGGCGGCAACCCCAATGACCCA 711
Db 253 GlySerLeuGlnGlyLeuValSerTrpGlyAspTyProCysAlaArgProAsnArgPro 272
QY 712 GGAGTCTACACTCAAGTGTCAAGTTCACCAAGTGGATAATGACACCATGAAA 765
Db 273 GlyValTyThrAsnLeuCysLysPheThrLysTrpIleGlnLuthrIleGln 290

RESULT 7
US-10-412-748-2
; Sequence 2, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-2
Alignment Scores:

Pred. No.: 8.12e-48 Length: 293
Score: 612.50 Matches: 114
Percent Similarity: 66.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 9
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-412-748-2 (1-293)
QY 76 GCAGGAGAAGAGCCAGGGTGAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAspAlaArgSerAspSerSerArgilelleAenGlySerAspCys 73
QY 124 GCAAGAGGCTCCACCCATGGAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyCys 93
QY 181 GGAGGGCTCTGCTCAATGAGCGCTGGTGCTCACTGCCGCCACCTGCACAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysVal 113
QY 241 TACACCGTGCACCTGGGCACTGATACGCTGGGC-----GACAGGAGAGCTCAGAGG 291
Db 114 PheArgValArgLeuGlyHisTySerLeuSerProValTyGluSerGlyGlnMet 133
QY 292 ATCAAGCCCTCGAAGTCATTCGCCACCCCGGCTACTCCACACAGACCCATGTTAATGAC 351
Db 134 PheGlnGlyValLysSerIleProHisProGlyTySerHisProGlyHisSerAsnAsp 153
QY 352 CTATCTCTGCTGAGCTCAATACCCAGGCGGCTGCTCCTCCGCTGGGCACTTACC 471
Db 174 ValSerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThr 193
QY 472 ACAGGCCAGATGTGACTTTCCTCTGACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
Db 194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSer 213
QY 532 CCCAGGAGCTGCAGAGGTTTACAGGACTTACTGGAAATTCATGCTGCTGCTGCTGCTGCT 591
Db 214 GlnLysArgCysGluAspAlaTyProArgGlnIleAspAspThrMetPheCysAlaGly 233
QY 592 ATCCCGAGCTCCAAAGAAAACGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
Db 234 ---AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsn 252
QY 652 GGTACCTCGAAGGTCTGGTGTCTCTGGGAACTTTCCTTGGCGGCAACCCCAATGACCCA 711
Db 253 GlySerLeuGlnGlyLeuValSerTrpGlyAspTyProCysAlaArgProAsnArgPro 272
QY 712 GGAGTCTACACTCAAGTGTCAAGTTCACCAAGTGGATAATGACACCATGAAA 765
Db 273 GlyValTyThrAsnLeuCysLysPheThrLysTrpIleGlnLuthrIleGln 290

RESULT 8
US-10-412-748-7
; Sequence 7, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-7

Alignment Scores:
Pred. No.: 293
Score: 612.50 Length: 293
Percent Similarity: 66.0% Matches: 114
Best Local Similarity: 47.9% Conservative: 43
Query Match: 34.4% Mismatches: 72
DB: 9 Indels: 9
Gaps: 4

US-09-905-083A-30 (1-969) x US-10-412-748-7 (1-293)

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QY 76 GCAGGAGAGAGCCAGGGTGAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAspAlaArgSerAspSerArgIleAlaHisCysArgCys 73
QY 124 GCAAGAGGCTCCACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaLeuLeuLeuArgProHsnGlnLeuTrCys 93
QY 181 GGAGGCGTCTGTGTCATAGAGCGCTGGTGCTCACTGCCGCCACTGCAAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysVal 113
QY 241 TACACCGTGCACCTGGCGAGTATACGCTGGGC-----GACAGGAGGCTCAGAGG 291
Db 114 PheArgValArgLeuGlyHisTySerLeuSerProValTyGluSerGlnGlnMet 133
QY 292 ATCAAGCGCTCGAAGTCATTCCGCCACCCGGCTACTCCACACAGACCATGTTAATGAC 351
Db 134 PheGlnGlyValLysSerLeuProHisProGlyTySerHisProGlyHisSerAsnAsp 153
QY 352 CTCATGCTCGTGAAGTCAATAGCCAGCGAGCGCTGTCTATCCATGTGTGAAGAAAGTCAGG 411
Db 154 LeuMetLeuIleLysLeuAsnArgAlaArgProThrLysAspValArgProHsnAsn 173
QY 412 CTGCGCTCCGTCGAGAACCCCTCGGAACCACTGTACTGTCTCCGGCTGGGGCACTACC 471
Db 174 ValSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThr 193
QY 472 ACGAGCCAGATGTGACCTTCCTCTGACCTCATGTGCTGATGTCAAGCTCATCTCC 531
Db 194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnLiesValLeuSer 213
QY 532 CCCCAGGACTGCAGCAAGCTTTTACAGGACTTTACTGGAAATTTCCATGCTGTGCGCTGCG 591
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QY 592 ATCCCGACTCCAGAAAACCGCTGCATGTGACTCAGGGGACCGTGTGTGTGCAGA 651
Db 234 ---AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsn 252
QY 652 GGTACCTCCAGGCTGTGTGCTCTGGGAACCTTTCCTTGGCGCAACCCCAATGACCA 711
Db 253 GlySerLeuGlnGlyLeuValSerTrpGlyAspTyProCysAlaArgProHsnArgPro 272
QY 712 GGAGTCTACACTCAAGTGTGCAAGTTTCACCAAGTGTGATAAATGACACCATGAAA 765
Db 273 GlyValTyThrAsnLeuCysLysPheThrLysTrpIleGlnGluThrIleGln 290
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RESULT 9

US-10-973-115B-456
; Sequence 456, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 456
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-456

Alignment Scores:
Pred. No.: 293
Score: 612.50 Length: 293
Percent Similarity: 66.0% Matches: 114
Best Local Similarity: 47.9% Conservative: 43
Query Match: 34.4% Mismatches: 72
DB: 9 Indels: 9
Gaps: 4

US-09-905-083A-30 (1-969) x US-10-973-115B-456 (1-293)

```
QY 76 GCAGGAGAGAGCCAGGGTGAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAspAlaArgSerAspSerArgIleAlaHisCysArgCys 73
QY 124 GCAAGAGGCTCCACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaLeuLeuLeuArgProHsnGlnLeuTrCys 93
QY 181 GGAGGCGTCTGTGTCATAGAGCGCTGGTGCTCACTGCCGCCACTGCAAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysVal 113
QY 241 TACACCGTGCACCTGGCGAGTATACGCTGGGC-----GACAGGAGGCTCAGAGG 291
Db 114 PheArgValArgLeuGlyHisTySerLeuSerProValTyGluSerGlnGlnMet 133
QY 292 ATCAAGCGCTCGAAGTCAATGAGCGCTGGTGCTCACTGCCGCCACTCCACAGACCCTGTTAATGAC 351
Db 134 PheGlnGlyValLysSerIleProHisProGlyTySerHisProGlyHisSerAsnAsp 153
QY 352 CTCATGCTCGTGAAGTCAATAGCCAGCGAGCGCTGTCTATCCATGTGTGAAGAAAGTCAGG 411
Db 154 LeuMetLeuIleLysLeuAsnArgAlaArgProThrLysAspValArgProHsn 173
QY 412 CTGCGCTCCGTCGAGAACCCCTCGGAACCACTGTACTGTGTCTCCGGCTGGGGCACTACC 471
```

```
Db 174 ValSerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThr 193
Qy 472 ACAGCCAGATGACCTTCCCTCTGACCTATGCTGCGTGGATGTCACATCTCC 531
Db 194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAAsnLeuSerValLeuSer 213
Qy 532 CCCAGGACTGCAGAGGTTTACAGGACTTACTGGAATTCATGCTGCGCTGGC 591
Db 214 GlnLysArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly 233
Qy 592 ATCCCCGACTCCAAAGAAACCGCTGCAATGGTGACTCAGGGGACCGTTGGTGCGAGA 651
Db 234 ---AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsn 252
Qy 652 GTTACCTGCAAGTCTGGTGTCTCTGGGAACTTCCCTTGGCGGCCAACCAATGACCCA 711
Db 253 GlySerLeuGlnGlyLeuValSerTrpGlyAspTyrProCysAlaArgProAsnArgPro 272
Qy 712 GGAGTCTACACTCAAGTGTCAAGTTCCACCAAGTGGATAATGACACCATGAAA 765
Db 273 GlyValTyrThrAsnLeuCysLysPheThrLysTrpIleGlnGlnThrIleGln 290

RESULT 10
US-10-995-561-552
; Sequence 552, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-552

Alignment Scores:
Pred. No.: 3,78e-45 Length: 267
Score: 583.00 Matches: 110
Percent Similarity: 61.2% Conservative: 43
Best Local Similarity: 44.0% Mismatches: 89
Query Match: 32.8% Indels: 8
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-995-561-552 (1-267)
Qy 28 CTCTCTCTGCGCTGACAGATCTTACTGCTATCTCTAGCCTTGGAACTGCAGGAGAA 87
Db 20 LeuLeuThrAlaLeuGlnValLeuAlaIleAlaMet-----ThrGlnSerGlnGlu 36
Qy 88 GCCCAGGCTGACAGATTATTGATGGCCGCCCTCCCAAGAGGCTCCCAACCCATGGCAG 147
Db 37 AspGlu---AsnLysIleIleGlyGlyHisThrCysThrArgSerSerGlnProTrpGln 55
Qy 148 GTGGCCCTGCTCAGTGGC-----ATCAGCTCCACTGCGGAGCGCTCTGGTCAATGAG 201
Db 56 AlaAlaLeuLeuAlaGlyProArgGlnValLeuArgValValArgGlnValThr 115
```

```
Qy 316 CACCCGGCTACTCCACACAGACCCCATGTTAATGACTCTCATGCTCGTGAAGCTCAATAGC 375
Db 116 HisProAsnTyrAsnSerArgThrHisAspAsnLeuMetLeuLeuGlnGlnGln 135
Qy 376 CAGGCAGGCTGTTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTCGGAACCCCT 435
Db 136 ProAlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro 155
Qy 436 GGAACCACTGTACTGCTCCGCTGGGCACTACCAAGAGCCAGATGTGACCTTTCC 495
Db 156 GlyThrSerCysArgValSerGlyTrpGlyThrIleSerSerProIleAlaArgTyrPro 175
Qy 496 TCTGACTCATGTCGCTGGATGTCAGCTCATCTCCCCCAGGACTGCACGAGGTTTAC 555
Db 176 AlaSerLeuGlnCysValAsnIleAsnIleSerProAspGluValCysGlnLysAlaTyr 195
Qy 556 AAGGACTTACTGTGAAAATTCATGCTGTGCGTCATCCCGACTCCCAAGAAACGCC 615
Db 196 ProArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyGlyLysAspSer 215
Qy 616 TGAATGGTGTACTCAGGGGACCGTTGGTGTGTGAGAGGTACCTCGCAAGGTCTGGTCTCC 675
Db 216 CysGlnGlyAspSerGlyGlyProLeuValCysArgGlyGlnLeuGlnGlyLeuValSer 235
Qy 676 TGGGGAACTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 236 TrpGlyMetGluArgCysAlaLeuProGlyTyrProGlyValTyrThrAsnLeuCysLys 255
Qy 736 TTCACCAAGTGGATAAATGACACCATGAAA 765
Db 256 TyrArgSerTrpIleGluThrMetArg 265

RESULT 11
US-10-995-561-553
; Sequence 553, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-553

Alignment Scores:
Pred. No.: 3,78e-45 Length: 267
Score: 583.00 Matches: 110
Percent Similarity: 61.2% Conservative: 43
Best Local Similarity: 44.0% Mismatches: 89
Query Match: 32.8% Indels: 8
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-995-561-553 (1-267)
Qy 28 CTCTCTCTGCGCTGACAGATCTTACTGCTATCTCTAGCCTTGGAACTGCAGGAGAA 87
Db 20 LeuLeuThrAlaLeuGlnValLeuAlaIleAlaMet-----ThrGlnSerGlnGlu 36
Qy 88 GCCCAGGCTGACAGATTATTGATGGCCGCCCTCCCAAGAGGCTCCCAACCCATGGCAG 147
Db 37 AspGlu---AsnLysIleIleGlyGlyHisThrCysThrArgSerSerGlnProTrpGln 55
Qy 148 GTGGCCCTGCTCAGTGGC-----ATCAGCTCCACTGCGGAGCGCTCTGGTCAATGAG 201
Db 56 AlaAlaLeuLeuAlaGlyProArgGlnValLeuArgValValArgGlnValThr 75
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```
QY 202 CGCTGGTGTCTACTCGCGCCCACTGCAAGATGAATGAGTACACCGTGACCTGGCGAGT 261
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 GlnTrpValIleThrAlaAlaHisCysGlyArgProIleLeuGlnValAlaLeuGlyLys 95
QY 262 GATACGCTG-----GGCGACGAGGAGCTCAGAGGATCAAGGCTCGAAGTCATTCGCG 315
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 HisAsnLeuArgArgTrpGluAlaThrGlnGlnValLeuArgValValArgGlnValThr 115
QY 316 CACCCCGGTACTCCACACGACCCATGTTAATGACCTATGCTCTGAGCTCAATAGC 375
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 HisProAsnTyraenSerArgThrHisAspAsnAspLeuMetLeuLeuGlnGln 135
QY 376 CAGGCAGGCTGCATCCATGTTGAGAAAGTCAGGCTGCCCTCCCGCTGCGAAGCCCT 435
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 ProAlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro 155
QY 436 GGAACACCTGTACTCTCCGCTGGGCACTACACGAGGCCAGATGTGACCTTTCCC 495
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 GlyThrSerCysArgValSerGlyTTPGlyThrIleSerSerProIleAlaArgTyrPro 175
QY 496 TCTGACCTCATGTGCTGATGTCAGGCTCATCTCCCCCAGGACTGCAGAGGTTTAC 555
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 AlaSerLeuGlnCysValAsnIleAsnIleSerProAspGluValCysGlnLysAlaTyr 195
QY 556 AAGGACTTACTGAAATTCATGCTGTGCTGGCATCCCGACTCCCAAGAAAAAGCC 615
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 ProArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyLysAspSer 215
QY 616 TGCATGTGTACTCAGGGGACCGTTGGTGTGAGAGGTACCTGCAAGGTCTGGTGTC 675
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
216 CysGlnGlyAspSerGlyGlyProLeuValCysArgGlyGlnLeuGlnGlyLeuValSer 235
QY 676 TGGGGAACCTTCCCTTGGCGCCAAACCAGTACCCAGGAGTCTACACTCAAGTGTCAAG 735
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 TrpGlyMetGluArgCysAlaLeuProGlyTyrProGlyValTyrThrAsnLeuCysLys 255
QY 736 TTCACCAAGTGGATAATGACACCATGAAA 765
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 TyrArgSerTrpIleGluGluThrMetArg 265
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RESULT 12

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US-10-131-826A-396
; Sequence 396, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 396
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-396

Alignment Scores:
Pred. No.: 4,18e-45 Length: 260
Score: 582.50 Matches: 118
Percent Similarity: 59.3% Conservative: 26
Best Local Similarity: 48.6% Mismatches: 88
Query Match: 32.7% Indels: 11
DB: 6 Gaps: 5

US-09-905-083A-30 (1-969) x US-10-131-826A-396 (1-260)

QY 46 ATCTTACTGCTATCTTAGCTTGGAAAATGTCAGGA---GAAGAAGCCCGAGGTGACAG 102
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13 MetPheLeuLeuLeuLeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLys 32
QY 103 ATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCCATGCGAGGTGGCTGCTGCTCAGT 162
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 ValLeuGlyGlyHisGluCysGlnProHisSerGlnProTrpGlnAlaAlaLeuPheGln 52
QY 163 GGCAATCAGTCCACTGGGAGGCTCTCTGTGTCATAGCGCTGGGTGTCTACTGCGCGC 222
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
53 GlyGlnGlnLeuLeuCysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAla 72
QY 223 CACTGCAAGATGAATGAGTACACCGTGCACCTGGCGAGTATACGCTG-----GCGGAC 276
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 HisCysLysLysProLysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAsp 92
QY 277 AGGAGAGCTCAGAGGATCAAGGCTCGAAGTCATTCCCGCCACCCCGGTCTACTCCACA--- 333
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
93 GlyProGluGlnGluIleProValValGlnSerIleProHisProCysTyrAsnSerSer 112
QY 334 -----CAGACCCATGTTAATGACTCATGTCTGTGAAGCTCAATAGCCAGCGCAGGCTG 387
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 AspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeu 132
QY 388 TCATCCATGTCGAAAGAAAGTACGGCTGCCCTCCCGCTGGGAACCCCTGGAACCACTGT 447
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
133 GlySerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
QY 448 ACTGTCTCGGCTGGGCACTTACCACGAGCCAGATGTGACCTTTCCCTCTGACCTCATG 507
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 ThrValSerGlyTyrGlyThrValThrSerProArgGluAsnPheProAspThrLeuAsn 172
QY 508 TCGTGGATGTCAAGCTCATCTCCCCCAGGACTGCACGAAAGTTTACAGGACTTACTG 567
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
QY 568 GAAAATTCATGCTGCTGGCTGGCATCCCCGACTCCAGAAAAAGCC-----TGCAAT 621
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 ThrAspGlyMetValCysAlaGly-----SerSerLysGlyAlaAspThrCysGln 209
```

| | | | |
|--|-----|---|------------------|
| Qy | 622 | GGTGACTCAGGGGACCGTGTGTGTCGACAGATACCTGCGAAGTCTGTGTGTCCTGGGGA | 688 |
| Db | 210 | GlyAaspSerGlyGlyProLeuValCysAaspGlyAlaLeuGlnGlyIleThrSerTrpGly | 229 |
| Qy | 682 | ACTTTTCCTCGCGGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTTCACC | 741 |
| Db | 230 | SerAaspProCysGlyArgSerAaspLysProGlyValIleThrAsnIleCysArgIyrLeu | 249 |
| Qy | 742 | AAGTGGATA 750 | |
| Db | 250 | AspTrpIle 252 | |
| RESULT 13 | | | |
| US-10-510-321-2 | | | |
| ; Sequence 2, Application US/10510321 | | | |
| ; Publication No. US20050287528A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Diamandis, Eleftherios P. | | | |
| ; APPLICANT: Kishi, Tadaaki | | | |
| ; TITLE OF INVENTION: Methods for Detecting Ovarian Cancer | | | |
| ; FILE REFERENCE: 11757.104USWO | | | |
| ; CURRENT APPLICATION NUMBER: US/10/510,321 | | | |
| ; CURRENT FILING DATE: 2004-10-04 | | | |
| ; PRIOR APPLICATION NUMBER: PCT/CA03/00495 | | | |
| ; PRIOR FILING DATE: 2003-04-04 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/370,559 | | | |
| ; PRIOR FILING DATE: 2002-04-04 | | | |
| ; NUMBER OF SEQ ID NOS: 4 | | | |
| ; SOFTWARE: Patent in version 3.3 | | | |
| ; SEQ ID NO 2 | | | |
| ; LENGTH: 260 | | | |
| ; TYPE: PRT | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-10-510-321-2 | | | |
| Alignment Scores: | | | |
| Pred. No.: | | 4.18e-45 | Length: 260 |
| Score: | | 582.50 | Matches: 118 |
| Percent Similarity: | | 59.3% | Conservative: 26 |
| Best Local Similarity: | | 48.6% | Mismatches: 88 |
| Query Match: | | 32.7% | Indels: 11 |
| DB: | | 6 | Gaps: 5 |
| US-09-905-083A-30 (1-969) x US-10-510-321-2 (1-260) | | | |
| Qy | 46 | ATCTTACTGCTATCCTTAGCTTGGAACTCGAGGA---GAAGAAGCCACGAGGTGCACAG | 102 |
| Db | 13 | MetPheLeuLeuLeuLeuGlyGlyAlaIrpAlaGlyHisSerArgAlaGlnLeuAaspLys | 32 |
| Qy | 103 | ATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCCATGCGCAGGTGGCCCTGTCAGT | 162 |
| Db | 33 | ValLeuGlyGlyHisGluCysGlnProHisSerGlnProIrpGlnAlaLeuPheGln | 52 |
| Qy | 163 | GGCAATCAGCTCCACTCGGAGGGCTCTGTGTCATAGCGCTGGGTGCTCACTCCCGCC | 222 |
| Db | 53 | GlyGlnGlnLeuLeuCysGlyValLeuValGlyGlyAsnTrpValLeuThrAlaIle | 72 |
| Qy | 223 | CACGTGAAGATGAATGAGTACACCGTGCACCTGGGCACGTATACCGCTG-----GGCGAC | 276 |
| Db | 73 | HisCysLysLysProLysIleThrValArgLeuGlyAaspHisSerLeuGlnAsnLysAasp | 92 |
| Qy | 277 | AGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCCGCACCCCGGCTACTCCACA--- | 333 |
| Db | 93 | GlyProGluGlnGluIleProValGlnSerIleProHisProCysIleTyrsnSerSer | 112 |
| Qy | 334 | -----CAGACCCCATGTTAATGACCTCATGTCTGCTGAAGCTCAATAGCCAGGCCAGGCTG | 387 |
| Db | 113 | AspValGluAaspHisAsnHisAaspLeuMetLeuLeuGlnLeuArgAaspGlnAlaSerLeu | 132 |
| Qy | 388 | TCATCCATGTTGAAGAAGTACAGGCTGCCCTCCCGCTCGGAACCCCTCGGAACCACTGT | 447 |
| Db | 133 | GlySerLysValLysProIleSerLeuAlaAaspHisCysThrGlnProGlyGlnLysCys | 152 |

| | | | |
|----|-----|--|-----|
| Qy | 448 | ACTGTCCTCCGGCTGGGGACATACACAGAGCCAGATGTGACCTTTCCCTCTGACCTCATG | 507 |
| Db | 153 | ThrValSerGlyTTPGlyThrValThrSerProArgGluAsnPheProAspThrLeuAen | 172 |
| Qy | 508 | TGCGTGGATGTCAGACTCATCTCCCGCCAGAGACTGCACGAAGGTTTACAGAGCTTACTG | 567 |
| Db | 173 | CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle | 192 |
| Qy | 568 | GAATAATTCCATGCTGTGGCTGGGCATCCCGACTCCAGAGAAAACGCC-----TGCAAT | 621 |
| Db | 193 | ThrAspGlyMetValCysAlaGly-----SerSerLysGlyAlaAspThrCysGln | 209 |
| Qy | 622 | GGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCTGCAGAGTCTGGTGTCTGGTGGGA | 681 |
| Db | 210 | GlyAspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly | 229 |
| Qy | 682 | ACTTTCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACTCAAGTGTGCNAGTTCACC | 741 |
| Db | 230 | SerAspProCysGlyArgSerAspLysProGlyValTyrThrAsnIleCysArgTyrLeu | 249 |
| Qy | 742 | AAGTGGATA | 750 |
| Db | 250 | AspTrpIle | 252 |

RESULT 14

US-10-973-115B-396

; Sequence 396, Application US/10973115B

; Publication No. US20060040351A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID

; TITLE OF INVENTION: SAME

; FILE REFERENCE: 39870-333031C300C1

; CURRENT APPLICATION NUMBER: US/10/973,115B

; CURRENT FILING DATE: 2004-10-22

; PRIOR APPLICATION NUMBER: US 10/145,747

; PRIOR FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: US 10/028,072

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: US 09/581,742

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: PCT/US00/05746

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/135,736

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: US 60/123,090

; PRIOR FILING DATE: 1999-03-05

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 396

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-973-115B-396

Alignment Scores:

Alignment Scores:


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Db      113 AspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeu 132
QY      388 TCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTCGGAACCCACCTGT 447
Db      133 GlySerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
QY      448 ACTGTCCTCCGGCTGGGGCACTACACGAGCCGAGATGTGACCTTCCCTCTGACCTCATG 507
Db      153 ThrValSerGlyTrpGlyThrValThrSerProArgGluAsnPheProAspThrLeuAsn 172
QY      508 TGGGTGGATGTCAGGCTCATCTCCCCCGGAGCTGCACGAGGTTTACAAGGACTTACTG 567
Db      173 CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
QY      568 GAAATTCATGTGTGCGTGGCATCCCGGATCCCAAGAAACGCGCC-----TGCAAT 621
Db      193 ThrAspGlyMetValCysAlaGly-----SerSerLysGlyAlaAspThrCysGln 209
QY      622 GGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCCTGCAAGGTCTGGTGTCTCTGGGA 681
Db      210 GlyAspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly 229
QY      682 ACTTTCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAGTTCCACC 741
Db      230 SerAspProCysGlyArgSerAspLysProGlyValTyrThrAsnIleCysArgTyrLeu 249
QY      742 AAGTGGATA 750
Db      250 AspTrpIle 252
```

Search completed: March 11, 2006, 02:21:42
Job time : 22.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 49 | 100.0 | 9 | 4 AAE08294 | Aae08294 Human str |
| 2 | 49 | 100.0 | 9 | 4 AAE08236 | Aae08236 Human str |
| 3 | 49 | 100.0 | 9 | 8 ADR68850 | Adr68850 Human str |
| 4 | 49 | 100.0 | 9 | 8 ADR68792 | Adr68792 Human str |
| 5 | 49 | 100.0 | 9 | 8 ADR68870 | Adr68870 Human str |
| 6 | 49 | 100.0 | 97 | 6 ADA05740 | Ada05740 Human str |
| 7 | 49 | 100.0 | 97 | 6 ADNG2904 | Adng2904 Human NOV |
| 8 | 49 | 100.0 | 136 | 4 ABG23378 | Abg23378 Novel hum |
| 9 | 49 | 100.0 | 144 | 8 ADI39727 | Adi39727 Stratum c |
| 10 | 49 | 100.0 | 144 | 8 ADI37151 | Adi37151 Stratum c |
| 11 | 49 | 100.0 | 181 | 6 ADA05738 | Ada05738 Human NOV |
| 12 | 49 | 100.0 | 181 | 8 ADNG2902 | Adng2902 Human NOV |
| 13 | 49 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 14 | 49 | 100.0 | 198 | 8 ADNG2900 | Adng2900 Human NOV |
| 15 | 49 | 100.0 | 224 | 6 ADA05744 | Ada05744 Human NOV |
| 16 | 49 | 100.0 | 224 | 8 ADNG2908 | Adng2908 Human NOV |
| 17 | 49 | 100.0 | 224 | 9 ADV21100 | Adv21100 Human str |
| 18 | 49 | 100.0 | 225 | 4 AAB98502 | Aab98502 Human str |
| 19 | 49 | 100.0 | 247 | 6 ADA05742 | Ada05742 Human NOV |
| 20 | 49 | 100.0 | 247 | 8 ADNG2906 | Adng2906 Human NOV |
| 21 | 49 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 22 | 49 | 100.0 | 250 | 8 ADNG2896 | Adng2896 Human NOV |
| 23 | 49 | 100.0 | 252 | 6 ADA05734 | Ada05734 Human NOV |
| 24 | 49 | 100.0 | 252 | 8 ADNG2898 | Adng2898 Human NOV |

| | | | | | |
|----|----|-------|-----|------------|--------------------|
| 25 | 49 | 100.0 | 253 | 2 AAR67888 | Aar67888 Human str |
| 26 | 49 | 100.0 | 253 | 2 AAU05383 | Aau05383 Human amy |
| 27 | 49 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 28 | 49 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 29 | 49 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 30 | 49 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 31 | 49 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 32 | 49 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |
| 33 | 49 | 100.0 | 253 | 7 ADR80484 | Adr80484 Ovarian c |
| 34 | 49 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 35 | 49 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/an |
| 36 | 49 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 37 | 49 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antipsori |
| 38 | 49 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 39 | 49 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 40 | 49 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 41 | 49 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |
| 42 | 40 | 81.6 | 226 | 5 ABB84422 | Abb84422 Rat SCCE |
| 43 | 39 | 79.6 | 9 | 4 AAE08326 | Aae08326 Human str |
| 44 | 39 | 79.6 | 9 | 8 ADR68883 | Adr68883 Human str |
| 45 | 37 | 75.5 | 9 | 4 AAE08298 | Aae08298 Human str |

ALIGNMENTS

RESULT 1
AAE08294
ID AAE08294 standard; peptide; 9 AA.
AC AAE08294;
XX XX

DT 01-NOV-2001 (first entry)

XX Human stratum corneum chymotrypsin enzyme peptide #59 (residues 72-80).

XX Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.

XX Homo sapiens.

XX WO200159158-A1.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US003977.

XX 11-FEB-2000; 2000US-00502600.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ;

XX WPI; 2001-514676/56.

XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

XX Disclosure; Page 115; 127pp; English.

XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

XX Sequence 9 AA;

SQ

```
Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 2
AAE08236
ID AAE08236 standard; peptide; 9 AA.
XX
AC AAE08236;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #1 (residues 72-80).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin
PT enzyme.
XX
PS Claim 25; Page 102; 127pp; English.
XX
CC The invention relates to diagnosing cancer especially ovarian cancer, by
CC screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
CC considered to be an integral part of tumour growth and metastasis, and
CC therefore, markers indicative of their presence or absence are useful for
CC the diagnosis of cancer. The method is useful for diagnosing cancer,
CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
CC to treat a cancer selected from ovarian, breast, lung, colon, prostate
CC and other cancers in which SCCE is overexpressed. The present sequence is
CC human SCCE peptide
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 3
ADR68850
ID ADR68850 standard; peptide; 9 AA.
XX
AC ADR68850;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide fragment SEQ ID NO:31.
KW serine protease; stratum corneum chymotryptic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.

DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:89.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.

XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/53.
XX
PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Disclosure; SEQ ID NO 89; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 49; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 4
ADR68792
ID ADR68792 standard; peptide; 9 AA.
XX
AC ADR68792;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:31.
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
```

XX 20-FEB-2004; 2004WO-US005134.
 XX 21-FEB-2003; 2003US-00372521.
 XX (UYAR-) UNIV ARKANSAS.
 XX O'brien TJ, Cannon MJ, Santin A;
 XX WPI; 2004-653294/63.
 XX Use of stratum corneum chymotryptic enzyme (SCCE) peptides, for
 PT vaccinating an individual against SCCE, and in monitoring and developing
 PT immunotherapies for ovarian and other malignancies.
 XX Claim 5; SEQ ID NO 31; 117pp; English.
 XX The invention relates to a novel method for vaccinating an individual
 CC against stratum corneum chymotryptic enzyme (SCCE), comprising inoculating
 CC an individual with a SCCE peptide, which elicits an immune response in
 CC the individual. A peptide of the invention acts as a stratum corneum
 CC chymotryptic enzyme inhibitor. The SCCE peptide is useful for vaccinating
 CC an individual against SCCE, particularly an individual having, suspected
 CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
 CC cancer. The oligonucleotide is useful for treating a neoplastic state in
 CC an individual, such as ovarian, breast, lung, colon, prostate, or
 CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
 CC peptides are also useful in the monitoring and development of
 CC immunotherapies for ovarian and other malignancies. The present sequence
 CC represents a peptide fragment of serine protease SCCE (stratum corneum
 CC chymotryptic enzyme).
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KMNEYTVHL 9
 Db |||||
 1 KMNEYTVHL 9
 RESULT 6
 ADA05740
 ID ADA05740 standard; protein; 97 AA.
 XX AC ADA05740;
 XX 06-NOV-2003 (first entry)
 DT Human NOV18e protein SEQ ID NO:100.
 DE human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 XX immunomodulator; cytostatic; neutropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX Homo sapiens.
 OS
 XX WO2003029424-A2.
 PN
 XX 10-APR-2003.
 PD
 XX 02-OCT-2002; 2002WO-US031373.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR
 XX 05-OCT-2001; 2001US-0327435P.
 PR
 XX 05-OCT-2001; 2001US-0327449P.
 PR
 XX 09-OCT-2001; 2001US-0327917P.
 PR
 XX 09-OCT-2001; 2001US-0328029P.
 PR
 XX 09-OCT-2001; 2001US-0328044P.
 PR
 XX 09-OCT-2001; 2001US-0328056P.
 PR
 XX 12-OCT-2001; 2001US-0328849P.
 PR
 XX 15-OCT-2001; 2001US-0329414P.
 PR
 XX 17-OCT-2001; 2001US-0330142P.
 PR
 XX 18-OCT-2001; 2001US-0330309P.
 PR
 XX 22-OCT-2001; 2001US-0341058P.
 PR
 XX 24-OCT-2001; 2001US-0339266P.
 PR
 XX 24-OCT-2001; 2001US-0343629P.
 PR
 XX 29-OCT-2001; 2001US-0349575P.
 PR
 XX 01-NOV-2001; 2001US-0346357P.

XX 20-FEB-2004; 2004WO-US005134.
 XX 21-FEB-2003; 2003US-00372521.
 XX (UYAR-) UNIV ARKANSAS.
 XX O'brien TJ, Cannon MJ, Santin A;
 XX WPI; 2004-653294/63.
 XX Use of stratum corneum chymotryptic enzyme (SCCE) peptides, for
 PT vaccinating an individual against SCCE, and in monitoring and developing
 PT immunotherapies for ovarian and other malignancies.
 XX Claim 5; SEQ ID NO 31; 117pp; English.
 XX The invention relates to a novel method for vaccinating an individual
 CC against stratum corneum chymotryptic enzyme (SCCE), comprising inoculating
 CC an individual with a SCCE peptide, which elicits an immune response in
 CC the individual. A peptide of the invention acts as a stratum corneum
 CC chymotryptic enzyme inhibitor. The SCCE peptide is useful for vaccinating
 CC an individual against SCCE, particularly an individual having, suspected
 CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
 CC cancer. The oligonucleotide is useful for treating a neoplastic state in
 CC an individual, such as ovarian, breast, lung, colon, prostate, or
 CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
 CC peptides are also useful in the monitoring and development of
 CC immunotherapies for ovarian and other malignancies. The present sequence
 CC represents a peptide fragment of serine protease SCCE (stratum corneum
 CC chymotryptic enzyme).
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KMNEYTVHL 9
 Db |||||
 1 KMNEYTVHL 9
 RESULT 5
 ADR68870
 ID ADR68870 standard; peptide; 9 AA.
 XX AC ADR68870;
 XX 02-DEC-2004 (first entry)
 DT Human stratum corneum chymotryptic enzyme peptide fragment SEQ ID NO:109.
 DE serine protease; stratum corneum chymotryptic enzyme; SCCE;
 KW immune response; ovarian cancer; lung cancer; prostate cancer;
 KW pancreatic cancer; colon cancer.
 XX Homo sapiens.
 OS
 XX WO2004075723-A2.
 PN
 XX 10-SEP-2004.
 PD
 XX 20-FEB-2004; 2004WO-US005134.
 PR
 XX 21-FEB-2003; 2003US-00372521.
 PR
 XX (UYAR-) UNIV ARKANSAS.
 PA
 XX O'brien TJ, Cannon MJ, Santin A;
 PI
 XX WPI; 2004-653294/63.
 DR
 XX


```

Db      78 KMNEYTVHL 86

RESULT 9
ADI39727
ID ADI39727 standard; protein; 144 AA.
XX
XX AC ADI39727;
XX
XX DT 15-APR-2004 (first entry)
XX
XX DE Stratum corneum chymotryptic enzyme (acce) catalytic domain.
XX
XX KW Immune T cell; dendritic cell; extracellular serine protease;
XX tumour antigen derived gene-14; TAGD-14; carcinoma;
XX KW stratum corneum chymotryptic enzyme; scce.
XX
XX OS Unidentified.
XX
XX PN US6642013-B1.
XX
XX PD 04-NOV-2003.
XX
XX PF 18-JUL-2000; 2000US-00618259.
XX
XX PR 21-AUG-1997; 97US-00915659.
XX 21-AUG-1998; 98US-00137944.
XX
XX PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
XX
XX PI O'brien TJ, Underwood LJ;
XX
XX DR WPI; 2004-118109/12.
XX
XX PT Production of activated immune cells or dendritic cells by exposing
XX immune cells to tumor antigen derived gene protein fragment consisting of
XX amino acid sequences.
XX
XX PS Example 1; SEQ ID NO 4; 44pp; English.
XX
XX CC The present invention relates to novel activated immune T cells or
XX dendritic cells directed toward extracellular serine protease termed
XX tumour antigen derived gene-14 (TAGD-14). The method of the invention
XX involves exposing the immune cells to a TAGD-14 protein fragment, where
XX exposure to the TAGD-14 protein fragment activates the immune cells. The
XX invention is used for the production of activated immune T cells or
XX dendritic cells. The invention allows screening to identify proteases
XX overexpressed in carcinoma. The present sequence is stratum corneum
XX chymotryptic enzyme (acce) catalytic domain. This sequence is used in the
XX invention.
XX
XX SQ Sequence 144 AA;

Query Match 100.0%; Score 49; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
DB 9 KMNEYTVHL 17

RESULT 10
ADI37151
ID ADI37151 standard; protein; 144 AA.
XX
XX AC ADI37151;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Stratum corneum chymotryptic enzyme (acce) catalytic domain.
XX
XX KW Serine protease; tumour antigen derived gene-14; TAGD-14;

KW neoplastic state; cancer; ovary; breast; lung; colon; prostate;
KW chymotryptic enzyme; scce; enzyme.
XX
XX OS Homo sapiens.
XX
XX PN US2003199010-A1.
XX
XX PD 23-OCT-2003.
XX
XX PF 13-JUN-2003; 2003US-00461787.
XX
XX PR 21-AUG-1997; 97US-00915659.
XX 21-AUG-1998; 98US-00137944.
XX 18-JUL-2000; 2000US-00618259.
XX
XX PA (UYAR-) UNIV ARKANSAS.
XX
XX PI O'brien TJ, Underwood LJ;
XX
XX DR WPI; 2004-141550/14.
XX
XX PT Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
XX for treating neoplastic state (such as ovarian cancer, breast cancer,
XX lung cancer, colon cancer, prostate cancer) in an individual.
XX
XX PS Example 1; SEQ ID NO 4; 46pp; English.
XX
XX CC The invention relates to extracellular serine protease termed tumour
XX antigen derived gene-14 (TAGD-14) and its nucleic acid. Composition
XX comprising TAGD-14 peptide is useful for treating a neoplastic state in
XX an individual. The neoplastic state is chosen from ovarian cancer, breast
XX cancer, lung cancer, colon cancer, prostate cancer in which TAGD-14 is
XX overexpressed. The present sequence is Stratum corneum chymotryptic
XX enzyme (scce) catalytic domain. This sequence is used in the
XX exemplification of the invention.
XX
XX SQ Sequence 144 AA;

Query Match 100.0%; Score 49; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
DB 9 KMNEYTVHL 17

RESULT 11
ADA05738
ID ADA05738 standard; protein; 181 AA.
XX
XX AC ADA05738;
XX
XX DT 06-NOV-2003 (first entry)
XX
XX DE Human NOVI8d protein SEQ ID NO:98.
XX
XX KW human; NOVI; antidiabetic; anorectic; antibacterial; virucide;
XX immunomodulator; cytostatic; nootropic; neuroprotective;
XX antiparkinsonian; antilipemic; gene therapy; human disease;
XX metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX immune disorder; haematopoietic disorder; dyslipidaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO2003029424-A2.
XX
XX PD 10-APR-2003.
XX
XX PF 02-OCT-2002; 2002WO-US031373.
XX
XX PR 02-OCT-2001; 2001US-0326483P.

```

PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327443P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ott T, Gorman L, Zechusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05737.
DR
XX
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Claim 1; Page 171; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 49; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9
Db 53 KMNEYTVHL 61
|||||||

RESULT 12
ADN62902
ID ADN62902 standard; protein; 181 AA.
XX
AC ADN62902;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18d.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
XX US2004038223-A1.
PN
XX
PD 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
PR

PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET J.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYK/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTI/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
XX Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62901.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 98; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,

CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 181 AA;
Query Match 100.0%; Score 49; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNEYTVVHL 9
DB 53 KNEYTVVHL 61
RESULT 13
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX
AC ADA05736;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18c protein SEQ ID NO:96.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0332666P.
PR 24-OCT-2001; 2001US-0332629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381039P.
PR 17-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytke KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI: 2003-381626/36.
DR N-PSDB; ADA05735.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipidemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.
XX
XX Sequence 198 AA;
XX
XX Query Match 100.0%; Score 49; DB 6; Length 198;
XX Best Local Similarity 100.0%; Pred. No. 0.27;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KNEYTVHL 9
XX Db 72 KNEYTVHL 80
XX
XX RESULT 14
XX ADN62900
XX ID ADN62900 standard; protein; 198 AA.
XX
XX AC ADN62900;

XX 01-JUL-2004 (first entry)
XX DE Human NOV18c.
XX
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
XX
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
XX (MILL/) MILLET I.
XX (PEYM/) PEYMAN J A.
XX (KEKU/) KEKUDA R.
XX (JUJU/) JU J.
XX (LILL/) LI L.
XX (GUOX/) GUO X.
XX (PATT/) PATTURAJAN M.
XX (SPYT/) SPYTEK K A.
XX (EDIN/) EDINGER S R.
XX (ELLE/) ELLERMAN K.
XX (MALI/) MALLYANKAR U M.
XX (ORTT/) ORT T.
XX (GORM/) GORMAN L.
XX (ZERR/) ZERHUSEN B D.
XX (ANDE/) ANDERSON D W.
XX (ZHON/) ZHONG M.
XX (CATT/) CATTERTON E.
XX (JIWW/) JI W.
XX (MILL/) MILLER C E.
XX (RAST/) RASTELLI L.
XX (STON/) STONE D J.
XX (PENNA/) PENA C E A.
XX (SHEN/) SHENOY S G.

CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders, such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.

XX Sequence 224 AA;

Query Match 100.0%; Score 49; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db |||||||
58 KNEYTVHL 66

Search completed: March 11, 2006, 00:24:09
Job time : 89.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 49 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 39 | 79.6 | 218 | 1 YVBPK3 | lysis protein t - |
| 3 | 39 | 79.6 | 218 | 1 YVBPT4 | lysis protein t - |
| 4 | 37 | 75.5 | 334 | 2 B98019 | conserved hypotet |
| 5 | 37 | 75.5 | 393 | 2 D75207 | hypothetical prote |
| 6 | 36 | 73.5 | 627 | 2 T25395 | hypothetical prote |
| 7 | 36 | 73.5 | 1829 | 2 T34239 | hypothetical prote |
| 8 | 35 | 71.4 | 159 | 2 A11406 | spermidine/spermin |
| 9 | 35 | 71.4 | 159 | 2 A11782 | spermidine/spermin |
| 10 | 35 | 71.4 | 505 | 2 H75431 | conserved hypotet |
| 11 | 35 | 71.4 | 555 | 2 AD1794 | acylase and dieste |
| 12 | 35 | 71.4 | 667 | 2 T09013 | RING finger protei |
| 13 | 35 | 71.4 | 667 | 2 T09482 | ring finger protei |
| 14 | 34 | 69.4 | 270 | 2 A43711 | replication protei |
| 15 | 34 | 69.4 | 270 | 2 S28582 | replication protei |
| 16 | 34 | 69.4 | 285 | 2 F70348 | hypothetical prote |
| 17 | 34 | 69.4 | 421 | 2 AH1120 | B. subtilis YwBN p |
| 18 | 34 | 69.4 | 421 | 2 AC1481 | conserved hypotet |
| 19 | 33 | 67.3 | 204 | 2 E95345 | FixJ Transcription |
| 20 | 33 | 67.3 | 204 | 2 B31227 | nitrogen fixation |
| 21 | 33 | 67.3 | 218 | 2 S53354 | calflagin Tb-24 - |
| 22 | 33 | 67.3 | 218 | 2 B83724 | hypothetical prote |
| 23 | 33 | 67.3 | 227 | 2 D83796 | two-component resp |
| 24 | 33 | 67.3 | 229 | 2 S53355 | calflagin Tb-1.7 - |
| 25 | 33 | 67.3 | 233 | 1 AQTU17 | flagellar calcium |
| 26 | 33 | 67.3 | 407 | 2 S53353 | calflagin Tb-44A - |
| 27 | 33 | 67.3 | 422 | 2 T11714 | hypothetical prote |
| 28 | 33 | 67.3 | 429 | 2 H70307 | preprotein translo |
| 29 | 33 | 67.3 | 525 | 2 B84028 | oligopeptide ABC t |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 33 | 67.3 | 664 | 2 C72379 | hypothetical prote |
| 31 | 33 | 67.3 | 677 | 2 A87470 | TonB-dependent rec |
| 32 | 33 | 67.3 | 1042 | 2 S23738 | pyr1-3 protein - s |
| 33 | 33 | 67.3 | 1308 | 2 E71622 | probable membrane |
| 34 | 33 | 67.3 | 1481 | 1 QZDOP3 | pyrimidine synthet |
| 35 | 32 | 65.3 | 49 | 2 H89308 | 50S ribosomal prot |
| 36 | 32 | 65.3 | 84 | 2 AE2172 | hypothetical prote |
| 37 | 32 | 65.3 | 116 | 2 S24989 | ribosomal protein |
| 38 | 32 | 65.3 | 130 | 2 E97262 | hypothetical prote |
| 39 | 32 | 65.3 | 144 | 2 F71215 | hypothetical prote |
| 40 | 32 | 65.3 | 192 | 2 G81301 | MdaB protein homol |
| 41 | 32 | 65.3 | 228 | 2 C90033 | hypothetical prote |
| 42 | 32 | 65.3 | 304 | 2 H75378 | hypothetical prote |
| 43 | 32 | 65.3 | 339 | 2 F97121 | probable membrane- |
| 44 | 32 | 65.3 | 371 | 2 A89800 | conserved hypotet |
| 45 | 32 | 65.3 | 448 | 2 F82280 | citrate/sodium sym |

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:g521214; PIDN:?
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRI>

Query Match 100.0%; Score 49; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVVHL 9
Db 72 KNEYTVVHL 80
|||||||

RESULT 2

YVBPK3
lysis protein t - phage K3
C;Species: phage K3
A;Note: host Escherichia coli
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A27083
R;Riede, I.
J. Bacteriol. 169, 2956-2961, 1987
A;Title: Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage
A;Reference number: A27083; MUID:87250254; PMID:3597316
A;Accession: A27083
A;Molecule type: DNA
A;Residues: 1-218 <RIE>
A;Cross-references: UNIPROT:PI0393; UNIPARC:UPI0000138941; GB:M16812; NID:g215503; PIDN:?
A;Note: the author translated the codon CAA for residue 85 as Ile and CAG for residue 20;

A;Gene: t
C;Superfamily: phage T4 lysis protein t
C;Keywords: host cell lysis

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Query Match          79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
   |:|||||
Db 139 MDEYTVHL 146

RESULT 3
YVBPT4
Lysis protein t - phage T4
C:Species: phage T4
A:Note: host Escherichia coli
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JF0028; S07395
R:Montag, D.; Degen, M.; Henning, U.
Nucleic Acids Res. 15, 6736, 1987
A:Title: Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.
A:Reference number: S07395; MUID:87316934; PMID:3628006
A:Accession: JF0028
A:Molecule type: DNA
A:Residues: 1-218 <MON>
A:Cross-references: UNIPROT:P06808; UNIPARC:UPI000005CBE7; GB:Y00408; NID:g15368; PIDN:C
A:Note: the sequence is almost identical with that of the E.coli phage K3
C:Comment: At the end of the growth cycle, phage T4 expresses two genes with lysis function
about the gene product of t, although it has been suggested that it acts as a phospholipase
C:Genetics:
A:Gene: t
A:Map position: 157.985-158.639
C:Superfamily: phage T4 lysis protein t
C:Keywords: host cell lysis; transmembrane protein
F:35-49/Domain: transmembrane #status predicted <TM>

Query Match          79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
   |:|||||
Db 139 MDEYTVHL 146

RESULT 4
B98019
conserved hypothetical protein spr1179 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98019
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B98019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KUR>
A:Cross-references: UNIPROT:Q8DPC2; UNIPARC:UPI00000E35BF; GB:AE007317; PIDN:AAK99982.1;
C:Genetics:
A:Gene: spr1179

Query Match          75.5%; Score 37; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 9.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
   |:|||||
Db 302 KMNEYITHI 310
```

```
RESULT 5
D75207
hypothetical protein PAB2235 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75207
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: D75207
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <KAW>
A:Cross-references: UNIPROT:Q9V291; UNIPARC:UPI0000063251; GB:AJ248283; GB:AL096836; NID:
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2235
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0196

Query Match          75.5%; Score 37; DB 2; Length 393;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
   |:|||||
Db 129 KLFYTHL 137

RESULT 6
T25395
hypothetical protein T28A8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25395
R:Illyod, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20027
A:Accession: T25395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-627 <WIL>
A:Cross-references: UNIPROT:Q9XU04; UNIPARC:UPI0000077722; EMBL:Z92813; PIDN:CAB07289.1;
A:Experimental source: clone T28A8
C:Genetics:
A:Gene: CESP:T28A8.6
A:Map position: 3
A:Introns: 51/2; 89/2; 183/2; 221/2; 296/2; 607/3
C:Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.d

Query Match          73.5%; Score 36; DB 2; Length 627;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
   |:|||||
Db 62 KMNEYSIEL 70

RESULT 7
T34239
hypothetical protein F26F12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34239
R:Wilson, R.; Bentley, D.; Gattung, S.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid F26F12.
A:Reference number: Z21493
A:Accession: T34239
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
```

A;Residues: 1-1829 <WIL>
A;Cross-references: UNIPROT:Q19815; UNIPARC:UPI00000765C9; EMBL:U55373; PIDN:AAC25894.1;
A;Experimental source: strain Bristol N2; clone F26F12
C;Genetics:
A;Gene: CBSP:F26F12.7
A;Map position: 5
A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1

Query Match 73.5%; Score 36; DB 2; Length 1829;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KMEYTVH 8
Db 765 KMEYTVH 771
:|||||

RESULT 8
A11406
spermidine/spermine N1-acetyl transferase homolog lmo2658 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11406
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <GLA>
A;Cross-references: UNIPROT:Q9Y419; UNIPARC:UPI000005520D; GB:NC_003210; PIDN:CAD00871.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2658

Query Match 71.4%; Score 35; DB 2; Length 159;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMEYTVH 8
Db 139 KMEYTVH 146
:|||||

RESULT 9
A11782
spermidine/spermine N1-acetyl transferase homolog lin2807 [imported] - Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11782
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11782
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <GLA>
A;Cross-references: UNIPROT:Q92711; UNIPARC:UPI00000CC9A2; GB:AL592022; PIDN:CAC98033.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin2807

Query Match 71.4%; Score 35; DB 2; Length 159;

Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMEYTVH 8
Db 139 KMEYTVH 146
:|||||

RESULT 10
H75431
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: H75431
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Fsihi, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maok, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-505 <WHI>
A;Cross-references: UNIPROT:Q9RV79; UNIPARC:UPI00000C18AC; GB:AE001964; GB:AE000513; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1150
A;Map position: 1
C;Superfamily: conserved hypothetical protein b0835

Query Match 71.4%; Score 35; DB 2; Length 505;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVH 9
Db 57 QMEYDTHL 65
:|||||

RESULT 11
AD1794
acylase and diesterase homolog lin2898 [imported] - Listeria innocua (strain Clp11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1794
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1794
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-555 <GLA>
A;Cross-references: UNIPROT:Q92621; UNIPARC:UPI00000CC9F2; GB:AL592022; PIDN:CAC98124.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin2898

Query Match 71.4%; Score 35; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMEYTVH 9
Db 483 KMEYDTHL 491
:|||||

RESULT 12

T09013
RING finger protein FXY - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
C:Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A:Title: A gene spans the pseudoautosomal boundary in mice.
A:Reference number: Z16531; MUID:98004518; PMID:9342357
A:Accession: T09013
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PAL>
A:Cross-references: UNIPARC:UPI000016C7E6; EMBL:AF026565; NID:g2589222; PIDN:AAB83986.1;
C:Genetics:
A:Gene: FXY
A:Map position: X; Y
C:Superfamily: rfp transforming protein
C:Keywords: zinc finger
P:6-65/Domain: RING finger homology <RRN>

Query Match 71.4%; Score 35; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KQNEYTVH 8
DB 444 KQNHVTVH 451

RESULT 13
T09482
ring finger protein FXY - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09482
R:Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A:Description: The human FXY maps to chromosome Xp22.3: Implications for evolution of th
A:Reference number: Z16687
A:Accession: T09482
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: UNIPROT:Q15344; UNIPARC:UPI000012F0E6; EMBL:AF035360; NID:g2827993;
C:Genetics:
A:Gene: FXY
A:Map position: Xp22.3
C:Superfamily: rfp transforming protein
P:6-65/Domain: RING finger homology <RRN>

Query Match 71.4%; Score 35; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KQNEYTVH 8
DB 444 KQNHVTVH 451

RESULT 14
A43711
replication protein repA 32K chain - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A43711
R:Erdile, L.F.; Wold, M.S.; Kelly, T.J.
J. Biol. Chem. 265, 3177-3182, 1990
A:Title: The primary structure of the 32-kDa subunit of human replication protein A.
A:Reference number: A43711; MUID:90153966; PMID:2406247
A:Accession: A43711
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-270 <ERD>
A:Cross-references: UNIPROT:P15927; UNIPARC:UPI000013379F; EMBL:J05249; NID:g337349; PIDN:
C:Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain

Query Match 69.4%; Score 34; DB 2; Length 270;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
DB 152 MNEFTTHI 159

RESULT 15
S28682
replication protein A 32K chain homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S28682
R:Nakagawa, M.; Tsukada, S.; Soma, T.; Shimizu, Y.; Miyake, S.; Iwamatsu, A.; Sugiyama, T.
Nucleic Acids Res. 19, 4292, 1991
A:Title: cDNA cloning of the murine 30-kDa protein homologous to the 32-kDa subunit of h
A:Reference number: S28682; MUID:91334146; PMID:1908076
A:Accession: S28682
A:Molecule type: mRNA
A:Residues: 1-270 <NAG>
A:Cross-references: UNIPROT:Q62193; UNIPARC:UPI0000028990; EMBL:D00812; NID:g220583; PIDN:
C:Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain

Query Match 69.4%; Score 34; DB 2; Length 270;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
DB 152 MNEFTTHI 159

Search completed: March 11, 2006, 00:40:44
Job time : 16.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KMWYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------|
| 1 | 49 | 100.0 | 253 | 1 | KLK7_HUMAN |
| 2 | 39 | 79.6 | 210 | 2 | Q9G0B3_BPAR1 |
| 3 | 39 | 79.6 | 218 | 1 | VLVS_BPK3 |
| 4 | 39 | 79.6 | 218 | 1 | VLVS_BPT4 |
| 5 | 38 | 77.6 | 261 | 1 | RFA4_HUMAN |
| 6 | 37 | 75.5 | 334 | 2 | Q8DFG2_STRR6 |
| 7 | 37 | 75.5 | 393 | 1 | PRIL_PYRAB |
| 8 | 37 | 75.5 | 401 | 2 | Q5LZS8_STRT1 |
| 9 | 37 | 75.5 | 401 | 2 | Q5M4D9_STRT2 |
| 10 | 37 | 75.5 | 498 | 2 | Q4UCK5_THEAN |
| 11 | 37 | 75.5 | 936 | 2 | Q633P6_BACZ2 |
| 12 | 36 | 73.5 | 445 | 2 | Q67Z18_ARATH |
| 13 | 36 | 73.5 | 446 | 2 | Q5WPT2_LUTLO |
| 14 | 36 | 73.5 | 603 | 2 | Q8L836_ARATH |
| 15 | 36 | 73.5 | 627 | 2 | Q9XU04_CABEL |
| 16 | 36 | 73.5 | 635 | 2 | Q9LQW1_ARATH |
| 17 | 36 | 73.5 | 733 | 2 | Q8VD00_STRMU |
| 18 | 36 | 73.5 | 753 | 2 | Q8E174_STRAS |
| 19 | 36 | 73.5 | 753 | 2 | Q8EGM8_STRAS |
| 20 | 36 | 73.5 | 1829 | 2 | Q19815_CABEL |
| 21 | 36 | 73.5 | 1849 | 2 | Q61KM2_CABEL |
| 22 | 36 | 73.5 | 6481 | 2 | Q4Q892_LEIMA |
| 23 | 35 | 71.4 | 47 | 2 | Q80274_MUSMA |
| 24 | 35 | 71.4 | 47 | 2 | Q80277_MUSCE |
| 25 | 35 | 71.4 | 47 | 2 | Q80280_SMURI |
| 26 | 35 | 71.4 | 47 | 2 | Q80283_ARVTE |
| 27 | 35 | 71.4 | 47 | 2 | Q802B4_MUSPL |
| 28 | 35 | 71.4 | 47 | 2 | Q810Y2_MUSSI |
| 29 | 35 | 71.4 | 48 | 2 | Q810X9_MUSSP |
| 30 | 35 | 71.4 | 159 | 2 | Q71WB4_LISTMA |
| 31 | 35 | 71.4 | 159 | 2 | Q8Y419_LISTMA |

| | | | | | | |
|----|----|------|-----|---|---------------|---------------------|
| 32 | 35 | 71.4 | 159 | 2 | Q92711_LISTIN | Q92711 listeria in |
| 33 | 35 | 71.4 | 197 | 2 | Q7T5S2_GVCL | Q7T5S2 cryptophleb |
| 34 | 35 | 71.4 | 232 | 2 | Q4RA68_TETNG | Q4RA68 tetraodon n |
| 35 | 35 | 71.4 | 258 | 2 | Q4X8E6_PLACH | Q4X8E6 plasmodium |
| 36 | 35 | 71.4 | 294 | 2 | Q4KC81_PSRF5 | Q4KC81 pseudomonas |
| 37 | 35 | 71.4 | 324 | 2 | Q4O709_LEIMA | Q4O709 leishmania |
| 38 | 35 | 71.4 | 394 | 2 | Q5SSA4_CRYNE | Q5SSA4 cryptococcus |
| 39 | 35 | 71.4 | 394 | 2 | Q5KGQ1_CRYNE | Q5KGQ1 cryptococcus |
| 40 | 35 | 71.4 | 400 | 2 | Q6PD02_MOUSE | Q6PD02 mus musculus |
| 41 | 35 | 71.4 | 429 | 2 | Q51YK5_MAGGR | Q51YK5 magnaporthe |
| 42 | 35 | 71.4 | 459 | 2 | Q4HB24_9DEIO | Q4HB24 deinococcus |
| 43 | 35 | 71.4 | 505 | 2 | Q9RV79_DEIRA | Q9RV79 deinococcus |
| 44 | 35 | 71.4 | 513 | 2 | Q5RFLO_PONPY | Q5RFLO pongo pygma |
| 45 | 35 | 71.4 | 555 | 2 | Q92621_LISTIN | Q92621 listeria in |

ALIGNMENTS

RESULT 1

KLK7_HUMAN STANDARD; PRT; 253 AA.

ID KLK7_HUMAN STANDARD; PRT; 253 AA.

AC P49862; Q8N5N9; Q8NFV7; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum chymotryptic enzyme) (hSCCE).

DE Name=KLK7; Synonyms=PRSS6, SCCE;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53. TISSUE=Skin;

RC MEDLINE=94308225; PubMed=8034709;

RA Hansson L., Stromqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;

RT "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";

RT J. Biol. Chem. 269:19420-19426(1994).

RL [2]

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION. TISSUE=Keratinocyte;

RC TISSUE=Keratinocyte;

RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., Diamandis E.P.;

RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal regulation.";

RL Gene 254:119-128(2000).

RN [3]

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RP PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;

RX Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Pieper B., Wang K.;

RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";

RL Gene 257:119-130(2000).

RN [4]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;

RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic itchy dermatitis.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY. TISSUE=Ovarian carcinoma;

CC RX MEDLINE=22623266; PubMed=12738725;
CC RA Dong Y., Kaushal A., Brattensand M., Nicklin J., Clements J.A.;
CC RT "differential splicing of KLK5 and KLK7 in epithelial ovarian cancer
CC RT produces novel variants with potential as cancer biomarkers.";
CC RL Clin. Cancer Res. 9:1710-1720(2003).
CC RN [6]
CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
CC RC TISSUE=Skin;
CC RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
CC RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
CC RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
CC RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
CC RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
CC RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
CC RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
CC RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
CC RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
CC RT "Generation and initial analysis of more than 15,000 full-length human
CC RT and mouse cDNA sequences.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC RN [7]
CC RP CHARACTERIZATION.
CC RX MEDLINE=95314630; PubMed=7794273;
CC RA Skjott A., Stroemqvist M., Egeirud T.;
CC RT "Primary substrate specificity of recombinant human stratum corneum
CC RT chymotryptic enzyme.";
CC RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
CC CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
CC CC structures in the cornified layer of the skin in the continuous
CC CC shedding of cells from the skin surface. Specific for amino acid
CC CC residues with aromatic side chains in the P1 position. SCCE
CC CC cleaves insulin B chain at 4-Thr-|-Cys-7, 16-Tyr-|-Leu-17, 25-
CC CC phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the
CC CC activation of precursors to inflammatory cytokines.
CC CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
CC CC also observed at the apical membrane and in cytoplasm at the
CC CC invasive front.
CC CC -!- ALTERNATIVE PRODUCTS:
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=1; Synonyms=Long;
CC CC IsoId=P49862-1; Sequence=Displayed;
CC CC Name=2; Synonyms=Short;
CC CC IsoId=P49862-2; Sequence=VSP_013581;
CC CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
CC CC expressed by keratinocytes in the epidermis. Also expressed in the
CC CC brain, mammary gland, cerebellum, spinal cord and kidney. Lower
CC CC levels in salivary glands, uterus, thymus, thyroid, placenta,
CC CC trachea and testis. Up-regulated in ovarian carcinoma, especially
CC CC late-stage serous carcinoma, compared with normal ovaries and
CC CC benign adenomas (at the protein level).
CC CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
CC CC cell line.
CC CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC CC subfamily.
CC CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC DR EMBL; L33404; AAC37551.1; -; mRNA.
CC DR EMBL; AF166330; AAD49718.1; -; Genomic_DNA.

DR EMBL; AF243527; AAG33360.1; -; Genomic_DNA.
DR EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
DR EMBL; AF411214; AAN03662.1; -; mRNA.
DR EMBL; AF411215; AAN03663.1; -; mRNA.
DR EMBL; BC032005; AAH32005.1; -; mRNA.
DR PIR; A53968; A53968.
DR HSSP; P00760; IEZX.
DR MEROPS; S01.300; -.
DR Ensemble; ENSG00000169035; Homo sapiens.
DR HGNC; HGNC:16368; KLK7.
DR H-InvDB; HIX0015373; -.
DR MIM; 604438; -.
DR GO; GO:0008236; F-serine-type peptidase activity; TAS.
DR GO; GO:0008544; P-epidermis development; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydrolyase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 22
FT PROPEP 23 29 Activation peptide.
FT CHAIN 30 253 Kallikrein 7.
FT DOMAIN 30 250 Peptidase S1.
FT ACT_SITE 70 70 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 205 205 Charge relay system (By similarity).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 C -> W (in Ref. 6; AAH32005).
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A68 CRC64;
SQ
Query Match 100.0%; Score 49; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXNEYTVHL 9
DB 72 KXNEYTVHL 80
RESULT 2
Q9G0B3 BPARI
ID Q9G0B3 BPARI PRELIMINARY; PRT; 210 AA.
AC Q9G0B3
DT 01-WAR-2001 (TRENBLrel. 16, Created)
DT 01-WAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE T protein (Fragment).
OS Bacteriophage AR1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=66711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20485545; PubMed=11029414;
RX DOI=10.1128/JB.182.21.5962-5968.2000;
RX Yu S.L., Ko K.L., Chen C.S., Chang Y.C., Syu W.J.;
RT "Characterization of the distal tail fiber locus and determination of
RT the receptor for phage AR1, which specifically infects Escherichia
RT coli O157:H7.";
RL J. Bacteriol. 182:5962-5968(2000).

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DR EMBL: AF208841; AAC29756.1; -; Genomic_DNA.
FT NEM_TER 210 210
SQ SEQUENCE 210 AA; 24348 MW; C6FF585F9F0DF68 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 210;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 139 MDEYTVHL 146

RESULT 3
VLVS_BPK3 STANDARD; PRT; 218 AA.
AC P10393;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lysis protein.
GN Name=T;
OS Bacteriophage K3.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=10674;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87250254; PubMed=3597316;
RA Riede I.;
RT "Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage genes have common ancestors.";
RL J. Bacteriol. 169:2956-2961(1987).
CC -----
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CC -----
CC EMBL; M16812; AAA88415.1; -; Genomic_DNA.
CC DR PIR; A27083; YVBPk3.
CC KW Phage lysis protein.
CC SQ SEQUENCE 218 AA; 25223 MW; 21B4DC02ACA0ECF6 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 139 MDEYTVHL 146

RESULT 4
VLVS_BPT4 STANDARD; PRT; 218 AA.
AC P06808;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lysis protein (Holin) (Protein rv).
GN Name=T; Synonyms=rv;
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87316934; PubMed=3628006;
RA Montag D., Degen M., Henning U.;
RT "Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.";
RL Nucleic Acids Res. 15:6736-6736(1987).
RN [2]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22514363; PubMed=12626685; DOI=10.1128/MMBR.67.1.86-156.2003;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome.";
RL Microbiol. Mol. Biol. Rev. 67:86-156(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-34.
RX MEDLINE=88011316; PubMed=2958637;
RA Montag D., Riede I., Eschbach M.-L., Degen M., Henning U.;
RT "Receptor-recognizing proteins of T-even type bacteriophages. Constant and hypervariable regions and an unusual case of evolution.";
RL J. Mol. Biol. 196:165-174(1987).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 202-218.
RC STRAIN=D;
RX MEDLINE=93106978; PubMed=8416914;
RA Orsini G., Ouhammouch M., Le Caer J.-P., Brody E.N.;
RT "The asfA gene of bacteriophage T4 codes for the anti-sigma 70 protein.";
RL J. Bacteriol. 175:85-93(1993).
CC -I- FUNCTION: At the end of the growth cycle, phage T4 expresses two genes with lysis function, e and t. Nothing is known about the gene product of t, although it has been suggested that it acts as a phospholipase.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL; Y00408; CAA68470.1; -; Genomic_DNA.
CC DR EMBL; AF158101; AAD42661.1; -; Genomic_DNA.
CC DR EMBL; X05677; CAA29164.1; -; Genomic_DNA.
CC DR EMBL; M99441; AAA32481.1; -; Genomic_DNA.
CC DR PIR; JF0028; YVBPf4.
CC KW Phage lysis protein; Transmembrane.
CC FT TRANSMEM 35 49 Potential.
CC SQ SEQUENCE 218 AA; 25176 MW; 9110BE11D772DF5 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 139 MDEYTVHL 146

RESULT 5
RFA4_HUMAN STANDARD; PRT; 261 AA.
ID ID_RFA4_HUMAN
AC Q13156;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Replication protein A 30 kDa subunit (RP-A) (RP-A) (Replication factor-A protein 4).
GN Name=RP24;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95280910; PubMed=7760808;
RA Keshav K.F., Chen C., Dutta A.;
RT "Rpa4, a homolog of the 34-kilodalton subunit of the replication protein A complex.";
RL Mol. Cell. Biol. 15:3119-3128(1995).
RN [2]
RP SEQUENCE REVISION TO 10.

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RA Keshav K.F.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT THR-33.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT "NIHGS-SNPs, environmental genome project, NIHES ES15478, Department
of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15772651; DOI=10.1038/nature03440;
RA Ross M.T., Graham D.V., Coffey A.J., Scherer S., McMay K., Muzny D.,
RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA Jones M.C., Hultes M.E., Andrews T.D., Scott C.E., Searle S.,
RA Ramser J., Whitaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA Cree A., Gunaratne P., Havlik P., Hodgson A., Metzker M.L.,
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Atadhyia S.,
RA Ashwell R.I., Babbage A.K., Baguley C.L., Ballabio A., Banerjee R.,
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.W.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blechnschmidt K., Brady N.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Bruford E.A., Buhaq C., Burch P., Burford D., Burgess J., Burrill W.,
RA Chavon J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA Chavez D., Chen G., Chen Y., Chen Z., Chinault C.,
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,
RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA Eades T., Ellwood M., Emery-Cohen A., Errington A.E., Evans K.L.,
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Gargoczy P.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA Hawes A., Heath P.D., Heilmann K., Hennig S., Hernandez J.,
RA Hinzmann B., Ho S., Hoffa M., Howden P.J., Huckle E.J., Hume J.,
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA Kioschis P., Klages S., Knights A.J., Kosiura A., Kovar-Smith C.,
RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA Lloyd C., Lloyd D.M., Loulsegod H., Loveland J.E., Lovell J.D.,
RA Lozada R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA McDowell J., McLaren S., McMurray A., Meidl P., Meitinger T.,
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA Mullikin J.C., Nguyen N., Nordliek G., Nyakatura G., O'dell C.N.,
RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA Ridler K.A., Schlessinger D., Schueler M.G., Sehra H.K.,
RA Shaw-Smith C., Shen H., Sheridan E.M., Showkeen R., Skuce C.D.,
RA Smith M.L., Sothran E.C., Steingrubner H.E., Steward C.A., Storey R.,
RA Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
RA Tronans A.C., d'Urso M., Verduzco D., Villaseña D., Waldron L.,
RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT "The DNA sequence of the human X chromosome.";
RL Nature 434:325-337(2005).
[5]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC "- FUNCTION: Absolutely required for simian virus 40 DNA replication
in vitro. It participates in a very early step in initiation. RP-A
is a single-stranded DNA-binding protein (By similarity).
CC "- SUBUNIT: Heterotrimer of 70, 32/30, and 14 kDa chains. The DNA-
binding activity may reside exclusively on the 70 kDa subunit.
CC "- SUBCELLULAR LOCATION: Nuclear.
CC "- TISSUE SPECIFICITY: Preferentially expressed in placental and
colon mucosa.
CC -----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; U24196; AAB08488.2; -; mRNA.
DR EMBL; AF494047; AAM09569.1; -; Genomic DNA.
DR EMBL; Z86061; CA142256.1; -; Genomic DNA.
DR EMBL; BC069791; AAB69791.1; -; mRNA.
DR EMBL; BC069808; AAB69808.1; -; mRNA.
DR EMBL; BC069824; AAB69824.1; -; mRNA.
DR HSSP; P15927; 1QUO.
DR HGNC; HGNC:30305; RPA4.
DR Reactome; Q13156; -;
DR GO; GO:0005662; C:DNA replication factor A complex; TAS.
DR GO; GO:0003697; F:single-stranded DNA binding; TAS.
DR GO; GO:0006270; P:DNA replication initiation; TAS.
DR GO; GO:0006270; P:DNA replication initiation; TAS.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR004365; OB_TRNA_NA_bd.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF01336; tRNA_anti; 1.
KW Alternative splicing; DNA replication; Nuclear protein; Polymorphism.
FT VARIANT 33 33 A -> T.
FT /FTID=VAR 019170.
SQ SEQUENCE 261 AA; 28868 MW; 6A925FAEDBE21718 CRC64;
Query Match 77.6%; Score 38; DB 1; Length 261;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 MNEYTVHL 9
DB 151 MNEFTVHI 158
RESULT 6
QBDPG2_STRR6
ID QBDPG2_STRR6 PRELIMINARY; PRT; 334 AA.
AC QBDPG2;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein sprl179.
GN Streptococcus pneumoniae-sprl179;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=21429245; PubMed=11544234;
RY DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA DeHoff B.S., Batrem S.T., Fritz L., Fu D.-J., Fuller W., Gerlinger C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AB008490; AAK99982.1; -; Genomic_DNA.
DR FIR; B98019; B98019.
DR InterPro; IPR006314; Dyp_peroxidase.
DR Pfam; PF04261; Dyp_perox; 1.
DR TIGRFAMs; TIGR01413; Dyp_perox fam; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 334 AA; 38137 MW; E207F1BC267334E5 CRC64;

Query Match 75.5%; Score 37; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
DB 302 KMEYITHI 310

RESULT 7
PRIL_PYRAB STANDARD; PRT; 393 AA.
AC Q9V291;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DNA primase large subunit (EC 2.7.7.-) (DNA primase 46 kDa subunit)
DE [p46].
GN Names=primB; OrderedLocNames=PYRAB01830; ORFNames=PAB2235;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RY DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Coost J., Weissbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
CC -1- FUNCTION: DNA primase is the polymerase that synthesizes small RNA
primers for the Okazaki fragments on both template strands at
replication forks during chromosomal DNA synthesis (By
similarity).
CC -1- SUBUNIT: Heterodimer of a small subunit and a large subunit. Both
participate in formation of the active center, but the ATP-binding
site is exclusively located on the small subunit (By similarity).
CC -1- SIMILARITY: Belongs to the eukaryotic-type primase large subunit
family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
CC EMBL; AJ248283; CAB49107.1; -; Genomic_DNA.
CC PIR; D75207; D75207.
CC HAMAP; MF 00701; -; 1.
CC InterPro; IPR007238; DNA_primase_lrg.
CC InterPro; IPR008918; HnH2.
CC Pfam; PF04104; DNA_primase_lrg; 1.
KW Complete proteome; DNA replication; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Primosome; Transferrase.
SQ SEQUENCE 393 AA; 45486 MW; 9448642FBB3FBF43 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 393;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
DB 129 KUPEYTHI 137

RESULT 8
Q5LZS8_STRT1 PRELIMINARY; PRT; 401 AA.
AC Q5LZS8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=stri1023;
OS Streptococcus thermophilus (strain CNRZ 1066).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=299768;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goldsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
RA Goffeau A., Hols F.;
RT "Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000024; AAV62601.1; -; Genomic_DNA.
DR InterPro; IPR006314; Dyp_peroxidase.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR006313; Tat_enzyme.
DR Pfam; PF04261; Dyp_perox; 1.
DR TIGRFAMs; TIGR01413; Dyp_perox fam; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
DR TIGRFAMs; TIGR01412; tat_substr_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 401 AA; 44973 MW; 1998CF52CB40CBAC CRC64;

Query Match 75.5%; Score 37; DB 2; Length 401;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
DB 370 KMEYITHI 378

RESULT 9
Q5M4D9_STRT2 PRELIMINARY; PRT; 401 AA.
AC Q5M4D9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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DE Hypothetical protein.
GN OrderedLocusNames=stul023;
OS Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=264199;
RN [1]
RX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngai K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
RT bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000023; AAV60681.1; -; Genomic_DNA.
DR InterPro; IPR006314; DYP_peroxidase.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR006313; Tat_enzyme.
DR Pfam; PF04261; DYP_perox; 1.
DR TIGRFAMs; TIGR01413; Dyp_perox_fam; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
DR TIGRFAMs; TIGR01412; tat_substr_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 401 AA; 44973 MW; 1998CF52CB40CBAC CRC64;

Query Match 75.5%; Score 37; DB 2; Length 401;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
DB 370 KMEYITHI 378

RESULT 10
Q4UCK5 THEN PRELIMINARY; PRT; 498 AA.
AC Q4UCK5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE RNA 3'-terminal phosphate cyclase like-protein, putative.
GN ORFNames=TA03460;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 3 genome sequence of Theileria annulata.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940352; CAI75446.1; -; Genomic DNA.
SQ SEQUENCE 498 AA; 55564 MW; 9135F3620AC4758A CRC64;

Query Match 75.5%; Score 37; DB 2; Length 498;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
DB 447 KLNRYSVHL 455

RESULT 11
Q633P6 BACCZ
ID Q633P6 BACCZ PRELIMINARY; PRT; 936 AA.
AC Q633P6;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BCE33L4292;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU15977.1; -; Genomic_DNA.
DR InterPro; IPR006635; NEA_transpt.
DR Pfam; PF05031; NEAT; 5.
DR SMART; SM00725; NEAT; 5.
DR PROSITE; PS50378; NEAT; 5.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 936 AA; 104539 MW; D05C843DBB02DF8A CRC64;

Query Match 75.5%; Score 37; DB 2; Length 936;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMEYTVH 8
DB 749 KMHDYTVH 756

RESULT 12
Q67Z18 ARATH PRELIMINARY; PRT; 445 AA.
AC Q67Z18;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE MRNA, partial cds, clone: RAFU23-25-J01 (MRNA, partial cds, clone:
DE RAFU23-09-L14) (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RP Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK176300; BAD44063.1; -; mRNA.
DR EMBL; AK176215; BAD43978.1; -; mRNA.
DR InterPro; IPR007145; MAP65_ASE1.
DR Pfam; PF03999; MAP65_ASE1; 1.
FT NON TER 1
SQ SEQUENCE 445 AA; 51244 MW; 00BD7C51A0D6EA45 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 445;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
DB 11 KUNEYQTHL 19

RESULT 13
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Q5WPT2_LUTLO
ID Q5WPT2_LUTLO PRELIMINARY; PRT; 446 AA.
AC Q5WPT2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 49 kDa salivary protein.
OS Lutzomyia longipalpis (Sand fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Lutzomyia; Lutzomyia.
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; AY455913; XAS16913.1; -; mRNA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 446 AA; 50670 MW; 0D8F747D8A6F1E30 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 446;
Best Local Similarity 75.0%; Pred. NO. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVH 8
Db 151 KSNIDTVH 158

RESULT 14
Q8L836_ARATH
ID Q8L836_ARATH PRELIMINARY; PRT; 603 AA.
AC Q8L836;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein Atgl14690.
GN Name=Atgl14690;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Heuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY120768; AAM53326.1; -; mRNA.
DR EMBL; BT008373; AAP37732.1; -; mRNA.

GO; GO:0005096; F:GTPase activator activity; IEA.
DR InterPro; IPR007145; MAP65_ASE1.
DR Pfam; PF03999; MAP65_ASE1; 1.
KW Hypothetical protein.
SQ SEQUENCE 603 AA; 69060 MW; 7C2B37A23CBB889D CRC64;

Query Match 73.5%; Score 36; DB 2; Length 603;
Best Local Similarity 66.7%; Pred. NO. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 169 KLINEYQTHL 177

RESULT 15
Q9XU04_CAEEL
ID Q9XU04_CAEEL PRELIMINARY; PRT; 627 AA.
AC Q9XU04;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein T28A8.6.
GN ORFNames=T28A8.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z52813; CAB07289.1; -; Genomic_DNA.
DR PIR; T25395; T25395.
DR WormBase; WBGene00012112; T28A8.6.
DR Ensembl; T28A8.6; CE18977.
DR WormPep; T28A8.6; CE18977.
DR InterPro; IPR006570; SPK.
DR Pfam; PF04435; SPK; 2.
DR SMART; SM00583; SPK; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 627 AA; 71794 MW; 4A56E4D3658EC1CC CRC64;

Query Match 73.5%; Score 36; DB 2; Length 627;
Best Local Similarity 66.7%; Pred. NO. 2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 62 KMNEYSIEL 70

Search completed: March 11, 2006, 00:38:33
Job time : 99.3333 secs
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-31

Perfect score: 49

Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 49 | 100.0 | 9 | 2 | US-09-502-600-31 |
| 2 | 49 | 100.0 | 9 | 2 | US-09-502-600-89 |
| 3 | 49 | 100.0 | 9 | 2 | US-09-502-600-109 |
| 4 | 49 | 100.0 | 9 | 2 | US-09-918-243-31 |
| 5 | 49 | 100.0 | 9 | 2 | US-09-918-243-89 |
| 6 | 49 | 100.0 | 9 | 2 | US-09-918-243-109 |
| 7 | 49 | 100.0 | 144 | 2 | US-09-618-259-4 |
| 8 | 49 | 100.0 | 154 | 2 | US-09-261-416-7 |
| 9 | 49 | 100.0 | 224 | 2 | US-08-944-483-33 |
| 10 | 49 | 100.0 | 225 | 1 | US-08-557-146-12 |
| 11 | 49 | 100.0 | 225 | 1 | US-09-027-337-4 |
| 12 | 49 | 100.0 | 225 | 1 | US-09-154-344-12 |
| 13 | 49 | 100.0 | 225 | 2 | US-09-644-600-4 |
| 14 | 49 | 100.0 | 225 | 2 | US-09-654-600A-4 |
| 15 | 49 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 16 | 49 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 17 | 49 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 18 | 49 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 19 | 49 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 20 | 49 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 21 | 49 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 22 | 49 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 23 | 39 | 79.6 | 9 | 2 | US-09-502-600-122 |
| 24 | 39 | 79.6 | 9 | 2 | US-09-918-243-122 |
| 25 | 37 | 75.5 | 9 | 2 | US-09-502-600-93 |
| 26 | 37 | 75.5 | 9 | 2 | US-09-918-243-93 |
| 27 | 37 | 75.5 | 463 | 2 | US-09-540-236-2942 |

28 35 71.4 415 2 US-09-949-016-11065 Sequence 11065, A
29 33 67.3 204 2 US-09-323-872A-13 Sequence 13, Appl
30 33 67.3 204 2 US-09-072-433-22 Sequence 22, Appl
31 33 67.3 358 2 US-09-710-279-2136 Sequence 2136, Ap
32 33 67.3 365 2 US-09-710-279-470 Sequence 470, App
33 33 67.3 366 2 US-09-134-001C-5502 Sequence 5502, Ap
34 33 67.3 799 2 US-08-909-954-4 Sequence 4, Appli
35 33 67.3 804 2 US-08-909-954-2 Sequence 2, Appli
36 32 65.3 60 2 US-09-134-001C-5184 Sequence 5184, Ap
37 32 65.3 116 2 US-09-732-210-882 Sequence 882, App
38 32 65.3 121 2 US-09-091-725-49 Sequence 49, Appl
39 32 65.3 144 2 US-09-270-767-47539 Sequence 47539, A
40 32 65.3 255 2 US-09-502-540-12375 Sequence 12375, A
41 32 65.3 393 2 US-09-248-796A-28699 Sequence 28699, A
42 32 65.3 698 2 US-09-949-016-10644 Sequence 10644, A
43 32 65.3 752 2 US-09-583-110-2714 Sequence 2714, Ap
44 32 65.3 755 2 US-09-107-433-4628 Sequence 4628, Ap
45 32 65.3 792 2 US-09-134-000C-5895 Sequence 5895, Ap

ALIGNMENTS

RESULT 1
US-09-502-600-31
; Sequence 31, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-31

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
| | | | | | | | |
Db 1 KNEYTVHL 9

RESULT 2
US-09-502-600-89
; Sequence 89, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-89

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 3

US-09-502-600-109
; Sequence 109, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR FILING DATE: 03/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-109

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 4

US-09-918-243-31
; Sequence 31, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-31

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 5

US-09-918-243-89
; Sequence 89, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-89

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 6

US-09-918-243-109
; Sequence 109, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-109

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 7

US-09-618-259-4
; Sequence 4, Application US/09618259
; Patent No. 6642013

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; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020C1P2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-618-259-4

Query Match      100.0%; Score 49; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNEYTVVHL 9
DB      9 KNEYTVVHL 17
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RESULT 8
US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: TAGD-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
; OTHER INFORMATION: domain in TAGD-12
US-09-261-416-7

Query Match      100.0%; Score 49; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNEYTVVHL 9
DB      18 KNEYTVVHL 26
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RESULT 9
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
```

```
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match      100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNEYTVVHL 9
DB      43 KNEYTVVHL 51
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RESULT 10
US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steiner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 49; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52

RESULT 11
US-09-027-337-4
/ Sequence 4, Application US/09027337B
/ Patent No. 5972616
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ APPLICANT: Tanimoto, Hirokoshi
/ TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease Overexpressed in
/ TITLE OF INVENTION: TAGD-15: Breast and Ovarian Carcinomas
/ FILE REFERENCE: D6064
/ CURRENT APPLICATION NUMBER: US/09/027,337B
/ CURRENT FILING DATE: 1998-02-20
/ NUMBER OF SEQ ID NOS: 13
/ SEQ ID NO 4
/ LENGTH: 225
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
/ OTHER INFORMATION: similar domain in TAGD-15
US-09-027-337-4

Query Match 100.0%; Score 49; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52

RESULT 12
US-09-154-344-12
/ Sequence 12, Application US/09154344
/ Patent No. 5981256
/ GENERAL INFORMATION:
/ APPLICANT: Egelrud, Torbjorn
/ APPLICANT: Hansson, Lennart
/ TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
/ TITLE OF INVENTION: Enzyme (SCCE)
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
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/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/154,344
/ FILING DATE: 16-SEP-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steiner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
US-09-154-344-12

Query Match 100.0%; Score 49; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52

RESULT 13
US-09-644-600-4
/ Sequence 4, Application US/09644600
/ Patent No. 6451500
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ APPLICANT: Tanimoto, Hirokoshi
/ TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
/ TITLE OF INVENTION: Overexpressed in Carcinomas
/ FILE REFERENCE: D6064CIP/D
/ CURRENT APPLICATION NUMBER: US/09/644,600
/ CURRENT FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: 09/421,213
/ PRIOR FILING DATE: 1999-10-20
/ PRIOR APPLICATION NUMBER: 09/027,337
/ PRIOR FILING DATE: 1998-02-20
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 4
/ LENGTH: 225
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: SCCE
US-09-644-600-4

Query Match 100.0%; Score 49; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52
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RESULT 14
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hiroto
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064C1P/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; 09/027,337
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4

Query Match 100.0%; Score 49; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
DB 44 KXNEYTVHL 52

RESULT 15
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-146-2
Query Match 100.0%; Score 49; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXNEYTVHL 9
DB 72 KXNEYTVHL 80
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Job time : 22.2222 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
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54.151 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 49 | 100.0 | 9 | 3 | US-09-918-243-31 |
| 2 | 49 | 100.0 | 9 | 3 | US-09-918-243-89 |
| 3 | 49 | 100.0 | 9 | 3 | US-09-918-243-109 |
| 4 | 49 | 100.0 | 9 | 3 | US-09-905-083-31 |
| 5 | 49 | 100.0 | 9 | 3 | US-09-905-083-89 |
| 6 | 49 | 100.0 | 9 | 3 | US-09-905-083-109 |
| 7 | 49 | 100.0 | 9 | 4 | US-10-372-521-31 |
| 8 | 49 | 100.0 | 9 | 4 | US-10-372-521-89 |
| 9 | 49 | 100.0 | 9 | 4 | US-10-372-521-109 |
| 10 | 49 | 100.0 | 9 | 5 | US-10-831-075-31 |
| 11 | 49 | 100.0 | 9 | 5 | US-10-831-075-89 |
| 12 | 49 | 100.0 | 9 | 5 | US-10-831-075-109 |
| 13 | 49 | 100.0 | 97 | 4 | US-10-262-511-100 |
| 14 | 49 | 100.0 | 136 | 5 | US-10-450-763-53737 |
| 15 | 49 | 100.0 | 144 | 3 | US-09-796-294-4 |
| 16 | 49 | 100.0 | 144 | 4 | US-10-461-787-4 |
| 17 | 49 | 100.0 | 181 | 4 | US-10-262-511-98 |
| 18 | 49 | 100.0 | 198 | 4 | US-10-262-511-96 |
| 19 | 49 | 100.0 | 224 | 3 | US-09-789-210-33 |
| 20 | 49 | 100.0 | 224 | 4 | US-10-262-511-104 |
| 21 | 49 | 100.0 | 225 | 4 | US-10-600-187-4 |
| 22 | 49 | 100.0 | 247 | 4 | US-10-262-511-102 |
| 23 | 49 | 100.0 | 250 | 4 | US-10-262-511-92 |
| 24 | 49 | 100.0 | 252 | 4 | US-10-262-511-94 |
| 25 | 49 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 26 | 49 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 27 | 49 | 100.0 | 253 | 4 | US-10-071-214-2 |

28 49 100.0 253 4 US-10-071-214-48 Sequence 48, Appl
29 49 100.0 253 4 US-10-264-283-90 Sequence 90, Appl
30 49 100.0 253 4 US-10-295-027-498 Sequence 498, App
31 49 100.0 253 4 US-10-173-999-48 Sequence 48, Appl
32 49 100.0 253 4 US-10-408-765A-639 Sequence 639, App
33 49 100.0 253 5 US-10-643-795A-95 Sequence 95, Appl
34 49 100.0 253 5 US-10-948-518-95 Sequence 95, Appl
35 49 100.0 253 5 US-10-868-490A-1 Sequence 1, Appl
36 49 100.0 257 4 US-10-344-394-38 Sequence 194726, Appl
37 40 81.6 141 4 US-10-437-963-194726 Sequence 194726, Appl
38 40 79.6 226 4 US-10-071-214-49 Sequence 49, Appl
39 39 79.6 9 3 US-09-918-243-122 Sequence 122, App
40 39 79.6 9 3 US-09-905-083-122 Sequence 122, App
41 39 79.6 9 4 US-10-372-521-122 Sequence 122, App
42 39 79.6 9 5 US-10-831-075-122 Sequence 122, App
43 39 79.6 81 4 US-10-424-599-175183 Sequence 175183, App
44 38 77.6 261 5 US-10-756-149-5592 Sequence 5592, Ap
45 37 75.5 9 3 US-09-918-243-93 Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-09-918-243-31
; Sequence 31, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-31

Query Match 100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
|||||||
Db 1 KNEYTVHL 9

RESULT 2
US-09-918-243-89
; Sequence 89, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-89

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 3
US-09-918-243-109
; Sequence 109, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-109

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 4
US-09-905-083-31
; Sequence 31, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-31

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 5
US-09-905-083-89
; Sequence 89, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-89

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 6
US-09-905-083-109
; Sequence 109, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-109

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 7
US-09-905-083-109
; Sequence 109, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-109

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9
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US-10-372-521-31
; Sequence 31, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-31
Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9
RESULT 8
US-10-372-521-89
; Sequence 89, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-89
Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9
RESULT 9
US-10-372-521-109
; Sequence 109, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
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; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-109
Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9
RESULT 10
US-10-831-075-31
; Sequence 31, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-31
Query Match 100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9
RESULT 11
US-10-831-075-89
; Sequence 89, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
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; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-89

Query Match      100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
DB      1 KMNEYTVHL 9

RESULT 12
US-10-831-075-109
; Sequence 109, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-109

Query Match      100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
DB      1 KMNEYTVHL 9

RESULT 13
US-10-262-511-100
; Sequence 100, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
```

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; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 100
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-100

Query Match      100.0%; Score 49; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
DB      53 KMNEYTVHL 61

RESULT 14
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
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; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

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Query Match 100.0%; Score 49; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KXNEYTVHL 9
Db 78 KXNEYTVHL 86

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RESULT 15
US-09-796-294-4
; Sequence 4, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4

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Query Match 100.0%; Score 49; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KXNEYTVHL 9
Db 9 KXNEYTVHL 17

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Job time : 70.4444 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 49 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 2 | 49 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 3 | 49 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 4 | 49 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 5 | 44 | 89.8 | 181 | 6 | US-10-412-748-19 |
| 6 | 33 | 67.3 | 176 | 7 | US-11-087-099-6304 |
| 7 | 33 | 67.3 | 358 | 6 | US-10-793-626-2136 |
| 8 | 33 | 67.3 | 365 | 6 | US-10-793-626-470 |
| 9 | 32 | 65.3 | 137 | 6 | US-10-485-517-159 |
| 10 | 32 | 65.3 | 688 | 7 | US-11-113-424-49 |
| 11 | 32 | 65.3 | 688 | 7 | US-11-040-218-25 |
| 12 | 32 | 65.3 | 1027 | 6 | US-10-330-773-265 |
| 13 | 32 | 65.3 | 1051 | 6 | US-10-330-773-268 |
| 14 | 31 | 63.3 | 22 | 6 | US-10-895-064-2480 |
| 15 | 31 | 63.3 | 22 | 7 | US-11-129-741-2480 |
| 16 | 31 | 63.3 | 178 | 7 | US-11-072-512-3741 |
| 17 | 31 | 63.3 | 306 | 6 | US-10-467-657-4304 |
| 18 | 31 | 63.3 | 690 | 7 | US-11-087-099-2239 |
| 19 | 30 | 61.2 | 245 | 7 | US-11-096-568A-10287 |
| 20 | 30 | 61.2 | 258 | 7 | US-11-096-568A-10286 |
| 21 | 30 | 61.2 | 357 | 7 | US-11-096-568A-9630 |
| 22 | 30 | 61.2 | 378 | 7 | US-11-096-568A-9629 |
| 23 | 30 | 61.2 | 336 | 7 | US-11-096-568A-9628 |
| 24 | 30 | 61.2 | 456 | 6 | US-10-966-483-34 |
| 25 | 30 | 61.2 | 456 | 7 | US-11-021-441-18 |

26 30 61.2 479 6 US-10-966-483-36 Sequence 36, Appl
27 30 61.2 479 7 US-11-021-441-20 Sequence 20, Appl
28 30 61.2 490 6 US-10-966-483-42 Sequence 42, Appl
29 30 61.2 490 7 US-11-021-441-26 Sequence 26, Appl
30 30 61.2 496 7 US-11-022-490A-4 Sequence 4, Appl
31 30 61.2 497 6 US-10-966-483-38 Sequence 38, Appl
32 30 61.2 497 6 US-10-966-483-40 Sequence 40, Appl
33 30 61.2 497 7 US-11-021-441-22 Sequence 22, Appl
34 30 61.2 497 6 US-10-966-483-2 Sequence 2, Appl
35 30 61.2 976 6 US-10-511-273-1 Sequence 1, Appl
36 30 61.2 976 7 US-11-233-796-2 Sequence 2, Appl
37 30 61.2 976 7 US-11-072-175-138 Sequence 138, App
38 30 61.2 976 7 US-11-203-251A-77 Sequence 77, Appl
39 30 61.2 1035 6 US-10-966-483-20 Sequence 20, Appl
40 30 61.2 1035 7 US-11-021-441-4 Sequence 4, Appl
41 30 61.2 1730 7 US-11-192-967-4 Sequence 4, Appl
42 30 61.2 1730 7 US-11-193-715-4 Sequence 4, Appl
43 30 61.2 25 6 US-10-986-501-283 Sequence 283, App
44 29 59.2 79 6 US-10-986-501-281 Sequence 281, App
45 29 59.2

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 49; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 72 KNEYTVHL 80

RESULT 2
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 49; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 72 KNEYTVHL 80

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 49; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 72 KNEYTVHL 80

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 49; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 72 KNEYTVHL 80

RESULT 5
US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

Query Match      89.8%; Score 44; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 1 MNEYTVHL 8

RESULT 6
US-11-087-099-6304
; Sequence 6304, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6304
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-11-087-099-6304

Query Match      67.3%; Score 33; DB 7; Length 176;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 34 RWNDYEAHL 42

RESULT 7
US-10-793-626-2136
; Sequence 2136, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09

```

; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2136
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2136

Query Match 67.3%; Score 33; DB 6; Length 358;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEYTVHL 9
Db 59 NEYLVHL 65

RESULT 8
US-10-793-626-470
; Sequence 470, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-470

Query Match 67.3%; Score 33; DB 6; Length 365;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEYTVHL 9
Db 66 NEYLVHL 72

RESULT 9
US-10-485-517-159
; Sequence 159, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 137

; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-159
Query Match 65.3%; Score 32; DB 6; Length 137;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 KMNEYTVH 8
Db 106 KLENYITH 113
RESULT 10
US-11-113-424-49
; Sequence 49, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-49

Query Match 65.3%; Score 32; DB 7; Length 688;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVH 8
Db 188 MNEFSVH 194

RESULT 11
US-11-040-218-25
; Sequence 25, Application US/11040218
; Publication No. US20060029983A1
; GENERAL INFORMATION:
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK.108
; CURRENT APPLICATION NUMBER: US/11/040,218
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US/10/788,197
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14581
; PRIOR FILING DATE: 2003-05-12

;
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 25
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-040-218-25

Query Match 65.3%; Score 32; DB 7; Length 688;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVH 8
Db 188 MNEFSVH 194

RESULT 12
US-10-330-773-265
; Sequence 265, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-330-773-265

Query Match 65.3%; Score 32; DB 6; Length 1027;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVH 8
Db 161 KLNHHTVH 168

RESULT 13
US-10-330-773-268
; Sequence 268, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773-268

Query Match 65.3%; Score 32; DB 6; Length 1051;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVH 8

Db 152 KLNHHTVH 159

RESULT 14
US-10-895-064-2480
; Sequence 2480, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2480
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Corononnavirus-HKU1
US-10-895-064-2480

Query Match 63.3%; Score 31; DB 6; Length 22;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVH 9
Db 6 MNDYWHV 13

RESULT 15
US-11-129-741-2480
; Sequence 2480, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR FUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2480
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Corononnavirus-HKU1
US-11-129-741-2480

Query Match 63.3%; Score 31; DB 7; Length 22;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVH 9
Db 6 MNDYWHV 13

Search completed: March 11, 2006, 01:38:38
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-32
Perfect score: 40
Sequence: 1 RLSSWVKV 9

Scoring table: BLOSUM62
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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqp1990s:*
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4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 40 | 100.0 | 9 | 4 AAE08237 | Aae08237 Human str |
| 2 | 40 | 100.0 | 9 | 8 ADR68793 | Adr68793 Human str |
| 3 | 40 | 100.0 | 144 | 8 ADI39727 | Adi39727 Stratum c |
| 4 | 40 | 100.0 | 144 | 8 ADI37151 | Adi37151 Stratum c |
| 5 | 40 | 100.0 | 224 | 6 ADA05744 | Ada05744 Human NOV |
| 6 | 40 | 100.0 | 224 | 8 ADN62908 | Adn62908 Human NOV |
| 7 | 40 | 100.0 | 224 | 8 ADV21100 | Adv21100 Human str |
| 8 | 40 | 100.0 | 225 | 4 AAB38502 | Aab38502 Human str |
| 9 | 40 | 100.0 | 247 | 6 ADA05742 | Ada05742 Human NOV |
| 10 | 40 | 100.0 | 247 | 8 ADN62906 | Adn62906 Human NOV |
| 11 | 40 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 12 | 40 | 100.0 | 250 | 8 ADN62896 | Adn62896 Human NOV |
| 13 | 40 | 100.0 | 252 | 6 ADA05734 | Ada05734 Human NOV |
| 14 | 40 | 100.0 | 252 | 8 ADN62898 | Adn62898 Human NOV |
| 15 | 40 | 100.0 | 253 | 2 AAR67888 | Aar67888 Human str |
| 16 | 40 | 100.0 | 253 | 2 AAW05383 | Aaw05383 Human amy |
| 17 | 40 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 18 | 40 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 19 | 40 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 20 | 40 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 21 | 40 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 22 | 40 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |
| 23 | 40 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 24 | 40 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |

| | | | | | |
|----|----|-------|-----|------------|--------------------|
| 25 | 40 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/an |
| 26 | 40 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 27 | 40 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antipsori |
| 28 | 40 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 29 | 40 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 30 | 40 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 31 | 40 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |
| 32 | 36 | 90.0 | 9 | 4 AAE08314 | Aae08314 Human str |
| 33 | 33 | 82.5 | 9 | 8 ADR68871 | Adr68871 Human str |
| 34 | 33 | 82.5 | 372 | 9 AEC03666 | Aec03666 Yeast gen |
| 35 | 33 | 82.5 | 394 | 5 ABP52834 | Abp52834 Anopheles |
| 36 | 33 | 82.5 | 394 | 7 ABR84477 | Abr84477 Mosquito |
| 37 | 33 | 82.5 | 417 | 7 ADD15250 | Add15250 African m |
| 38 | 32 | 80.0 | 258 | 8 ADY05796 | Ady05796 Plant ful |
| 39 | 32 | 80.0 | 293 | 8 ADX79907 | Adx79907 Plant ful |
| 40 | 32 | 80.0 | 295 | 8 ADX97198 | Adx97198 Plant ful |
| 41 | 32 | 80.0 | 295 | 8 ADX74001 | Adx74001 Plant ful |
| 42 | 32 | 80.0 | 296 | 8 ADX91086 | Adx91086 Plant ful |
| 43 | 32 | 80.0 | 298 | 8 ADY07861 | Ady07861 Plant ful |
| 44 | 32 | 80.0 | 589 | 6 ABU48685 | Abu48685 Protein e |
| 45 | 31 | 77.5 | 9 | 4 AAE08292 | Aae08292 Human str |

ALIGNMENTS

RESULT 1

AAE08237
ID AAE08237 standard; peptide; 9 AA.
XX AAE08237;
AC AAE08237;
XX
DT 01-NOV-2001 (first entry)
XX Human stratum corneum chymotrypsin enzyme peptide #2 (residues 123-131).
DE Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
FN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX (UYAR-) UNIV ARKANSAS.
XX O'brien TJ;
XX
XX WPI; 2001-514676/56.
XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
XX Claim 25; Page 102; 127pp; English.
XX
XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX Sequence 9 AA;
SQ

```

Query Match      100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 2
ADR68793
ID ADR68793 standard; peptide; 9 AA.
XX
AC ADR68793;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme peptide fragment SEQ ID NO:32.
XX
KW serine protease; stratum corneum chymotryptic enzyme; SCCE;
KW Immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon WJ, Santin A;
DR WPI; 2004-653294/63.
XX
PT Use of stratum corneum chymotryptic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Claim 5; SEQ ID NO 32; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotryptic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotryptic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotryptic enzyme).
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 3
ADI39727

Query Match      100.0%; Score 40; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.9; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 60 RLSSMVKKV 68

RESULT 4
ADI37151
ID ADI37151 standard; protein; 144 AA.
XX
AC ADI37151;
XX
DT 06-MAY-2004 (first entry)
XX
DE Stratum corneum chymotryptic enzyme (scce) catalytic domain.
XX
KW Serine protease; tumour antigen derived gene-14; TADG-14;
KW neoplastic state; cancer; ovary; breast; lung; colon; prostate;
KW chymotryptic enzyme; scce; enzyme.
XX
OS Homo sapiens.
XX

```


CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 CC

XX Sequence 224 AA;

Query Match 100.0%; Score 40; DB 6; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 109 RUSSMVKKV 117

RESULT 6

ADN62908

ID ADN62908 standard; protein; 224 AA.

XX AC ADN62908;

XX 01-JUL-2004 (first entry)

XX Human NOV18g.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX

XX Homo sapiens.

XX OS

XX US2004038223-A1.

XX 26-FEB-2004.

XX 01-OCT-2002; 2002US-00262511.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 09-OCT-2001; 2001US-0327449P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

XX 09-OCT-2001; 2001US-0328044P.

XX 12-OCT-2001; 2001US-0328056P.

XX 15-OCT-2001; 2001US-0328949P.

XX 17-OCT-2001; 2001US-0329414P.

XX 18-OCT-2001; 2001US-0330142P.

XX 18-OCT-2001; 2001US-0330309P.

XX 22-OCT-2001; 2001US-0341058P.

XX 24-OCT-2001; 2001US-0339266P.

XX 24-OCT-2001; 2001US-0343629P.

XX 29-OCT-2001; 2001US-0349575P.

XX 01-NOV-2001; 2001US-0346357P.

XX 17-APR-2002; 2002US-0373260P.

XX 19-APR-2002; 2002US-0373815P.

XX 19-APR-2002; 2002US-0373817P.

XX 19-APR-2002; 2002US-0373826P.

XX 19-APR-2002; 2002US-0373884P.

XX 22-APR-2002; 2002US-0374977P.

XX 16-MAY-2002; 2002US-0381037P.

XX 16-MAY-2002; 2002US-0381038P.

XX 17-MAY-2002; 2002US-0381042P.

XX 17-MAY-2002; 2002US-0381642P.

XX 28-MAY-2002; 2002US-0383656P.

XX 29-MAY-2002; 2002US-0383831P.

XX 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.

XX (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGRE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIP1/) DIPIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62907.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 DR diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 PT Claim 1; SEQ ID NO 104; 395pp; English.

PS The invention relates to isolated NOVX polypeptides and polynucleotides.

CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 40; DB 8; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 109 RLSSMVKKV 117

RESULT 7

ADV21100
ID ADV21100 standard; protein; 224 AA.

XX
AC ADV21100;

XX 24-FEB-2005 (first entry)

XX Human stratum corneum chymotrypsin protein.

XX Protein purification; PS133 protein; serine protease; prostate disease;
KW andrology; genitourinary disease; prostatic cancer; cytostatic;
KW protein therapy; chymotrypsin; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 26..42
/note = Catalytically functional motif
FT Domain 83..87
/note = Catalytically functional motif
FT Domain 174..179
/note = Catalytically functional motif

XX US2004241646-A1.

XX 02-DEC-2004.

XX 20-FEB-2001; 2001US-00789210.

XX 06-OCT-1997; 97US-00944483.

XX (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GRAN/) GRANADOS E.

PA (KLAS/) KLAS M R.

PA (RUSS/) RUSSELL J C.

PA (STEW/) STEWART K D.

PA (STRO/) STROUPE S D.

XX Cohen M, Colpitts TL, Friedman PN, Granados E, KLAS MR;

PI Russell JC, Stewart KD, Stroupe SD;

XX WPI; 2005-011614/01.

DR GENBANK; L33404.

XX New isolated polypeptides, useful for detecting, diagnosing, staging,
PT monitoring, prognosticating, preventing or treating, or determining
PT predisposition to diseases or conditions of the prostate such as prostate
PT cancer.

XX Example 1; SEQ ID NO 33; 96pp; English.

XX The invention relates to PS133 protein, a member of the human serine
CC protease family and its corresponding nucleic acid sequence. PS133
CC polypeptide is useful for detecting, diagnosing, staging, monitoring,
CC prognosticating, preventing or treating or determining predisposition to

CC diseases or conditions of the prostate such as prostatic cancer. The
CC present sequence is the human stratum corneum chymotrypsin protein. This
CC sequence is used to align with PS133 consensus protein.

XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 40; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 94 RLSSMVKKV 102

RESULT 8

AAB98502
ID AAB98502 standard; protein; 225 AA.

XX
AC AAB98502;

XX 03-AUG-2001 (first entry)

XX Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.

XX Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
KW tumour antigen-derived gene 15; serine protease;
KW Stratum Corneum Chymotryptic Enzyme; SCCE.

XX Homo sapiens.

XX WO200129056-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000WO-US029095.

XX 20-OCT-1999; 99US-00421213.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ, Tanimoto H;

XX WPI; 2001-381031/40.

XX Novel extracellular serine protease, termed tumor antigen-derived gene 15
PT protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
PT treatment, prevention of cancer, particularly breast, ovarian cancer.

XX Example 10; Fig 1; 130pp; English.

XX The present invention relates to human tumour antigen-derived gene 15
CC (TADG-15) protein and coding sequence (see AAB21601 and AAB98500). TADG-
CC 15 is an extracellular serine protease. It was found that TADG-15 is over-
CC -expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20
CC residues that lack TADG-15 protease activity are useful for vaccinating
CC an individual against TADG-15, having, suspected of having or at risk of
CC getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic
CC or therapeutic target in cancer. The present sequence was used in a
CC sequence homology alignment with the catalytic domain of TADG-15

XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 40; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 95 RLSSMVKKV 103

RESULT 9

ADA05742
ID ADA05742 standard; protein; 247 AA.
XX
AC ADA05742;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18f protein SEQ ID NO:102.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328499P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383566P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Raestelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05741.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 172; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 247 AA;
SQ

Query Match 100.0%; Score 40; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSNVKKV 9
|||||
Db 109 RLSSNVKKV 117

RESULT 10
ADN62906
ID ADN62906 standard; protein; 247 AA.
XX
AC ADN62906;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18f.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.

05-OCT-2001; 2001US-0327449P.
 09-OCT-2001; 2001US-0327517P.
 09-OCT-2001; 2001US-0328029P.
 09-OCT-2001; 2001US-0328044P.
 09-OCT-2001; 2001US-0328056P.
 12-OCT-2001; 2001US-0328849P.
 15-OCT-2001; 2001US-0329414P.
 17-OCT-2001; 2001US-0330142P.
 18-OCT-2001; 2001US-0330309P.
 22-OCT-2001; 2001US-0341058P.
 24-OCT-2001; 2001US-0339266P.
 24-OCT-2001; 2001US-0343629P.
 29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
 16-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383556P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 (SMIT/) SMITHSON G.
 (MILL/) MILLET I.
 (PEYM/) PEYMAN J A.
 (KEKU/) KEKUDA R.
 (JUJ/) JU J.
 (LILL/) LI L.
 (GUOX/) GUO X.
 (PAT/) PATTURAJAN M.
 (SPYT/) SPYTEK K A.
 (EDIN/) EDINGER S R.
 (ELLE/) ELLERMAN K.
 (MALY/) MALYANKAR U M.
 (ORTT/) ORT T.
 (GORM/) GORMAN L.
 (ZERH/) ZERHUSEN B D.
 (ANDE/) ANDERSON D W.
 (ZHON/) ZHONG M.
 (CATT/) CATTERTON E.
 (JINW/) JI W.
 (MILL/) MILLER C E.
 (RAST/) RASTELLI L.
 (STON/) STONE D J.
 (PENA/) PENNA C E A.
 (SHEN/) SHENOY S G.
 (SHIM/) SHIMKETS R A.
 (ROTH/) ROTHENBERG M E.
 (LEAC/) LEACH M D.
 (AGEE/) AGEE M L.
 (BERG/) BERGHS C.
 (DIP/) DIPIPPO V A.
 (EISE/) EISEN A.
 (GANG/) GANGOLLI E A.
 (RIEG/) RIEGER D K.
 (SPAD/) SPADERNA S K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI; 2004-213931/20.
 N-PSDB; ADN62905.

Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 Claim 1; SEQ ID NO 102; 395pp; English.
 The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polynucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious diseases, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.

Sequence 247 AA;
 Query Match 100.0%; Score 40; DB 8; Length 247;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
 Db 109 RLSSMVKKV 117
 |||||
 |||||

RESULT 11
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX
 AC ADA05732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18a protein SEQ ID NO:92.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373826P.
PR 22-APR-2002; 2002US-0373884P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eissen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05731.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 169-170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 40; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 120 RLSSMVKKV 128
|||||||

RESULT 12
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
AC ADN62896;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV19a.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327445P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373826P.
PR 22-APR-2002; 2002US-0373884P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JULJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTI/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATI/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62895.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX Claim 1; SEQ ID NO 92; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative

CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 250 AA;

Query Match 100.0%; Score 40; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 120 RLSSMVKKV 128
|||||||

RESULT 13

ADA05734
ID ADA05734 standard; protein; 252 AA.

XX

AC ADA05734;

XX

DT 06-NOV-2003 (first entry)

XX

DE Human NOV18b protein SEQ ID NO:94.

XX

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

KW immunomodulator; cytostatic; neurotropic; neuroprotective;

KW antiparkinsonian; antilipemic; gene therapy; human disease;

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003029424-A2.

XX

PD 10-APR-2003.

XX

PF 02-OCT-2002; 2002WO-US031373.

XX

PR 02-OCT-2001; 2001US-0326483P.

PR

PR 05-OCT-2001; 2001US-0327435P.

PR

PR 09-OCT-2001; 2001US-0327917P.

PR

PR 09-OCT-2001; 2001US-0328029P.

PR

PR 09-OCT-2001; 2001US-0328044P.

PR

PR 09-OCT-2001; 2001US-0328056P.

PR

PR 12-OCT-2001; 2001US-0328849P.

PR

PR 15-OCT-2001; 2001US-0329414P.

PR

PR 17-OCT-2001; 2001US-0330142P.

PR

PR 18-OCT-2001; 2001US-0330309P.

PR

PR 22-OCT-2001; 2001US-0341058P.

PR

PR 24-OCT-2001; 2001US-0342666P.

PR

PR 24-OCT-2001; 2001US-0343629P.

PR

PR 29-OCT-2001; 2001US-0349575P.

PR

PR 01-NOV-2001; 2001US-0346357P.

PR

PR 17-APR-2002; 2002US-0373260P.

PR

PR 19-APR-2002; 2002US-0373815P.

PR

PR 19-APR-2002; 2002US-0373817P.

PR

PR 19-APR-2002; 2002US-0373826P.

PR

PR 19-APR-2002; 2002US-0373884P.

PR

PR 22-APR-2002; 2002US-0374977P.

PR

PR 16-MAY-2002; 2002US-0381037P.

PR

PR 16-MAY-2002; 2002US-0381038P.

PR

PR 16-MAY-2002; 2002US-0381042P.

PR

PR 17-MAY-2002; 2002US-0381642P.

PR

PR 28-MAY-2002; 2002US-0383656P.

PR

PR 29-MAY-2002; 2002US-0383831P.

PR

PR 25-JUN-2002; 2002US-0391335P.

PR

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI: 2003-381626/36.
DR N-PSDB; ADA05733.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 170; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antihypertensive activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 252 AA;
SQ
Query Match 100.0%; Score 40; DB 6; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLSSMVKKV 9
Db 122 RLSSMVKKV 130
RESULT 14
ADN62898
ID ADN62898 standard; protein; 252 AA.
XX
AC ADN62898;
XX
DT 01-JUL-2004 (first entry)

XX DE Human NOV18b.
XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX OS Homo sapiens.
XX PN US2004038223-A1.
XX PD 26-FEB-2004.
XX PF 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-032914P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-32
Perfect score: 40
Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 40 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 33 | 82.5 | 282 | 2 T35294 | probable endo alpha |
| 3 | 33 | 82.5 | 372 | 2 S20056 | para-hydroxybenzoa |
| 4 | 33 | 82.5 | 560 | 2 S50401 | hypothetical prote |
| 5 | 32 | 80.0 | 350 | 1 C70009 | ABC transporter (l |
| 6 | 32 | 80.0 | 351 | 2 D90264 | biotin synthase (b |
| 7 | 32 | 80.0 | 358 | 2 T38914 | para-hydroxybenzoa |
| 8 | 32 | 80.0 | 589 | 2 A71277 | arginine-tRNA liga |
| 9 | 32 | 80.0 | 664 | 2 T50316 | hypothetical Armad |
| 10 | 31 | 77.5 | 912 | 2 H85470 | hypothetical prote |
| 11 | 31 | 77.5 | 925 | 2 T05012 | hypothetical prote |
| 12 | 30 | 75.0 | 239 | 2 T02473 | hypothetical prote |
| 13 | 30 | 75.0 | 240 | 2 T32363 | hypothetical prote |
| 14 | 30 | 75.0 | 318 | 2 I56519 | taipoxin-associate |
| 15 | 30 | 75.0 | 319 | 2 JCS402 | vitamin D receptor |
| 16 | 30 | 75.0 | 373 | 2 G75073 | hypothetical prote |
| 17 | 30 | 75.0 | 457 | 2 D85429 | cytochrome P450 11 |
| 18 | 30 | 75.0 | 532 | 2 T01759 | glycine hydroxymet |
| 19 | 30 | 75.0 | 647 | 2 A49218 | hemagglutinin homo |
| 20 | 30 | 75.0 | 833 | 2 A47528 | transcription fact |
| 21 | 30 | 75.0 | 986 | 2 E90220 | isoleucine-tRNA sy |
| 22 | 30 | 75.0 | 1167 | 2 A82543 | chromosome segrega |
| 23 | 30 | 75.0 | 1846 | 2 T33079 | hypothetical prote |
| 24 | 29 | 72.5 | 253 | 2 JCS511 | TATA-binding prote |
| 25 | 29 | 72.5 | 285 | 2 A97255 | S-adenosylmethioni |
| 26 | 29 | 72.5 | 336 | 2 E69214 | GTP-binding protei |
| 27 | 29 | 72.5 | 337 | 2 AH2591 | membrane lipoprote |
| 28 | 29 | 72.5 | 337 | 2 B97374 | Deinococcus radiod |
| 29 | 29 | 72.5 | 345 | 2 F90194 | threonine synthase |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 29 | 72.5 | 349 | 2 F84246 | hypothetical prote |
| 31 | 29 | 72.5 | 357 | 2 D96986 | probable lipoprote |
| 32 | 29 | 72.5 | 379 | 2 H75318 | membrane lipoprote |
| 33 | 29 | 72.5 | 553 | 2 A72228 | hypothetical prote |
| 34 | 29 | 72.5 | 571 | 2 S65060 | phytoene desaturas |
| 35 | 29 | 72.5 | 578 | 2 H82872 | hypothetical prote |
| 36 | 29 | 72.5 | 582 | 2 S29314 | phytoene dehydroge |
| 37 | 29 | 72.5 | 583 | 2 A45381 | phytoene dehydroge |
| 38 | 29 | 72.5 | 656 | 2 T23338 | hypothetical prote |
| 39 | 29 | 72.5 | 691 | 2 E70906 | probable beta-gluc |
| 40 | 29 | 72.5 | 839 | 2 S62963 | hypothetical prote |
| 41 | 29 | 72.5 | 1360 | 2 F66596 | hypothetical prote |
| 42 | 29 | 72.5 | 4077 | 2 T17484 | hypothetical prote |
| 43 | 29 | 72.5 | 4589 | 2 T14914 | dynein beta heavy |
| 44 | 28 | 70.0 | 41 | 2 G71376 | hypothetical prote |
| 45 | 28 | 70.0 | 63 | 2 AH2565 | hypothetical prote |

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:7
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 123 RLSSMVKKV 131

RESULT 2

T35294
probable endo alpha-1,4 polygalactosaminidase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T35294
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Accession: T35294
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-282 <SEE>
A;Cross-references: UNIPROT:Q9S208; UNIPARC:UPI000000DB294; EMBL:AL096872; PIDN:CAB51262.1
C;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5F7.23c

Query Match 82.5%; Score 33; DB 2; Length 282;
Best Local Similarity 87.5%; Pred. No. 13;

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| Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |
| QY 1 RLSSMVKK 8 : | |
| Db 265 RLSSMLKK 272 | |
| RESULT 3 | |
| S20056 | |
| para-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-) precursor - yeast (Saccharomyces | |
| N)Alternate names: 4-hydroxybenzoate hexaprenyltransferase; protein N3419; protein YNR04 | |
| C:Species: Saccharomyces cerevisiae | |
| C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004 | |
| C:Accession: S20056; S63372; J02317 | |
| J. Ashby, M.N.; Kutsunat, S.Y.; Ackerman, S.; Tzagoloff, A.; Edwards, P.A. | |
| J. Biol. Chem. 267, 4128-4136, 1992 | |
| A:Title: COQ2 is a candidate for the structural gene encoding para-hydroxybenzoate:polyp | |
| A:Reference number: S20056; MUID:92156158; PMID:1740455 | |
| A:Accession: S20056 | |
| A:Molecule type: DNA | |
| A:Residues: 1-372 <ASH> | |
| A:Cross-references: UNIPROT:P32378; UNIPARC:UPI0000127BF7; EMBL:M81698; NID:gl171252; PID | |
| R:Pohl, T.M. | |
| Submitted to the Protein Sequence Database, April 1996 | |
| A:Reference number: S63346 | |
| A:Accession: S63372 | |
| A:Molecule type: DNA | |
| A:Residues: 1-372 <POH> | |
| A:Cross-references: UNIPARC:UPI0000127BF7; EMBL:Z71656; NID:gl1302546; PID:e239832; PID:g | |
| A:Experimental source: strain S288C | |
| C:Genetics: | |
| A:Gene: SGD:COQ2 | |
| A:Cross-references: SGD:S0005324; MIPS:YNR041c | |
| A:Map position: 14R | |
| C:Keywords: isoprenoid biosynthesis; mitochondrion; transferase; transmembrane protein | |
| F:1-22/Domain: transit peptide (mitochondrion) #status predicted <TRP> | |
| F:117-133/Domain: transmembrane #status predicted <TM1> | |
| F:172-188/Domain: transmembrane #status predicted <TM2> | |
| F:203-225/Region: polyprenyl diphosphate binding #status predicted | |
| Query Match 82.5%; Score 33; DB 2; Length 372; | |
| Best Local Similarity 77.8%; Pred. No. 17; | |
| Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |
| QY 1 RLSSMVKK 9 : | |
| Db 326 RLFSMIKK 334 | |
| RESULT 4 | |
| S50401 | |
| hypothetical protein YMR145c - yeast (Saccharomyces cerevisiae) | |
| N)Alternate names: hypothetical protein YM9375.14c | |
| C:Species: Saccharomyces cerevisiae | |
| C:Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004 | |
| C:Accession: S50401 | |
| R:Badcock, K.; Churcher, C. | |
| submitted to the EMBL Data Library, December 1994 | |
| A:Reference number: S50388 | |
| A:Accession: S50401 | |
| A:Molecule type: DNA | |
| A:Residues: 1-560 <BAD> | |
| A:Cross-references: UNIPROT:P40215; UNIPARC:UPI000013B8C3; EMBL:Z47071; NID:g606429; PID | |
| C:Genetics: | |
| A:Gene: MIPS:YMR145c | |
| A:Cross-references: SGD:S0004753 | |
| A:Map position: 13R | |
| C:Superfamily: NADH dehydrogenase | |
| Query Match 82.5%; Score 33; DB 2; Length 560; | |
| Best Local Similarity 77.8%; Pred. No. 26; | |
| Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |

| | |
|--|--|
| Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |
| QY 1 RLSSMVKK 9 : | |
| Db 347 RLKTMVKV 355 | |
| RESULT 5 | |
| C70009 | |
| ABC transporter (lipoprotein) homolog yufN - Bacillus subtilis | |
| C:Species: Bacillus subtilis | |
| C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 | |
| C:Accession: C70009 | |
| R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter | |
| C:Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi | |
| A:Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; | |
| Nature 330, 249-256, 1997 | |
| A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert | |
| iech, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; | |
| Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, | |
| A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel, | |
| Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, | |
| Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, | |
| A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, | |
| akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, | |
| T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. | |
| A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. | |
| A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. | |
| A:Reference number: A69580; MUID:98044033; PMID:9384377 | |
| A:Accession: C70009 | |
| A:Status: preliminary; nucleic acid sequence not shown; translation not shown | |
| A:Molecule type: DNA | |
| A:Residues: 1-350 <KUN> | |
| A:Cross-references: UNIPROT:C05252; UNIPARC:UPI00000609A4; GB:Z99120; GB:AL009136; NID:g | |
| A:Experimental source: strain 168 | |
| C:Genetics: | |
| A:Gene: yufN | |
| C:Superfamily: ABC transporter yufN | |
| Query Match 80.0%; Score 32; DB 1; Length 350; | |
| Best Local Similarity 87.5%; Pred. No. 28; | |
| Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |
| QY 2 LSSMVKK 9 : | |
| Db 269 LTSVMKK 276 | |
| RESULT 6 | |
| D90264 | |
| biotin synthase (bioB) [imported] - Sulfolobus solfataricus | |
| C:Species: Sulfolobus solfataricus | |
| C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 | |
| C:Accession: D90264 | |
| R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-v | |
| Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. | |
| arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J. | |
| submitted to GenBank, April 2001 | |
| A:Description: Sulfolobus solfataricus complete genome. | |
| A:Reference number: A99139 | |
| A:Accession: D90264 | |
| A:Status: preliminary | |
| A:Molecule type: DNA | |
| A:Residues: 1-351 <KUB> | |
| A:Cross-references: UNIPROT:Q97226; UNIPARC:UPI0000064360; GB:AE006641; NID:gl13814305; P | |
| C:Genetics: | |
| A:Gene: bioB | |
| Query Match 80.0%; Score 32; DB 2; Length 351; | |
| Best Local Similarity 66.7%; Pred. No. 28; | |
| Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; | |
| QY 1 RLSSMVKK 9 : | |
| Db 341 RLDSLKKV 349 | |

RESULT 7

T38914
pata-hydroxybenzoate-polyphenyltransferase (EC 2.5.1.1.-) precursor, mitochondrial - fission
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38914
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21817
A:Accession: T38914
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-358 <PEA>
A:Cross-references: UNIPROT:Q10252; UNIPARC:UPI0000127EF6; EMBL:Z69728; PIDN:CAA93575.1
A:Experimental source: strain 972h-; cosmid c56F8
C:Genetics:
A:Gene: SPDB:SPAC56F8.04C
A:Map position: 1
A:Genome: nuclear
C:Keywords: mitochondrion; transferase

Query Match 80.0%; Score 32; DB 2; Length 358;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 311 RLSSMIYKV 319
|||||:|

RESULT 8

A71277
arginine-tRNA ligase (EC 6.1.1.19) (args) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: A71277
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: A71277
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-589 <COL>
A:Cross-references: UNIPROT:O83803; UNIPARC:UPI000013666B; GB:AE001253; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Superfamily: Bacillus arginine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 80.0%; Score 32; DB 2; Length 589;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 473 RISSLLKKV 481
|:|:|:|

RESULT 9

T50316
hypotheical Armadillo/beta-catenin domain protein [imported] - fission yeast (Schizosac
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: T50316
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, F
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25061

A:Accession: T50316
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-664 <MCD>
A:Cross-references: UNIPROT:Q9P7W7; UNIPARC:UPI000006B097; EMBL:AL136536; PIDN:CAB66447.1
A:Experimental source: strain 972h(-); cosmid c1703
C:Genetics:
A:Gene: SPDB:SPBC1703.03c
A:Map position: 2
A:Introns: 43/3

Query Match 80.0%; Score 32; DB 2; Length 664;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 624 RLQNMVKKI 632
|||:|:|

RESULT 10

H85470
hypotheical protein AT4g39750 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85470
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85470
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-912 <STO>
A:Cross-references: UNIPROT:Q9LDK6; UNIPARC:UPI00000A9562; GB:NC_001268; NID:g7270959; P1
C:Genetics:
A:Gene: AT4g39750
A:Map position: 4

Query Match 77.5%; Score 31; DB 2; Length 912;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 403 RFSSMIRKI 411
|:|:|:|

RESULT 11

T05012
hypotheical protein T19P19.140 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05012
R:Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.; N
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15394
A:Accession: T05012
A:Molecule type: DNA
A:Residues: 1-925 <BEV>
A:Cross-references: UNIPROT:Q9LDK6; UNIPARC:UPI000017AFB3; EMBL:AL022605
A:Experimental source: cultivar Columbia; BAC clone T19P19
C:Genetics:
A:Map position: 4
A:Introns: 142/3; 193/1; 551/1
A:Note: T19P19.140

Query Match 77.5%; Score 31; DB 2; Length 925;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|:|:|:|

Db 416 RFSSMIRKI 424

RESULT 12

T02473
hypothetical protein At2g45740 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F4118.28
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02473; C94894
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talton, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C94894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <ROU>
A:Cross-references: UNIPROT:O80845; UNIPARC:UPI000017AF99; EMBL:AC004665; NID:G3386593;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talton, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C94894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <STO>
A:Cross-references: UNIPARC:UPI000017AF99; GB:AE002093; NID:G3386621; PIDN:AAC28551.1; C
C:Genetics:
A:Gene: At2g45740; F4118.28
A:Map position: 2
A:Introns: 65/3; 90/3; 115/3; 142/3; 167/3

Query Match 75.0%; Score 30; DB 2; Length 239;

Best Local Similarity 66.7%; Pred. No. 54;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 148 RLSSSMKKI 156

RESULT 13

T32363
hypothetical protein C08E3.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32363
R:Miller, N.; Kramer, J.; Keppler, D.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid C08E3.
A:Reference number: Z21155
A:Accession: T32363
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-240 <MIL>
A:Cross-references: UNIPROT:O17203; UNIPARC:UPI000007F654; EMBL:AF025457; PIDN:AAB70970.
A:Experimental source: strain Bristol N2; clone C08E3
C:Genetics:
A:Gene: CESP:C08E3.12
A:Map position: 2
A:Introns: 167/3

Query Match 75.0%; Score 30; DB 2; Length 240;

Best Local Similarity 66.7%; Pred. No. 54;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 193 RIPSMLKKV 201

RESULT 14

156519
taipoxin-associated calcium binding protein-49 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56519
R:Dodds, D.; Schlingens, A.K.; Lu, S.Y.; Perin, M.S.
J. Neurochem. 64, 2339-2344, 1995
A:Title: Novel reticular calcium binding protein is purified on taipoxin columns.
A:Reference number: I56519; MUID:95239201; PMID:7722520
A:Accession: I56519
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-318 <RES>
A:Cross-references: UNIPROT:Q62703; UNIPARC:UPI0000133470; EMBL:U15734; NID:G606967; PID:
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:62-94/Domain: calmodulin repeat homology <EF1>
F:120-152/Domain: calmodulin repeat homology <EF2>
F:187-219/Domain: calmodulin repeat homology <EF3>
F:228-260/Domain: calmodulin repeat homology <EF4>
F:264-296/Domain: calmodulin repeat homology <EF5>

Query Match 75.0%; Score 30; DB 2; Length 318;

Best Local Similarity 55.6%; Pred. No. 71;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 66 RLQSIKKI 74

RESULT 15

JC5402
vitamin D receptor associated factor 1 - mouse
N:Alternate names: ERC-55 protein
C:Species: Mus musculus (house mouse)
C>Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5402
R:Imai, T.; Matsuda, K.; Shimojima, T.; Hashimoto, T.; Masuhiro, Y.; Kitamoto, T.; Sugita, Biochem. Biophys. Res. Commun. 233, 765-769, 1997
A:Title: ERC-55, a binding protein for the papilloma virus E6 oncoprotein, specifically
A:Reference number: JC5402; MUID:97312489; PMID:9168930
A:Accession: JC5402
A:Molecule type: mRNA
A:Residues: 1-319 <IMA>
A:Cross-references: UNIPROT:O70341; UNIPARC:UPI0000177892
C:Comment: This protein acts as a vitamin D receptor-specific cofactor modulating its fu
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
F:63-95/Domain: calmodulin repeat homology <EF1>
F:99-131/Domain: calmodulin repeat homology <EF2>
F:151-183/Domain: calmodulin repeat homology <EF3>
F:188-220/Domain: calmodulin repeat homology <EF4>
F:229-261/Domain: calmodulin repeat homology <EF5>
F:265-297/Domain: calmodulin repeat homology <EF6>

Query Match 75.0%; Score 30; DB 2; Length 319;

Best Local Similarity 55.6%; Pred. No. 72;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 67 RLQSIKKI 75

Search completed: March 11, 2006, 00:40:46

Job time : 16.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083a-32
Perfect score: 40
Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|--------------------|
| 1 | 40 | 100.0 | 140 | 2 Q5R567_PONPY | Q5R567 pongo pygma |
| 2 | 40 | 100.0 | 253 | 1 KLK7_HUMAN | P49862 homo sapien |
| 3 | 33 | 82.5 | 202 | 2 Q6VPM5_ANOGA | Q6VPM5 anopheles g |
| 4 | 33 | 82.5 | 259 | 2 Q7QIV3_ANOGA | Q7QIV3 anopheles g |
| 5 | 33 | 82.5 | 282 | 2 Q9S2Q8_STRCO | Q9S2Q8 streptomyce |
| 6 | 33 | 82.5 | 297 | 2 Q7P141_CHRVO | Q7P141 chromobacte |
| 7 | 33 | 82.5 | 372 | 1 COQ2_YEAST | P32378 saccharomyc |
| 8 | 33 | 82.5 | 417 | 1 OR1_ANOGA | Q8WTE7 anopheles g |
| 9 | 33 | 82.5 | 530 | 2 Q6FE58_CANGA | Q6FE58 candida gla |
| 10 | 33 | 82.5 | 560 | 1 YM23_YEAST | P40215 saccharomyc |
| 11 | 22 | 80.0 | 107 | 2 Q616B7_ECOLI | Q616B7 escherichia |
| 12 | 32 | 80.0 | 169 | 2 Q899C6_CLOFE | Q899C6 clostridium |
| 13 | 32 | 80.0 | 288 | 2 Q6AIB5_DESPS | Q6AIB5 desulfotale |
| 14 | 32 | 80.0 | 330 | 2 Q7NVJ5_CHRVO | Q7NVJ5 chromobacte |
| 15 | 32 | 80.0 | 350 | 1 YUFN_BAGSU | Q05252 bacillus su |
| 16 | 32 | 80.0 | 351 | 2 Q97Z26_SULSO | Q97Z26 sulfolobus |
| 17 | 22 | 80.0 | 358 | 1 COQ2_SCHPO | Q10252 schizosacch |
| 18 | 32 | 80.0 | 589 | 1 SYR_TREPA | Q83803 treponema p |
| 19 | 32 | 80.0 | 664 | 2 Q9P7W7_SCHPO | Q9P7W7 schizosacch |
| 20 | 32 | 80.0 | 697 | 2 Q4WGZ9_ASPFU | Q4WGZ9 aspergillus |
| 21 | 31 | 77.5 | 97 | 2 Q9B021_9VIRU | Q9B021 bacteriopho |
| 22 | 31 | 77.5 | 355 | 2 Q67Q22_SYMTH | Q67Q22 symbiobacte |
| 23 | 31 | 77.5 | 390 | 2 Q8LSQ6_ARATH | Q8LSQ6 arabidopsis |
| 24 | 31 | 77.5 | 510 | 2 Q5K028_ORYLA | Q5K028 oryza lat |
| 25 | 31 | 77.5 | 550 | 2 Q8W607_9CAUD | Q8W607 bacteriopho |
| 26 | 31 | 77.5 | 589 | 2 Q7XS95_ORYSA | Q7XS95 oryza sativ |
| 27 | 31 | 77.5 | 610 | 2 Q72M04_LEPIC | Q72M04 leptospira |
| 28 | 31 | 77.5 | 610 | 2 Q8EYH8_LEPIN | Q8EYH8 leptospira |
| 29 | 31 | 77.5 | 751 | 2 Q7XMH8_ORYSA | Q7XMH8 oryza sativ |
| 30 | 31 | 77.5 | 814 | 2 Q6L2C3_PICTO | Q6L2C3 picrophilus |
| 31 | 31 | 77.5 | 839 | 2 Q6LC09_CAEBR | Q6LC09 caenorhabdi |

| | | | | | |
|----|----|------|------|----------------|--------------------|
| 32 | 31 | 77.5 | 912 | 2 Q9LDK6_ARATH | Q9LDK6 arabidopsis |
| 33 | 31 | 77.5 | 2159 | 2 Q8RUQ1_MAIZE | Q8RUQ1 zea mays (m |
| 34 | 31 | 77.5 | 2159 | 2 Q8RVLI_MAIZE | Q8RVLI zea mays (m |
| 35 | 30 | 75.0 | 103 | 2 Q73IJ1_WOLFM | Q73IJ1 wolbachia p |
| 36 | 30 | 75.0 | 105 | 2 Q93W83_ARATH | Q93W83 arabidopsis |
| 37 | 30 | 75.0 | 124 | 2 Q8BP39_MOUSE | Q8BP39 mus musculu |
| 38 | 30 | 75.0 | 131 | 2 Q85IX1_ORYSA | Q85IX1 oryza sativ |
| 39 | 30 | 75.0 | 207 | 2 Q6AV20_ORYSA | Q6AV20 oryza sativ |
| 40 | 30 | 75.0 | 217 | 2 Q73E11_BACC1 | Q73E11 bacillus ce |
| 41 | 30 | 75.0 | 236 | 2 Q80845_ARATH | Q80845 arabidopsis |
| 42 | 30 | 75.0 | 240 | 2 Q17203_CABEL | Q17203 caenorhabdi |
| 43 | 30 | 75.0 | 266 | 2 Q5U925_CLODI | Q5U925 clostridium |
| 44 | 30 | 75.0 | 308 | 2 Q75K11_DICDI | Q75K11 dictyosteli |
| 45 | 30 | 75.0 | 320 | 1 KCN2_MOUSE | Q8BP32 mus musculu |

ALIGNMENTS

```
RESULT 1
Q5R567_PONPY
ID Q5R567_PONPY PRELIMINARY; PRT; 140 AA.
AC Q5R567;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp459E0918.
GN Name=DKFZp459E0918;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Suarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German CDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR860999; CAH93099.1; -; mRNA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
SQ SEQUENCE 140 AA; 15127 MW; 8DD6280252A39311 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
    |||||
Db 10 RLSSMVKKV 18

RESULT 2
KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8NSN9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
 RP TISSUE=Skin;
 RX MEDLINE=94308225; PubMed=8034709;
 RA Hanson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
 RA Egelrud T.,
 RT Cloning, expression, and characterization of stratum corneum
 RT chymotryptic enzyme. A skin-specific human serine proteinase.";
 RL J. Biol. Chem. 269:19420-19426(1994).
 RN [2]
 RC NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
 RP TISSUE=Keratinoocyte;
 RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
 RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
 RA Diamandis E.P.,
 RT The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
 RT enzyme is a new member of the human kallikrein gene family - genomic
 RT characterization, mapping, tissue expression and hormonal
 RT regulation.";
 RL Gene 254:119-128(2000).
 RN [3]
 RC NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepel B., Wang K.,
 RT Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Hansson L., Baekman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.,
 RT Epidermal overexpression of stratum corneum chymotryptic enzyme in
 RT mice; a model for chronic itchy dermatitis.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RC NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
 RP AND TISSUE SPECIFICITY.
 RC TISSUE=Ovarian carcinoma;
 RX MEDLINE=22623266; PubMed=12738725;
 RA Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.,
 RT Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer
 RT produces novel variants with potential as cancer biomarkers.";
 RL Clin. Cancer Res. 9:1710-1720(2003).
 RN [6]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RP TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Fawer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RC CHARACTERIZATION.

RX MEDLINE=95314630; PubMed=7794273;
 RA Skytt A., Stroemqvist M., Egelrud T.,
 RT Primary substrate specificity of recombinant human stratum corneum
 RT chymotryptic enzyme.";
 RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
 CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
 CC structures in the cornified layer of the skin in the continuous
 CC shedding of cells from the skin surface. Specific for amino acid
 CC residues with aromatic side chains in the P1 position. SCCE
 CC cleaves insulin B chain at 6-Leu|-Cys-7, 16-Tyr|-Leu-17, 25-
 CC Phe|-Tyr-26, and 26-Tyr|-Thr-27. Could play a role in the
 CC activation of precursors to inflammatory cytokines.
 CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
 CC also observed at the apical membrane and in cytoplasm at the
 CC invasive front.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=P49862-1; Sequences=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=P49862-2; Sequence=VSP_013581;
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
 CC expressed by keratinocytes in the epidermis. Also expressed in the
 CC brain, mammary gland, cerebellum, spinal cord and kidney. Lower
 CC levels in salivary glands, uterus, thymus, thyroid, placenta,
 CC trachea and testis. Up-regulated in ovarian carcinoma, especially
 CC late-stage serous carcinoma, compared with normal ovaries and
 CC benign adenomas (at the protein level).
 CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
 CC cell line.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; L33404; AAC37551.1; -; mRNA.
 CC EMBL; AF166330; AAD49718.1; -; Genomic DNA.
 CC EMBL; AF243527; AAG33360.1; -; Genomic DNA.
 CC EMBL; AF332583; AAK69624.1; -; Genomic DNA.
 CC EMBL; AF411214; AAN03662.1; -; mRNA.
 CC EMBL; AF411215; AAN03663.1; -; mRNA.
 CC EMBL; BC032005; AAH32005.1; -; mRNA.
 CC PIR; A53968; A53968.
 CC HSP; P00760; IEZX.
 CC MEROPS; S01.300; -.
 CC Ensembl; ENSG00000169035; Homo sapiens.
 CC HGNC; HGNC:6368; KLK7.
 CC H-InvDB; HIX0015373; -.
 CC MIM; 604438; -.
 CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
 CC GO; GO:0008544; P:epidermis development; TAS.
 CC InterPro; IPR001254; Peptidase S1_S6.
 CC InterPro; IPR001314; Peptidase_S1a.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM0020; TRYP_SPC; 1.
 CC PROSITE; PS0240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Alternative splicing; Direct protein sequencing; Glycoprotein;
 CC Hydroxylase; Protease; Serine protease; Signal; Zymogen.
 CC SIGNAL 1 22
 CC PROPEP 23 29 Activation peptide.
 CC CHAIN 30 253 Kallikrein 7.
 CC DOMAIN 30 250 Peptidase S1.
 CC ACT_SITE 70 70 Charge relay system (By similarity).
 CC ACT_SITE 112 112 Charge relay system (By similarity).
 CC ACT_SITE 205 205 Charge relay system (By similarity).

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FT CARBOHYD 246 246 N-linked (GlcNAc... ) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARGPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTId=VSP_013581.
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A7A668 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 123 RLSSMVKKV 131
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|

RESULT 3
Q6VPM5 ANOGA
ID Q6VPM5_ANOGA PRELIMINARY; PRT; 202 AA.
AC Q6VPM5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Odorant receptor 1 (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4ARR, Yaounde, and L3-5;
RA Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY334006; AAR01131.1; -; Genomic DNA.
DR EMBL; AY334007; AAR01132.1; -; Genomic DNA.
DR EMBL; AY334005; AAR01130.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005549; F:odorant binding; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007608; P:perception of smell; IEA.
DR InterPro; IPR004117; 7tm_olftrecept.
DR Pfam; PF02949; 7tm_6; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 202
FT SEQUENCE 202 AA; 23639 MW; E4F6334A7FC8EBA0 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 202;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 185 RLSSMVKKL 193
|||||
|

RESULT 4
Q7QIV3 ANOGA
ID Q7QIV3_ANOGA PRELIMINARY; PRT; 259 AA.
AC Q7QIV3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000011096.
GN ORFNames=ENSANG000000008607;
OS Anopheles gambiae str. PEST.

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008807; EAA04012.2; -; Genomic DNA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_TYP.
DR Pfam; PF00560; LRR 1; 5.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00369; LRR_TYP; 5.
KW Leucine-rich repeat; Repeat.
SQ SEQUENCE 259 AA; 28975 MW; EFB47C010FDEF6A4 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 259;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 77 RVASMVKKI 85
|||||
|

RESULT 5
Q9S2Q8 STRCO PRELIMINARY; PRT; 282 AA.
AC Q9S2Q8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Putative endo alpha-1,4 polygalactosaminidase.
GN OrderedLocustNames=SCO2178; ORFNames=SCSP7.23c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417.141-147(2002).
DR EMBL; AL939111; CAB51262.1; -; Genomic DNA.
DR PIR; T35294; T35294.
KW Complete proteome.
SQ SEQUENCE 282 AA; 30789 MW; BEECFE1743703A33 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 282;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RLSSMVKK 8
Db      265 RLSSMLKK 272

RESULT 6
O7P141_CHRVO
ID      O7P141_CHRVO PRELIMINARY;      PRT;      297 AA.
AC      O7P141;
DT      01-WAR-2004 (TREMELrel. 26, Created)
DT      01-WAR-2004 (TREMELrel. 26, Last sequence update)
DT      01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE      Hypothetical protein.
GN      OrderedLocusNames=CO0373;
OS      Chromobacterium violaceum.
OC      Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC      Neisseriaceae; Chromobacterium.
OX      NCBI_TaxID=536;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=ATCC 12472 / DSM 30191;
RX      MEDLINE=22882980; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA      Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA      Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA      Alves-Gomes J.A., Aradeo E.M., Avarize J., de Araujo M.F.F.,
RA      Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA      Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA      Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA      Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA      Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
RA      Crezinek-Paes T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA      Paninatti P., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA      Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R.,
RA      Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA      Grattapaglia D., Griard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA      Leoi L.C.T., Lima L.F.A., Loureiro M.P., Lyra M.C.C.P.,
RA      Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA      di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA      Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA      Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA      Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA      Ramalho-Neco C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA      Santos E.B.P., Santos F.R., Schneider M.P.C., Seunarez H.N.,
RA      Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA      Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA      Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA      Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT      "The complete genome sequence of Chromobacterium violaceum reveals
RT      remarkable and exploitable bacterial adaptability."
RL      Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR      EMBL; AB016911; AAQ58051.1; -; Genomic_DNA.
DR      InterPro; IPR002790; DUF88.
DR      Pfam; PF01936; DUF88; 1.
DR      ProDom; PD010896; DUF88; 1.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 297 AA; 3242 MW; FCDD2708D8087690 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 297;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      225 RLSQMVKKL 233

RESULT 7
COQ2_YEAST
ID      COQ2_YEAST
AC      P32378; Q6B113;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)

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10-MAY-2005 (Rel. 47, Last annotation update)
Para-hydroxybenzoate-polyprenyltransferase, mitochondrial precursor
(EC 2.5.1.-) [PHB:polyprenyltransferase]
Name=COQ2; OrderedLocusNames=YNR041C; ORFNames=N3419;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92156158; PubMed=1740455;
RA Ashby M.N., Kutsunai S.Y., Ackerman S., Tzagoloff A., Edwards P.A.;
RT "COQ2 is a candidate for the structural gene encoding para-
hydroxybenzoate:polyprenyltransferase.";
RL J. Biol. Chem. 267:4128-4136(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97313269; PubMed=9169873;
RA Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K.,
RA Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albertmann K.,
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
RA Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,
RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., Del Rey F.,
RA Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,
RA Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,
RA Goffeau A., Gueldener U., Herbert C.J., Heumann K., Heuss-Neitzel D.,
RA Hilbert H., Hinni K., Iraqui Housaini I., Jacquet M., Jimenez A.,
RA Joniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,
RA Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,
RA Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,
RA Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Plantia R.J.,
RA Pohl T.M., Purnelle B., Rebeschung C., Remacha M.A., Revuelta J.L.,
RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,
RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhaeselt P.,
RA Viendecels F., Visiers S., Voet M., Volckaert G., Wach A.,
RA Wambutt R., Wedler H., Zollner A., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
and its evolutionary implications.";
RL Nature 387:93-98(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAINS=S288C;
RA Marischky G., Rols A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Congaza L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the prenylation of para-hydroxybenzoate with
an all-trans polyprenyl group.
CC -!- PATHWAY: Coenzyme Q biosynthesis; second step.
CC -!- INTERACTION: Q05946:UTP13; NDEXP=1; IntAct=EBI-4919, EBI-34702;
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -!- SIMILARITY: Belongs to the ubia prenyltransferase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; M81698; AAA34507.1; -; Genomic DNA.
CC EMBL; Z71656; CAA96321.1; -; Genomic DNA.
CC EMBL; AY693097; AAT93116.1; -; Genomic DNA.
CC PIR; S20056; S20056.
CC InterAct; P32378; -;
CC GenOnline; I43386; -;
CC Ensembl; YNR041C; Saccharomyces cerevisiae.
CC SGD; S000005324; COQ2.

```

DR GO: GO:0005743; C-mitochondrial inner membrane; TAS.
DR GO: GO:0005386; F-carrier activity; TAS.
DR GO: GO:0019840; F-isoprenoid binding; TAS.
DR GO: GO:0004659; F:prenyltransferase activity; IMP.
DR GO: GO:0006743; P:ubiquinone metabolism; IMP.
DR InterPro: IPR000537; UbiA prenyltrans.
DR InterPro: IPR006370; UbiA proteo.
DR Pfam: PF01040; UbiA; 1.
DR TRIPFAM; TIGR01474; ubiA proteo; 1.
DR PROSITE; PS00943; UBI1; 1.
KW Complete proteome; Isoprene biosynthesis; Mitochondrion; Transferase;
FT TRANSIT 1 22 Mitochondrion (Potential).
FT CHAIN 23 372 Para-hydroxybenzoate--
FT TRANSMEM 92 112 polyprenyltransferase.
FT TRANSMEM 114 133 1 (Potential).
FT TRANSMEM 170 191 2 (Potential).
FT TRANSMEM 193 210 3 (Potential).
FT TRANSMEM 229 249 4 (Potential).
FT TRANSMEM 298 318 5 (Potential).
FT REGION 134 156 6 (Potential).
FT COMPIAS 29 49 Allylic polyprenyl diphosphate-binding
FT CONFLICT 273 273 site (Potential).
FT SEQUENCE 372 AA; 41001 MW; 4D9738CE248B4AD6 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 372;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 326 RLFSMIKKV 334

RESULT 8
ORI_ ANOGA STANDARD; PRT; 417 AA.
AC Q8WTE7; Q7Q1T3;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Odorant receptor Or1 (Agor1).
GN Name=ORI;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
RC STRAIN=G3;
RX MEDLINE=21593012; PubMed=11724964; DOI=10.1073/pnas.261432998;
RA Fox A.N., Pitts R.J., Robertson H.M., Carlson J.R., Zwiebel L.J.;
RT "Candidate odorant receptors from the malaria vector mosquito
RT Anopheles gambiae and evidence of down-regulation in response to blood
RT feeding.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14693-14697(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PEST;
RG Anopheles genome sequencing consortium;
RN Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION, AND INDUCTION.
RX PubMed=14724626; DOI=10.1038/427212a;
RA Hallen E.A., Fox A.N., Zwiebel L.J., Carlson J.R.;
RT "Olfaction: mosquito receptor for human-sweat odorant.";
RL Nature 427:212-213(2004).
RN [4]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RX PubMed=12364795; DOI=10.1126/science.1076196;

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RA Hill C.A., Fox A.N., Pitts R.J., Kent L.B., Tan P.L., Chrystal M.A.,
RA Cravchik A., Collins F.H., Robertson H.M., Zwiebel L.J.;
RT "G protein-coupled receptors in Anopheles gambiae.";
RL Science 298:176-178(2002).
CC -!- FUNCTION: Plays a critical role in the anthropophilic host-seeking
CC behavior; establishes the host preference to transmit malaria. May
CC participate in the phenomenon of decreased host-seeking behavior
CC in disease vector mosquitoes after blood feeding.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Female-specific antennae and maxillary palp
CC expression.
CC -!- INDUCTION: Strong response to the odorant 4-methylphenol, a
CC component of human sweat, when expressed in odorant receptor
CC deficient Drosophila. In vivo, decreased expression in antennae
CC after a blood meal.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor Dr-or
CC family.
CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 44 of February 2004;
CC WWW="http://www.expasy.org/spotlight/back_issues/sptl044.shtml".
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF364130; AAL35506.1; -; Genomic DNA.
CC EMBL; AAAB01008980; EAA13838.1; -; Genomic DNA.
CC Ensembl; ENSANG00000007844; Anopheles gambiae.
CC GO; GO:0016021; C:integral to membrane; NAS.
CC GO; GO:0005549; F:odorant binding; IDA.
CC GO; GO:0004984; F:olfactory receptor activity; IDA.
CC GO; GO:0042048; P:olfactory behavior; IDA.
CC GO; GO:0007608; P:perception of smell; IDA.
CC InterPro: IPR004117; 7tm6_olfrrecept.
CC Pfam: PF02949; 7tm6; 1.
KW G-protein coupled receptor; Multigene family; Olfaction; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 2 Extracellular (Potential).
FT TRANSMEM 3 23 1 (Potential).
FT TOPO_DOM 24 45 Cytoplasmic (Potential).
FT TRANSMEM 46 66 2 (Potential).
FT TOPO_DOM 67 73 Extracellular (Potential).
FT TRANSMEM 74 94 3 (Potential).
FT TOPO_DOM 95 133 Cytoplasmic (Potential).
FT TRANSMEM 134 154 4 (Potential).
FT TOPO_DOM 155 178 Extracellular (Potential).
FT TRANSMEM 179 199 5 (Potential).
FT TOPO_DOM 200 284 Cytoplasmic (Potential).
FT TRANSMEM 285 305 6 (Potential).
FT TOPO_DOM 306 317 Extracellular (Potential).
FT TRANSMEM 318 338 7 (Potential).
FT TOPO_DOM 339 417 Cytoplasmic (Potential).
SQ SEQUENCE 417 AA; 48520 MW; F6D07D7BD93D37F2 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 417;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 219 RLGSVMKKL 227

RESULT 9
Q8FR58 CANGA
ID Q8FR58 CANGA PRELIMINARY; PRT; 530 AA.
AC Q6FR58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P40215|Saccharomyces cerevisiae YMR145c NDHL.
GN OrderedLocusNames=CAGL01007489;

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OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boirame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller R.,
RA Niclaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulou O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380955; CAG60223.1; -; Genomic DNA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001327; FAD_pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
KW Complete proteome.
SQ SEQUENCE 530 AA; 59726 MW; 9BF95A03A0347248 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 530;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 316 RLKTMVKV 324

RESULT 10
ID YM23 YEAST STANDARD; PRT; 560 AA.
AC P40215;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 62.8 kDa protein in RPS16A-TIF34 intergenic region.
GN OrderedLocusNames=YM145C; ORFNames=YM9375.14C;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetales; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9159872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye K., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrett B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=S288c;
RA Marisichy G., Rolfs A., Richardson A., Kane M., Baqui M., Tavcher E.,
RA Hu Y., Vannberg F., Meger J., Kramer J., Moreira D., Kelley F.,
RA Zhu D., Raphael J., Hogle J., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;

RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
EMBL; Z47071; CAA87359.1; -; Genomic_DNA.
EMBL; AY632785; AAT92804.1; -; Genomic_DNA.
PIR; S50401; S50401.
IntAct; P40215; -.
GeneOnline; 142815; -.
Ensembl; YMR145C; Saccharomyces cerevisiae.
SGD; S000004753; NDEL.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0003954; P:NADH dehydrogenase activity; IDA.
DR GO; GO:0019655; P:ethanol fermentation; IMP.
DR GO; GO:0006116; P:NADH oxidation; IDA.
DR InterPro; IPR001327; FAD_pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
KW Complete proteome; FAD; Flavoprotein; Hypothetical protein; NAD;
KW Oxidoreductase; Ubiquinone.
SQ SEQUENCE 560 AA; 62774 MW; 10B1795E12E29C34 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 560;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 347 RLKTMVKV 355

RESULT 11
Q616B7 ECOLI
ID Q616B7 ECOLI PRELIMINARY; PRT; 107 AA.
AC Q616B7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Escherichia coli.
OG Plasmid R388.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Anbutsu H., Tauda M.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB182370; BAD24124.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 107 AA; 12021 MW; 1E128007B7367B5B CRC64;

Query Match 80.0%; Score 32; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 52 RVSSNVKSV 60

RESULT 12
Q899C6 CLOTE
ID Q899C6 CLOTE PRELIMINARY; PRT; 169 AA.
AC Q899C6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

DE Anaerobic ribonucleoside-triphosphate reductase activating protein
 (EC 1.97.1.1.).
 GN OrderedLocusNames=CTC00258;
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Massachusetts / E88;
 RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
 RA Brueggemann H., Baumeister S., Fricke W.F., Wiezer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 RT tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321 (2003).
 DR EMBL; AB015936; AAC34903.1; -; Genomic DNA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0014491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IEA.
 DR InterPro; IPR001989; Radical activat.
 DR InterPro; IPR007197; Radical SAM.
 DR Pfam; PF04055; Radical SAM; I.
 DR PROSITE; PS01087; RADICAL_ACTIVATING; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 169 AA; 19292 MW; CC7AB2511D3844C1 CRC64;
 Query Match 80.0%; Score 32; DB 2; Length 169;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLSSMVKK 8
 DB 85 RLASMIKK 92
 RESULT 13
 QGAIB5 DESPS
 ID Q6AIB5 DESPS PRELIMINARY; PRT; 288 AA.
 AC Q6AIB5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Probable UTP-glucose-1-phosphate uridylyltransferase.
 GN OrderedLocusNames=DPPB68;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=LSV54 / DSM 12343;
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Kuepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902 (2004).
 DR EMBL; CR522871; CAG37932.1; -; Genomic DNA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0003983; F:UTP-glucose-1-phosphate uridylyltransferase. . .; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR GO; GO:0006011; P:UDP-glucose metabolism; IEA.
 DR InterPro; IPR005771; Galu trans.
 DR InterPro; IPR005835; NTP transferase.
 DR Pfam; PF00483; NTP transferase; 1.
 DR TIGRFAMs; TIGR01099; galu; 1.
 KW Complete proteome; Nucleotidyltransferase; Transferase.
 SQ SEQUENCE 288 AA; 31782 MW; FID28AC4A04EE3CB CRC64;

Query Match 80.0%; Score 32; DB 2; Length 288;
 Best Local Similarity 87.5%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLSSMVKK 8
 DB 184 RLSSMVKK 191
 RESULT 14
 Q7NVJ5 CHRVO
 ID Q7NVJ5 CHRVO PRELIMINARY; PRT; 330 AA.
 AC Q7NVJ5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Probable membrane lipoprotein.
 GN OrderedLocusNames=CV2347;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.P.,
 RA Atolffi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogio M., Bonatto S.,
 RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasek T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunarez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
 DR EMBL; AB016918; AAQ60019.1; -; Genomic DNA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR Pfam; PF02608; Bmp; 1.
 DR Complete proteome; Lipoprotein.
 SQ SEQUENCE 330 AA; 35382 MW; 2AFAB050961AF87F CRC64;

Query Match 80.0%; Score 32; DB 2; Length 330;
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LSSMVKKV 9
 DB 247 LSSMVKKV 254

RESULT 15
 YUFN_BACSU

ID YUFN BACSU STANDARD; PRT; 350 AA.
AC O05252;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical lipoprotein yufN precursor.
GN Name=yufN; OrderedLocNames=BSU31540;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RX MEDLINE=97419515; PubMed=9274030;
RA Oudega B., Koningshoeft A., Pohl T.M., Weitzenecker T.,
RA Hilbert H., Duesterhoeft A., Pohl T.M., Weitzenecker T.,
RT "Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (rnb) and 284 degrees
(pat).";
RL Microbiology 143:2769-2774 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RX MEDLINE=9804033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Goltightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-W., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescean E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tonato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC -!- SIMILARITY: Belongs to the BMP lipoprotein family.
CC
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CC
CC EMBL; Z93937; CAB07936.1; -; Genomic DNA.
CC EMBL; Z99120; CAB15143.1; -; Genomic DNA.
CC FIC; C70009; C70009.
CC Subtilin; BG12349; yufN.
CC InterPro; IPR003760; Bmp.
CC InterPro; IPR000437; Prok_lipoprot_s.
CC Pfam; PF02608; Bmp; 1.

DR PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE_NEG.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
KW Palmitate; Signal.
FT SIGNAL 1 13 Probable.
FT CHAIN 14 350 Hypothetical lipoprotein yufN.
FT LIPID 14 14 N-palmitoyl cysteine (Probable).
FT LIPID 14 14 S-diacylglycerol cysteine (Probable).
SQ SEQUENCE 350 AA; 37349 MW; 16D5176A52A99284 CRC64;
Query Match 80.0%; Score 32; DB 1; Length 350;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LSSMVKKV 9
DB 269 LSSMVKKV 276
Search completed: March 11, 2006, 00:38:38
Job time : 100.333 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-32

Perfect score: 40

Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5-COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6-COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS-COMB.pep.*
5: /cgn2_6/prodata/1/iaa/R8-COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 40 | 100.0 | 9 | 2 | US-09-502-600-32 |
| 2 | 40 | 100.0 | 9 | 2 | US-09-918-243-32 |
| 3 | 40 | 100.0 | 144 | 2 | US-09-618-259-4 |
| 4 | 40 | 100.0 | 154 | 2 | US-09-261-416-7 |
| 5 | 40 | 100.0 | 161 | 2 | US-09-261-416-8 |
| 6 | 40 | 100.0 | 224 | 2 | US-08-944-483-33 |
| 7 | 40 | 100.0 | 225 | 1 | US-08-557-146-12 |
| 8 | 40 | 100.0 | 225 | 1 | US-09-027-337-4 |
| 9 | 40 | 100.0 | 225 | 1 | US-09-154-344-12 |
| 10 | 40 | 100.0 | 225 | 2 | US-09-644-600-4 |
| 11 | 40 | 100.0 | 225 | 2 | US-09-654-600A-4 |
| 12 | 40 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 13 | 40 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 14 | 40 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 15 | 40 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 16 | 40 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 17 | 40 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 18 | 40 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 19 | 40 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 20 | 36 | 90.0 | 9 | 2 | US-09-502-600-110 |
| 21 | 36 | 90.0 | 9 | 2 | US-09-918-243-110 |
| 22 | 31 | 77.5 | 9 | 2 | US-09-502-600-79 |
| 23 | 31 | 77.5 | 9 | 2 | US-09-502-600-87 |
| 24 | 31 | 77.5 | 9 | 2 | US-09-918-243-79 |
| 25 | 31 | 77.5 | 9 | 2 | US-09-918-243-87 |
| 26 | 30 | 75.0 | 156 | 2 | US-09-328-352-7506 |
| 27 | 29 | 72.5 | 571 | 2 | US-09-690-942-15 |

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28 29 72.5 582 1 US-08-261-086-2 Sequence 2, Appli
29 29 72.5 582 1 US-08-261-086-4 Sequence 4, Appli
30 29 72.5 582 1 US-08-261-086-6 Sequence 6, Appli
31 28 70.0 90 2 US-09-248-796A-23383 Sequence 23383, A
32 28 70.0 154 2 US-09-328-352-7990 Sequence 7990, Ap
33 28 70.0 174 2 US-09-248-796A-18044 Sequence 18044, A
34 28 70.0 214 2 US-09-583-110-3154 Sequence 3154, Ap
35 28 70.0 217 2 US-09-107-433-4867 Sequence 4867, Ap
36 28 70.0 218 2 US-09-270-767-49085 Sequence 49085, A
37 28 70.0 250 2 US-09-107-532A-4737 Sequence 4737, Ap
38 28 70.0 289 2 US-09-107-532A-6154 Sequence 6154, Ap
39 28 70.0 341 2 US-09-134-001C-3650 Sequence 3650, Ap
40 28 70.0 357 2 US-09-710-279-1360 Sequence 1360, Ap
41 28 70.0 405 2 US-09-134-000C-5465 Sequence 5465, Ap
42 28 70.0 448 2 US-09-871-212-8 Sequence 8, Appli
43 28 70.0 459 2 US-09-491-785-2 Sequence 2, Appli
44 28 70.0 459 2 US-09-710-279-2462 Sequence 2462, Ap
45 28 70.0 464 2 US-09-134-001C-4562 Sequence 4562, Ap

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ALIGNMENTS

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RESULT 1
US-09-502-600-32
; Sequence 32, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-502-600-32

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Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

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RESULT 2
US-09-918-243-32
; Sequence 32, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-918-243-32

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 1 RLSSMVKKV 9

RESULT 3

US-09-618-259-4
; Sequence 4, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (sccc) catalytic domain
US-09-618-259-4

Query Match 100.0%; Score 40; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 60 RLSSMVKKV 68

RESULT 4

US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: chymotryptic enzyme (Sccc) homologous to similar
; OTHER INFORMATION: domain in TADG-12
US-09-261-416-7

Query Match 100.0%; Score 40; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 69 RLSSMVKKV 77

RESULT 5

US-09-261-416-8
; Sequence 8, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 8
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of hepsin (Heps)
; OTHER INFORMATION: homologous to similar domain in TADG-12
US-09-261-416-8

Query Match 100.0%; Score 40; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 75 RLSSMVKKV 83

RESULT 6

US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

US-08-944-483-33

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183 US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 40; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||||
DB 94 RLSSMVKKV 102

RESULT 7
US-08-557-146-12
Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

DB 95 RLSSMVKKV 103
|||||

RESULT 8

US-09-027-337-4
Sequence 4, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotooshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Query Match 100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||||
DB 95 RLSSMVKKV 103

RESULT 9

US-09-154-344-12
Sequence 12, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-09-154-344-12

Query Match          100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 95 RLSSMVKKV 103

RESULT 10
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4

Query Match          100.0%; Score 40; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 95 RLSSMVKKV 103

RESULT 11
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4

Query Match          100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 95 RLSSMVKKV 103

RESULT 12
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match          100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 13
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-08-824-874-3

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 14
US-09-154-344-2
Sequence 2, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 15
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bialock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMYKKV 9
| | | | |
Db 123 RLSSMYKKV 131

Search completed: March 11, 2006, 01:24:24
Job time : 22.2222 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-32

Perfect score: 40

Sequence: 1 RLSSWVKV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 40 | 100.0 | 9 | 3 | US-09-918-243-32 |
| 2 | 40 | 100.0 | 9 | 3 | US-09-905-083-32 |
| 3 | 40 | 100.0 | 9 | 4 | US-10-372-521-32 |
| 4 | 40 | 100.0 | 9 | 5 | US-10-831-075-32 |
| 5 | 40 | 100.0 | 30 | 5 | US-10-831-075-137 |
| 6 | 40 | 100.0 | 144 | 3 | US-09-796-294-4 |
| 7 | 40 | 100.0 | 144 | 4 | US-10-461-787-4 |
| 8 | 40 | 100.0 | 224 | 3 | US-09-789-210-33 |
| 9 | 40 | 100.0 | 224 | 4 | US-10-262-511-104 |
| 10 | 40 | 100.0 | 225 | 4 | US-10-600-187-4 |
| 11 | 40 | 100.0 | 247 | 4 | US-10-262-511-102 |
| 12 | 40 | 100.0 | 250 | 4 | US-10-262-511-92 |
| 13 | 40 | 100.0 | 252 | 4 | US-10-262-511-94 |
| 14 | 40 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 15 | 40 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 16 | 40 | 100.0 | 253 | 4 | US-10-071-214-2 |
| 17 | 40 | 100.0 | 253 | 4 | US-10-071-214-48 |
| 18 | 40 | 100.0 | 253 | 4 | US-10-264-283-90 |
| 19 | 40 | 100.0 | 253 | 4 | US-10-295-027-498 |
| 20 | 40 | 100.0 | 253 | 4 | US-10-173-999-48 |
| 21 | 40 | 100.0 | 253 | 4 | US-10-408-765A-639 |
| 22 | 40 | 100.0 | 253 | 5 | US-10-643-795A-95 |
| 23 | 40 | 100.0 | 253 | 5 | US-10-948-518-95 |
| 24 | 40 | 100.0 | 253 | 5 | US-10-868-490A-1 |
| 25 | 40 | 100.0 | 257 | 4 | US-10-344-394-38 |
| 26 | 36 | 90.0 | 9 | 3 | US-09-918-243-110 |
| 27 | 36 | 90.0 | 9 | 3 | US-09-905-083-110 |

28 36 90.0 9 4 US-10-372-521-110 Sequence 110, App
29 36 90.0 9 5 US-10-831-075-110 Sequence 110, App
30 33 82.5 84 4 US-10-424-599-244024 Sequence 244024,
31 33 82.5 369 4 US-10-437-963-155539 Sequence 155539,
32 33 82.5 394 4 US-10-094-240-4 Sequence 4, Appli
33 33 82.5 394 4 US-10-056-405-4 Sequence 4, Appli
34 33 82.5 417 5 US-10-954-778-1 Sequence 1, Appli
35 32 80.0 258 4 US-10-425-114-61611 Sequence 61611, A
36 32 80.0 293 4 US-10-425-114-49273 Sequence 49273, A
37 32 80.0 295 4 US-10-425-114-43367 Sequence 43367, A
38 32 80.0 295 4 US-10-425-114-59862 Sequence 59862, A
39 32 80.0 296 4 US-10-425-114-53750 Sequence 53750, A
40 32 80.0 298 4 US-10-425-114-63676 Sequence 63676, A
41 32 80.0 589 4 US-10-282-122A-78609 Sequence 78609, A
42 31 77.5 9 3 US-09-918-243-79 Sequence 79, Appl
43 31 77.5 9 3 US-09-918-243-87 Sequence 87, Appl
44 31 77.5 9 3 US-09-905-083-79 Sequence 79, Appl
45 31 77.5 9 3 US-09-905-083-87 Sequence 87, Appl

ALIGNMENTS

RESULT 1

US-09-918-243-32

; Sequence 32, Application US/09918243

; Patent No. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santini, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 32

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 123-131 of the SCCE protein

US-09-918-243-32

Query Match 100.0%; Score 40; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSWVKV 9

|||||||

Db 1 RLSSWVKV 9

RESULT 2

US-09-905-083-32

; Sequence 32, Application US/09905083

; Patent No. US20020146708A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP/C/Div

; CURRENT APPLICATION NUMBER: US/09/905,083

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 09/502,600

; PRIOR FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 32

; LENGTH: 9

; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-905-083-32

Query Match      100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 3
US-10-372-521-32
; Sequence 32, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-10-372-521-32

Query Match      100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 4
US-10-831-075-32
; Sequence 32, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-10-831-075-32

Query Match      100.0%; Score 40; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 5
US-10-831-075-137
; Sequence 137, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 137
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 110-139 of the SCCE protein
US-10-831-075-137

Query Match      100.0%; Score 40; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 14 RLSSMVKKV 22

RESULT 6
US-09-796-294-4
; Sequence 4, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4

Query Match      100.0%; Score 40; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 60 RLSSMVKKV 68
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RESULT 7
US-10-461-787-4
; Sequence 4, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. US20030199010A1 Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/618,259
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (sccc) catalytic domain
US-10-461-787-4

Query Match      100.0%; Score 40; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY      1 RLSSMVKKV 9
        |||||
Db       60 RLSSMVKKV 68

RESULT 8
US-09-789-210-33
; Sequence 33, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,210
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,483
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183. US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match      100.0%; Score 40; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY      1 RLSSMVKKV 9
        |||||
Db       94 RLSSMVKKV 102

RESULT 9
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
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; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104

Query Match      100.0%; Score 40; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
        |||||
Db      109 RLSSMVKKV 117

RESULT 10
US-10-600-187-4
; Sequence 4, Application US/10600187
; Publication No. US20040086910A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotochi
; TITLE OF INVENTION: TAG-15: An Extracellular Serine Protease
; FILE OF INVENTION: Overexpressed in Carcinomas
; CURRENT APPLICATION NUMBER: US/10/600,187
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/654,600A
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; 09/027,337
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-10-600-187-4

Query Match      100.0%; Score 40; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
        |||||
Db      95 RLSSMVKKV 103

RESULT 11
US-10-262-511-102
; Sequence 102, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.

```

```

; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 102
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-102

Query Match      100.0%; Score 40; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
        |||||
Db      109 RLSSMVKKV 117

RESULT 12
US-10-262-511-92
; Sequence 92, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-05-17
; PRIOR FILING DATE: 2002-10-09
; PRIOR FILING DATE: 2002-05-16
; PRIOR FILING DATE: 2002-04-17
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SEQ ID NO 92
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92

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Query Match 100.0%; Score 40; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RLSSMVKKV 9
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Db 120 RLSSMVKKV 128

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RESULT 13
US-10-262-511-94

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; Sequence 94, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-05-17
; PRIOR FILING DATE: 2002-10-09
; PRIOR FILING DATE: 2002-05-16
; PRIOR FILING DATE: 2002-04-17
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 94
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-94

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Query Match 100.0%; Score 40; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RLSSMVKKV 9
    |||||
Db 122 RLSSMVKKV 130

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-32

Perfect score: 40

Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 40 | 100.0 | 181 | 6 | US-10-412-748-19 |
| 2 | 40 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 3 | 40 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 4 | 40 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 5 | 40 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 6 | 30 | 75.0 | 220 | 7 | US-11-096-568A-29743 |
| 7 | 30 | 75.0 | 236 | 7 | US-11-096-568A-29742 |
| 8 | 30 | 75.0 | 334 | 7 | US-11-096-568A-32412 |
| 9 | 30 | 75.0 | 385 | 7 | US-11-096-568A-32411 |
| 10 | 30 | 75.0 | 390 | 7 | US-11-096-568A-32410 |
| 11 | 30 | 75.0 | 457 | 7 | US-11-208-308-13 |
| 12 | 30 | 75.0 | 524 | 6 | US-11-208-308-11 |
| 13 | 30 | 75.0 | 524 | 7 | US-11-208-308-11 |
| 14 | 30 | 75.0 | 524 | 7 | US-11-208-308-12 |
| 15 | 29 | 72.5 | 187 | 7 | US-11-096-568A-24167 |
| 16 | 29 | 72.5 | 235 | 7 | US-11-096-568A-24166 |
| 17 | 29 | 72.5 | 247 | 7 | US-11-096-568A-24165 |
| 18 | 29 | 72.5 | 691 | 7 | US-11-087-099-4595 |
| 19 | 28 | 70.0 | 185 | 7 | US-11-087-099-12061 |
| 20 | 28 | 70.0 | 235 | 7 | US-11-087-099-9520 |
| 21 | 28 | 70.0 | 235 | 7 | US-11-087-099-11057 |
| 22 | 28 | 70.0 | 236 | 7 | US-11-098-686-10100 |
| 23 | 28 | 70.0 | 238 | 7 | US-11-087-099-3228 |
| 24 | 28 | 70.0 | 249 | 7 | US-11-087-099-6428 |
| 25 | 28 | 70.0 | 319 | 6 | US-10-510-941-4 |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 26 | 28 | 70.0 | 357 | 6 | US-10-793-626-1360 | Sequence 1360, Ap |
| 27 | 28 | 70.0 | 459 | 6 | US-10-793-626-2462 | Sequence 2462, Ap |
| 28 | 28 | 70.0 | 523 | 7 | US-11-094-917-37 | Sequence 37, Appl |
| 29 | 28 | 70.0 | 896 | 7 | US-11-192-219-3 | Sequence 3, Appli |
| 30 | 28 | 70.0 | 898 | 7 | US-11-166-730-3 | Sequence 3, Appli |
| 31 | 28 | 70.0 | 923 | 7 | US-11-192-219-4 | Sequence 4, Appli |
| 32 | 28 | 70.0 | 1165 | 7 | US-11-192-219-2 | Sequence 2, Appli |
| 33 | 28 | 70.0 | 1165 | 7 | US-11-202-330-4 | Sequence 4, Appli |
| 34 | 27 | 67.5 | 235 | 7 | US-11-087-099-4958 | Sequence 4958, Ap |
| 35 | 27 | 67.5 | 236 | 7 | US-11-087-099-330 | Sequence 330, App |
| 36 | 27 | 67.5 | 317 | 6 | US-10-329-258-29 | Sequence 29, Appl |
| 37 | 27 | 67.5 | 357 | 7 | US-11-264-728-44 | Sequence 44, Appl |
| 38 | 27 | 67.5 | 366 | 7 | US-11-087-099-1085 | Sequence 1085, Ap |
| 39 | 27 | 67.5 | 368 | 7 | US-11-087-099-11516 | Sequence 11516, A |
| 40 | 27 | 67.5 | 396 | 7 | US-11-096-568A-33127 | Sequence 33127, A |
| 41 | 27 | 67.5 | 422 | 7 | US-11-116-203-4 | Sequence 4, Appli |
| 42 | 27 | 67.5 | 423 | 6 | US-10-063-703-106 | Sequence 106, App |
| 43 | 27 | 67.5 | 423 | 7 | US-11-102-240-106 | Sequence 106, App |
| 44 | 27 | 67.5 | 425 | 7 | US-11-098-686-10671 | Sequence 10671, A |
| 45 | 27 | 67.5 | 441 | 7 | US-11-096-568A-30776 | Sequence 30776, A |

ALIGNMENTS

RESULT 1
US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

Query Match 100.0%; Score 40; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

QY 1 RLSSMVKKV 9
|||||
Db 51 RLSSMVKKV 59

RESULT 2
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 5
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 123 RLSSMVKKV 131

RESULT 6
US-11-096-568A-29743
; Sequence 29743, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29743
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(220)
; OTHER INFORMATION: Ceres Seq. ID no. 4927738
US-11-096-568A-29743

Query Match      75.0%; Score 30; DB 7; Length 220;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 132 RLSSMVKKI 140

RESULT 7
US-11-096-568A-29742
; Sequence 29742, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29742
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(236)
; OTHER INFORMATION: Ceres Seq. ID no. 4927737
US-11-096-568A-29742

Query Match 75.0%; Score 30; DB 7; Length 236;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 148 RLSSMKKI 156
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RESULT 8
US-11-096-568A-32412
; Sequence 32412, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32412
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(334)
; OTHER INFORMATION: Ceres Seq. ID no. 13592964
US-11-096-568A-32412

Query Match 75.0%; Score 30; DB 7; Length 334;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSMVKK 8
Db 316 LSSMIKK 322
|||||

RESULT 9
US-11-096-568A-32411
; Sequence 32411, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32411
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (1)..(385)
; OTHER INFORMATION: Ceres Seq. ID no. 13592963
US-11-096-568A-32411

Query Match 75.0%; Score 30; DB 7; Length 385;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSMVKK 8
Db 367 LSSMIKK 373
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RESULT 10
US-11-096-568A-32410
; Sequence 32410, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32410
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(390)
; OTHER INFORMATION: Ceres Seq. ID no. 13592962
US-11-096-568A-32410

Query Match 75.0%; Score 30; DB 7; Length 390;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSMVKK 8
Db 372 LSSMIKK 378
|||||

RESULT 11
US-11-208-308-13
; Sequence 13, Application US/11208308
; Publication No. US20060041952A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong C.
; TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
; FILE REFERENCE: 18207-006001
; CURRENT APPLICATION NUMBER: US/11/208,308
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: 60/603,533
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(457)
; OTHER INFORMATION: Public GI no. 4006922
US-11-208-308-13

Query Match 75.0%; Score 30; DB 7; Length 457;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 RLSSMVKKV 9
Db 199 RLKMKVKV 207

RESULT 12
US-10-507-106-4
; Sequence 4, Application US/10507106
; Publication No. US20050246797A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Agency
; TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
; FILE REFERENCE: 26352U (P503-311pCt)
; CURRENT APPLICATION NUMBER: US/10/507,106
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-507-106-4
Query Match 75.0%; Score 30; DB 6; Length 524;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 266 RLKMKVKV 274

RESULT 13
US-11-208-308-11
; Sequence 11, Application US/11208308
; Publication No. US20060041952A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong C.
; TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
; FILE REFERENCE: 18207-006001
; CURRENT APPLICATION NUMBER: US/11/208,308
; PRIOR FILING DATE: 2005-08-19
; CURRENT APPLICATION NUMBER: 60/603,533
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(524)
; OTHER INFORMATION: Public GI no. 13878393
US-11-208-308-11
Query Match 75.0%; Score 30; DB 7; Length 524;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 266 RLKMKVKV 274

RESULT 14
US-11-208-308-12
; Sequence 12, Application US/11208308
; Publication No. US20060041952A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong C.
; TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
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; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 18207-006001
; CURRENT APPLICATION NUMBER: US/11/208,308
; PRIOR FILING DATE: 2005-08-19
; CURRENT APPLICATION NUMBER: 60/603,533
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(524)
; OTHER INFORMATION: Public GI no. 18419825
US-11-208-308-12
Query Match 75.0%; Score 30; DB 7; Length 524;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 266 RLKMKVKV 274

RESULT 15
US-11-096-568A-24167
; Sequence 24167, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; PRIOR FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24167
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(187)
; OTHER INFORMATION: Ceres Seq. ID no. 12419624
US-11-096-568A-24167
Query Match 72.5%; Score 29; DB 7; Length 187;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 152 RLSECVKKI 160

Search completed: March 11, 2006, 01:38:39
Job time : 9 secs
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1990s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 40 | 100.0 | 9 | 4 AAE08238 | Aae08238 Human str |
| 2 | 40 | 100.0 | 9 | 8 ADR68794 | Adr68794 Human str |
| 3 | 40 | 100.0 | 136 | 4 ABG23378 | Abg23378 Novel hum |
| 4 | 40 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 5 | 40 | 100.0 | 198 | 8 ADN62900 | Adn62900 Human NOV |
| 6 | 40 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 7 | 40 | 100.0 | 250 | 8 ADN62896 | Adn62896 Human NOV |
| 8 | 40 | 100.0 | 253 | 2 AAR05383 | Aar05383 Human str |
| 9 | 40 | 100.0 | 253 | 2 AAW05383 | Aaw05383 Human amy |
| 10 | 40 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 11 | 40 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 12 | 40 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 13 | 40 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 14 | 40 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 15 | 40 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |
| 16 | 40 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 17 | 40 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 18 | 40 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/tu |
| 19 | 40 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 20 | 40 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antiporci |
| 21 | 40 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 22 | 40 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 23 | 40 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 24 | 40 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |

| | | | | | | |
|----|----|------|-----|---|----------|--------------------|
| 25 | 38 | 95.0 | 812 | 7 | ABO65558 | Abo65558 Klebsiell |
| 26 | 36 | 90.0 | 9 | 4 | AAE08240 | Aae08240 Human str |
| 27 | 36 | 90.0 | 9 | 4 | AAE08241 | Aae08241 Human str |
| 28 | 36 | 90.0 | 9 | 8 | ADR68796 | Adr68796 Human str |
| 29 | 36 | 90.0 | 9 | 8 | ADR68797 | Adr68797 Human str |
| 30 | 35 | 87.5 | 61 | 4 | AAO12472 | Aao12472 Human pol |
| 31 | 35 | 87.5 | 142 | 4 | AAB63580 | Aab63580 Human gas |
| 32 | 35 | 87.5 | 156 | 4 | AAB63578 | Aab63578 Human gas |
| 33 | 35 | 87.5 | 159 | 4 | AAB63582 | Aab63582 Human gas |
| 34 | 34 | 85.0 | 23 | 4 | ABB43858 | Abb43858 Peptide # |
| 35 | 34 | 85.0 | 23 | 4 | AAM37771 | Aam37771 Peptide # |
| 36 | 34 | 85.0 | 23 | 4 | AAM64837 | Aam64837 Human bra |
| 37 | 34 | 85.0 | 23 | 4 | ABG59233 | Abg59233 Human liv |
| 38 | 34 | 85.0 | 23 | 5 | ABG46617 | Abg46617 Human pep |
| 39 | 34 | 85.0 | 115 | 7 | ADP59165 | Adp59165 Human pol |
| 40 | 34 | 85.0 | 187 | 8 | ADX94464 | Adx94464 Plant ful |
| 41 | 34 | 85.0 | 201 | 5 | ABB78636 | Abb78636 Rat OST10 |
| 42 | 34 | 85.0 | 369 | 8 | ADL91113 | Adl91113 Bovine lu |
| 43 | 34 | 85.0 | 369 | 8 | ADL91117 | Adl91117 Bovine lu |
| 44 | 34 | 85.0 | 369 | 8 | ADL91127 | Adl91127 Bovine lu |
| 45 | 34 | 85.0 | 371 | 2 | AAR75642 | Aar75642 Bovine co |

ALIGNMENTS

RESULT 1
AAE08238
ID AAE08238 standard; peptide; 9 AA.
XX AC AAE08238;
XX XX
DT 01-NOV-2001 (first entry)
XX XX Human stratum corneum chymotrypsin enzyme peptide #3 (residues 5-13).
XX DE Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX OS Homo sapiens.
XX XX
FN WO200159158-A1.
XX XX
PD 16-AUG-2001.
XX XX
PF 07-FEB-2001; 2001WO-US003977.
XX XX
PR 11-FEB-2000; 2000US-00502600.
XX XX (UYAR-) UNIV ARKANSAS.
XX XX O'brien TJ;
XX XX WPI; 2001-514676/56.
XX XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX XX Claim 25; Page 102; 127pp; English.
XX XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX Sequence 9 AA;
SQ

```
Query Match      100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLILL 9
Db 1 LLLPLQLILL 9

RESULT 2
ADR68794
ID ADR68794 standard; peptide; 9 AA.
XX
AC ADR68794;
XX
XX 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:33.
XX
XX serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
XX Homo sapiens.
OS
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005134.
PF
XX 21-FEB-2003; 2003US-00372521.
PR
XX (UYAR-) UNIV ARKANSAS.
PA
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/63.
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX Claim 5; SEQ ID NO 33; 117pp; English.
XX
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;
XX
Query Match      100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLILL 9
Db 1 LLLPLQLILL 9

RESULT 3
ABG23378
ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #23369.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
PF
XX 31-MAR-2000; 2000US-00540217.
PR
XX 23-AUG-2000; 2000US-00649167.
PR
XX (HYSE-) HYSEQ INC.
PA
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
XX WPI; 2001-639362/73.
DR
XX N-PSDB; AAS87565.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 53737; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 136 AA;
XX
Query Match      100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLILL 9
Db 11 LLLPLQLILL 19

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX
```

AC ADA05736;
 DT 06-NOV-2003 (first entry)
 XX Human NOV18c protein SEQ ID NO:96.
 XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipidemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO2003029424-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-US031373.
 XX
 XX 02-OCT-2001; 2001US-0326483P.
 XX 05-OCT-2001; 2001US-0327435P.
 XX 05-OCT-2001; 2001US-0327449P.
 XX 09-OCT-2001; 2001US-0327917P.
 XX 09-OCT-2001; 2001US-0328029P.
 XX 09-OCT-2001; 2001US-0328044P.
 XX 09-OCT-2001; 2001US-0328056P.
 XX 12-OCT-2001; 2001US-0328849P.
 XX 15-OCT-2001; 2001US-0329414P.
 XX 17-OCT-2001; 2001US-0330142P.
 XX 18-OCT-2001; 2001US-0330309P.
 XX 22-OCT-2001; 2001US-0341058P.
 XX 24-OCT-2001; 2001US-0339266P.
 XX 24-OCT-2001; 2001US-0343629P.
 XX 29-OCT-2001; 2001US-0349575P.
 XX 01-NOV-2001; 2001US-0346357P.
 XX 17-APR-2002; 2002US-0373260P.
 XX 19-APR-2002; 2002US-0373815P.
 XX 19-APR-2002; 2002US-0373817P.
 XX 19-APR-2002; 2002US-0373826P.
 XX 19-APR-2002; 2002US-0373884P.
 XX 22-APR-2002; 2002US-0374377P.
 XX 16-MAY-2002; 2002US-0381037P.
 XX 16-MAY-2002; 2002US-0381038P.
 XX 16-MAY-2002; 2002US-0381042P.
 XX 27-MAY-2002; 2002US-0381642P.
 XX 28-MAY-2002; 2002US-0383566P.
 XX 29-MAY-2002; 2002US-0383566P.
 XX 25-JUN-2002; 2002US-0391335P.
 XX 01-OCT-2002; 2002US-00262511.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerkhus BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shency SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 XX WPI; 2003-381626/36.
 DR N-PSDB; ADA05735.
 XX
 XX
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 XX Claim 1; Page 170; 586pp; English.
 PS
 XX The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method or screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipidemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

Query Match 100.0%; Score 40; DB 6; Length 198;
 Best Local Similarity 100.0%, Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
 Db 5 LLLPLQLLL 13
 |||||
 |||||

RESULT 5
 ADM62900
 ID ADM62900 standard; protein; 198 AA.
 XX
 AC ADM62900;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 XX Human NOV18c.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 XX US2004038223-A1.
 XX
 XX 26-FEB-2004.
 PD
 XX 01-OCT-2002; 2002US-00262511.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.

09-OCT-2001; 2001US-0328044P.
 09-OCT-2001; 2001US-0328056P.
 12-OCT-2001; 2001US-0328849P.
 15-OCT-2001; 2001US-0329414P.
 17-OCT-2001; 2001US-0330142P.
 18-OCT-2001; 2001US-0330309P.
 22-OCT-2001; 2001US-0341058P.
 24-OCT-2001; 2001US-0339266P.
 24-OCT-2001; 2001US-0343629P.
 29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
 17-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383566P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 (SMIT/) SMITHSON G.
 (MILL/) MILLET I.
 (PEYM/) PEYMAN J A.
 (KEKU/) KEKUDA R.
 (JUJJ/) JU J.
 (LILL/) LI L.
 (GUOX/) GUO X.
 (PAT/) PATTURAJAN M.
 (SPYT/) SPYTEK K A.
 (EDIN/) EDINGER S R.
 (ELLE/) ELLERMAN K.
 (MALX/) MALYANKAR U M.
 (ORTT/) ORT T.
 (GORM/) GORMAN L.
 (ZERH/) ZERHUSEN B D.
 (ANDE/) ANDERSON D W.
 (ZHON/) ZHONG M.
 (CATT/) CATTERTON E.
 (JIW/) JI W.
 (MILL/) MILLER C E.
 (RAST/) RASTELLI L.
 (STON/) STONE D J.
 (PENA/) PENA C E A.
 (SHEN/) SHENOY S G.
 (SHIM/) SHIMKETS R A.
 (ROTH/) ROTHENBERG M E.
 (LEAC/) LEACH M D.
 (AGEE/) AGEE M L.
 (BERG/) BERGHS C.
 (DIPI/) DIPPO V A.
 (EISE/) EISEN A.
 (GANG/) GANGOLLI E A.
 (RIEG/) RIEGER D K.
 (SPAD/) SPADERNA S K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spyttek KA, Edinger SR, Ellerman K, Malvankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI: 2004-213931/20.
 N-PSDB; ADN62899.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disorders, Alzheimer's Disease, cancer-associated cachexia, neurodegenerative
 CC disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 40; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLLPLQILL 9
 DB 5 LLLPLQILL 13
 RESULT 6
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX
 AC ADA05732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18a protein SEQ ID NO:92.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkete RA, Rothenberg ME, Leach MD, Agee NA, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05731.
XX
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Claim 1; Page 169-170; 586pp; English.
XX
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nontropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 40; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLLPLQILL 9
Db 2 LLLPLQILL 10
RESULT 7
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
AC ADN62896;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18a.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 09-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381642P.
PR 17-MAY-2002; 2002US-0383656P.
PR 28-MAY-2002; 2002US-0383831P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPVT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPL/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62895.
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 92; 395pp; English.
XX
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient with
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX SQ Sequence 250 AA;

Query Match 100.0%; Score 40; DB 8; Length 250;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9

Db 2 LLLPLQILL 10

RESULT 8

AAR67888

ID AAR67888 standard; protein; 253 AA.

XX AC AAR67888;

XX DT 25-MAR-2003 (revised)

XX DT 09-AUG-1995 (first entry)

XX DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).

XX KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
XX KW callosities; keratosis pilaris; ichthyoses; eczema.

XX OS Homo sapiens.

XX PN WO9500651-A1.

XX PD 05-JAN-1995.

XX PF 20-JUN-1994; 94WO-IB000166.

XX PR 18-JUN-1993; 93DK-00000725.

XX PA (SYMB-) SYMBICOM AB.

XX PI Egelrud T, Hansson L;

XX DR WPI; 1995-052088/07.

XX DR N-PSDB; AAQ81203.

XX PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
XX PT related vectors, transformed cells and polypeptides, useful for treating
XX PT skin disorders, e.g. acne or psoriasis, and for identification of
XX PT specific inhibitors.

XX PS Disclosure; Page 97; 137pp; English.

XX CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
XX CC and skin care products, especially to treat and prevent acne, xeroderma,
XX CC or other hyperkeratotic conditions (e.g. callosities or keratosis
XX CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
XX CC recombinantly following mammal, insect, plant, or microorganism
XX CC transformation with plasmid pBS07. (Updated on 25-MAR-2003 to correct PN
XX CC field.)

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 40; DB 2; Length 253;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9

Db 5 LLLPLQILL 13

RESULT 9

| | | |
|----------|-----------------------|---|
| XX | PD | AAW05383 |
| XX | ID | AAW05383 standard; protein; 253 AA. |
| XX | AC | AAW05383; |
| XX | PF | 31-DEC-1996 (first entry) |
| XX | PR | Human amyloid precursor protein protease. |
| XX | DE | Amyloid precursor protein protease; Alzheimer's disease; diagnosis; therapy. |
| XX | KW | Homo sapiens. |
| XX | KM | WO9631122-A1. |
| XX | PX | 10-OCT-1996. |
| XX | PD | 02-APR-1996; 96WO-US004294. |
| XX | PF | 04-APR-1995; 95US-00416257. |
| XX | PR | (ELIL) LILLY & CO ELI. |
| XX | PA | Dixon EP, Johnstone EM, Little SP; |
| XX | PI | WPI; 1996-464694/46. |
| XX | DR | N-PSDB; AAT39783. |
| XX | DR | New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease. |
| XX | PT | Claim 1; Page 44-45; 55pp; English. |
| XX | PS | Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic (partic. AV-120 host cells. It is used to develop products for the design and testing of cpds. useful for treating or preventing conditions CC associated with beta-amyloid peptide, esp. Alzheimer's disease XX |
| XX | SQ | Sequence 253 AA; |
| | Query Match | 100.0%; Score 40; DB 2; Length 253; |
| | Best Local Similarity | 100.0%; Pred. No. 26; |
| | Matches | 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 | LLLLPLQLL 9 |
| Db | 5 | LLLLPLQLL 13 |
| | RESULT 10 | |
| ABBB4421 | ID | ABBB4421 standard; peptide; 253 AA. |
| XX | AC | ABBB4421; |
| XX | DT | 08-NOV-2002 (first entry) |
| XX | DE | Human SCCE protein N-terminal fragment SEQ ID 48. |
| XX | KW | SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme. |
| XX | OS | Homo sapiens. |
| XX | PN | WO200262135-A2. |

| | | |
|----------|-----------------------|--|
| XX | PD | 15-AUG-2002. |
| XX | AC | 08-FEB-2002; 2002WO-IB001300. |
| XX | PF | 09-FEB-2001; 2001CA-02332655. |
| XX | PR | 09-FEB-2001; 2001DK-00000218. |
| XX | DE | (EGEL/) EGELRUD T. |
| XX | PA | (HANS/) HANSSON L. |
| XX | PI | Egelrud T, Hansson L; |
| XX | DR | WPI; 2002-643380/69. |
| XX | PT | Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin. |
| XX | PS | Example 6; Page 37; 74pp; English. |
| XX | CC | This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal fragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the transgenic mammals described in the invention |
| XX | SQ | Sequence 253 AA; |
| | Query Match | 100.0%; Score 40; DB 5; Length 253; |
| | Best Local Similarity | 100.0%; Pred. No. 26; |
| | Matches | 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 | LLLLPLQLL 9 |
| Db | 5 | LLLLPLQLL 13 |
| | RESULT 11 | |
| ABB84406 | ID | ABB84406 standard; protein; 253 AA. |
| XX | AC | ABB84406; |
| XX | DT | 08-NOV-2002 (first entry) |
| XX | DE | Human SCCE protein. |
| XX | KW | SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme. |
| XX | OS | Homo sapiens. |

XX WO200262135-A2.
 PN 15-AUG-2002.
 PD 08-FEB-2002; 2002WO-IB001300.
 PF 09-FEB-2001; 2001CA-02332655.
 PR 09-FEB-2001; 2001DK-00000218.
 XX (EGEL/) EGELRUD T.
 PA (HANS/) HANSSON L.
 XX Egelrud T, Hansson L;
 XX WPI; 2002-643380/69.
 DR N-PSDB; ABQ76226.
 XX Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 XX
 PS Claim 10; Page 58-59; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide
 CC sequence comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous scce
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathogenic condition, for development or testing of a
 CC cosmetic or a pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC compound or composition effective for the prevention or treatment of
 CC inflammatory skin diseases selected from diseases consisting of epidermal
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful
 CC as a model for further studies of itch mechanisms and the testing of
 CC potential compounds and compositions for relieve of various skin diseases
 CC where itch is a component. This sequence represents the human stratum
 CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
 CC with human kallikrein 7 (KLK7) and is used in the development of the
 CC transgenic mammals described in the invention
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLLPLQILL 9
 Db 5 LLLPLQILL 13
 RESULT 12
 AAU82740
 ID AAU82740 standard; protein; 253 AA.
 XX
 AC AAU82740;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Amino acid sequence of novel human protease #39.
 XX Human; protease; cancer; immune-related disorder; cardiovascular disease;
 KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 XX

KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 KW ocular disease; cytostatic; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200200860-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-US020171.
 XX
 PR 26-JUN-2000; 2000US-0214047P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 XX Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepel S;
 PI Charyczak G;
 XX
 DR WPI; 2002-139913/18.
 XX N-PSDB; ABK31782.
 XX
 PT Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related diseases
 PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 PT disorders.
 XX
 PS Claim 6; Fig 2N; 313pp; English.
 XX
 CC The present invention relates to the isolation of novel human proteases,
 CC and the nucleic acids encoding them. The sequences of the invention are
 CC useful for treating diseases and disorders such as cancers (e.g. breast,
 CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
 CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
 CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
 CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
 CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
 CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
 CC disorders, neurological disorders, hypotension, hypertension, psychotic
 CC disease) and dyskinesias. The nucleic acids and polypeptides are also
 CC useful for treating viral infections caused by human immunodeficiency
 CC virus (HIV), and non-viral infections such as ocular disease (e.g.
 CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
 CC human proteases of the invention
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLLPLQILL 9
 Db 5 LLLPLQILL 13
 RESULT 13
 ABU07440
 ID ABU07440 standard; protein; 253 AA.
 XX
 AC ABU07440;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Protein differentially regulated in prostate cancer #43.
 XX
 KW Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX
 OS Homo sapiens.
 XX

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 15
ABR58471
ID ABR58471 standard; protein; 253 AA.
XX
AC ABR58471;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX
KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX
OS Homo sapiens.
XX
PN WO2003029468-A1.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031467.
XX
PR 02-OCT-2001; 2001US-0327135P.
PR 30-MAY-2002; 2002US-0384531P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Mannion J;
XX
DR WPI; 2003-372001/35.
XX
PT New polynucleotide and polypeptide useful for diagnosing and/or treating
cancer, particularly ovarian cancer, and as a vaccine.
XX
PS Claim 2; Page 157-158; 169pp; English.
XX
CC The invention relates to a novel isolated polynucleotide. The
CC polynucleotides of the invention have cytostatic activity, and may have a
CC use in gene therapy, and in a vaccine. The composition and methods are
CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
CC The composition may also be used as a vaccine to prevent cancer. The
CC present sequence is used in the exemplification of the invention
XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

Search completed: March 11, 2006, 00:24:13
Job time : 88.6667 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 40 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 36 | 90.0 | 146 | 2 H75201 | hypothetical prote |
| 3 | 34 | 85.0 | 277 | 2 H84314 | cytochrome aa3 con |
| 4 | 34 | 85.0 | 369 | 2 S33603 | surfactant protein |
| 5 | 34 | 85.0 | 371 | 1 JN0450 | conglutinin precu |
| 6 | 34 | 85.0 | 371 | 2 I45878 | conglutinin - bovi |
| 7 | 34 | 85.0 | 754 | 2 AE0614 | probable competenc |
| 8 | 34 | 85.0 | 845 | 2 D97163 | cation transport p |
| 9 | 33 | 82.5 | 196 | 2 G65039 | hypothetical prote |
| 10 | 33 | 82.5 | 282 | 2 E70890 | hypothetical prote |
| 11 | 33 | 82.5 | 370 | 2 AB3334 | daunorubicin resis |
| 12 | 33 | 82.5 | 398 | 2 C91063 | hypothetical prote |
| 13 | 33 | 82.5 | 413 | 2 AC0834 | probable membrane |
| 14 | 33 | 82.5 | 426 | 2 C83103 | hypothetical prote |
| 15 | 33 | 82.5 | 470 | 2 A90083 | hypothetical prote |
| 16 | 33 | 82.5 | 475 | 1 A69149 | O-antigen transpor |
| 17 | 33 | 82.5 | 653 | 2 A46362 | amyloid precursor- |
| 18 | 32 | 80.0 | 198 | 2 S25656 | T-cell surface gly |
| 19 | 32 | 80.0 | 235 | 1 RWHTU8 | T-cell surface gly |
| 20 | 32 | 80.0 | 238 | 1 LNR7MA | mannose-binding le |
| 21 | 32 | 80.0 | 247 | 1 KYHUCM | chymase (EC 3.4.21 |
| 22 | 32 | 80.0 | 249 | 2 F91095 | type III secretion |
| 23 | 32 | 80.0 | 249 | 2 B85941 | hypothetical prote |
| 24 | 32 | 80.0 | 264 | 2 C97402 | probable acyltrans |
| 25 | 32 | 80.0 | 264 | 2 AC2620 | 1-acyl-sn-glycerol |
| 26 | 32 | 80.0 | 266 | 2 JC7300 | tax-responsive ele |
| 27 | 32 | 80.0 | 267 | 2 JC4857 | hepatocarcinogenes |
| 28 | 32 | 80.0 | 491 | 2 JC6197 | stromelysin 3 (EC |
| 29 | 32 | 80.0 | 492 | 2 A44399 | stromelysin 3 (EC |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 32 | 80.0 | 543 | 2 AI2088 | Na+/H+-exchanging |
| 31 | 32 | 80.0 | 1306 | 1 A31759 | peptidyl-dipeptida |
| 32 | 31 | 77.5 | 100 | 2 A38685 | apolipoprotein C-I |
| 33 | 31 | 77.5 | 155 | 2 A31278 | interleukin-2 prec |
| 34 | 31 | 77.5 | 159 | 2 G75555 | conserved hypother |
| 35 | 31 | 77.5 | 184 | 2 S10125 | alpha-2u-globulin |
| 36 | 31 | 77.5 | 189 | 2 T43766 | hypothetical prote |
| 37 | 31 | 77.5 | 244 | 2 F69260 | nitrate ABC transp |
| 38 | 31 | 77.5 | 249 | 2 T35589 | probable secreted |
| 39 | 31 | 77.5 | 269 | 2 T38931 | hypothetical prote |
| 40 | 31 | 77.5 | 303 | 2 C84914 | hypothetical prote |
| 41 | 31 | 77.5 | 372 | 2 A98157 | probable permease |
| 42 | 31 | 77.5 | 372 | 2 AH3130 | ABC transporter, m |
| 43 | 31 | 77.5 | 392 | 2 D83934 | hypothetical prote |
| 44 | 31 | 77.5 | 447 | 2 C84306 | hypothetical prote |
| 45 | 31 | 77.5 | 493 | 2 A71875 | hypothetical prote |

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:g521214; PIDN:7
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

RESULT 2

H75201
hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75201
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: H75201
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <XAW>
A;Cross-references: UNIPROT:Q9V2D5; UNIPARC:UPI0000063243; GB:AJ248283; GB:AL096836; NID
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0088
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

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Query Match      90.0%; Score 36; DB 2; Length 146;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 67 LLLPLQIII 75

RESULT 3
H84314
cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84314
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
; LeiChausser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84314
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <STO>
A:Cross-references: UNIPROT:Q9HP13; UNIPARC:UPI0000063931; GB:AE004437; NID:g10581096; E
C:Genetics:
A:Gene: ccp

Query Match      85.0%; Score 34; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 97 VLLPLQVIL 105

RESULT 4
S33603
surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S33603
R:Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A:Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro
A:Reference number: S33603; MUID:93170856; PMID:8436402
A:Accession: S33603
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-369 <DIM>
A:Cross-references: UNIPARC:UPI0000177932
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-367/Domain: C-type lectin homology <LCH>

Query Match      85.0%; Score 34; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 2 LLLPLSVLL 10

RESULT 5
JN0450
conglutinin precursor - bovine
N:Alternate names: C3b-binding protein
N:Contains: conglutinin-N
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

```

```

C:Accession: JN0450; JC2396; S33235; A23740; S36879; S35044; I46010; A29416; S34054
R:Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A:Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
A:Reference number: JN0450; MUID:93213261; PMID:8460993
A:Accession: JN0450
A:Molecule type: mRNA
A:Residues: 1-371 <SUZ>
A:Cross-references: UNIPROT:P23805; UNIPARC:UPI0000127EB3; DDBJ:D14085; NID:g285643; PIDN:
A:Experimental source: liver
R:Kawasaki, N.; Itoh, N.; Kawasaki, T.
Biochem. Biophys. Res. Commun. 198, 597-604, 1994
A:Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamme
A:Reference number: JC2396; MUID:94128104; PMID:8297370
A:Accession: JC2396
A:Molecule type: mRNA
A:Residues: 1-371 <KA2>
A:Cross-references: UNIPARC:UPI0000127EB3
A>Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R:Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 157-162, 1993
A:Title: The cDNA cloning of conglutinin and identification of liver as a primary site of
A:Reference number: S3235; MUID:93277452; PMID:7684896
A:Accession: S3235
A:Molecule type: mRNA
A:Residues: 1-172, 'H', 174-217, 'A', 219-271, 'V', 273-371 <LUJ>
A:Cross-references: UNIPARC:UPI000016C2E3; EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PII
A:Experimental source: liver
R:Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarna, T.B.
J. Biol. Chem. 266, 2715-2723, 1991
A:Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin fa
A:Reference number: A23740; MUID:91131556; PMID:1993651
A:Accession: A23740
A:Molecule type: protein
A:Residues: 21-209, 'S', 211-371 <LEB>
A:Cross-references: UNIPARC:UPI000014DF2A
R:Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Biochem. Biophys. 305, 533-540, 1993
A:Title: Differentiation of conglutination activity and sugar-binding activity of conglu
A:Reference number: S36879; MUID:93384312; PMID:8373191
A:Accession: S36879
A:Molecule type: protein
A:Residues: 21-54; 75-86, 'X', 88-89, 'X', 91, 'X', 93-94; 208-209, 'X', 211-227 <KAW>
A:Cross-references: UNIPARC:UPI00001741A3; UNIPARC:UPI00001741A4; UNIPARC:UPI00001741A5
A:Experimental source: serum
R:Lu, J.; Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
Eur. J. Biochem. 215, 793-799, 1993
A:Title: Structural similarity between lung surfactant protein D and conglutinin. Two di
A:Reference number: S35044; MUID:93358905; PMID:8354286
A:Accession: S35044
A:Molecule type: protein
A:Residues: 75-86, 'X', 88-89, 'X', 91, 'I', 'I' <LUA>
A:Cross-references: UNIPARC:UPI00001741A6
A:Experimental source: lung
R:Young, N.M.; Leon, M.A.
Biochem. Biophys. Res. Commun. 143, 645-651, 1987
A:Title: The carbohydrate specificity of conglutinin and its homology to proteins in the
A:Reference number: A29416; MUID:87184551; PMID:3566740
A:Contents: annotation
R:Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
Biochem. J. 293, 15-19, 1993
A:Title: Research Communication. Localization of the receptor-binding site in the collect
A:Reference number: S34054; MUID:93319501; PMID:8328957
A:Contents: annotation
R:Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarna, T.B.; Tauber, A.I.; Sastry,
J. Immunol. 153, 173-180, 1994
A:Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to
A:Reference number: I46010; MUID:94267222; PMID:8207234
A:Accession: I46010
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-371 <LIO>
A:Cross-references: UNIPARC:UPI0000127EB3; EMBL:U06860; NID:gs07183; PIDN:AAB60624.1; PII

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C;Comment: This protein mediates the agglutination of erythrocytes with antibody and complement. This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamin C;Genetics:

A;Gene: CGN1
 A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 C;Keywords: calcium binding; glycoprotein; hydroxyllysine; hydroxyproline
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-371/Product: conglutinin #status predicted <MAT>
 F;46-214/Region: collagen-like
 F;75-371/Product: conglutinin-N #status predicted <MA2>
 F;248-369/Domain: C-type lectin homology <LCH>
 F;63,87,99,135,141,159,162,198,210/Binding site: carbohydrate (Lys) (covalent) #status predicted <LCH>
 F;63,87,99,135,141,159,162,198,210/Modified site: 5-hydroxyllysine (Lys) #status experimental
 F;78,96,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (Pro) #status experimental
 F;337/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 85.0%; Score 34; DB 1; Length 371;
 Best Local Similarity 77.8%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 2 LLLPLSVLL 10

RESULT 6
 I45878
 conglutinin - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
 C;Accession: I45878
 R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, Gene 141, 277-281, 1994
 A;Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of Gene 141, 277-281, 1994
 A;Reference number: I45878; MUID:94215917; PMID:8163202
 A;Accession: I45878
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-371 <LIO>
 A;Cross-references: UNIPROT:P23805; UNIPARC:UPI000016C2E0; GB:L18871; NID:g495012; PIDN: C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 F;248-369/Domain: C-type lectin homology <LCH>

Query Match 85.0%; Score 34; DB 2; Length 371;
 Best Local Similarity 77.8%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 2 LLLPLSVLL 10

RESULT 7
 AE0614
 probable competence-related protein STY0984 [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: This species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
 C;Accession: AE0614
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P. Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AE0614
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-754 <PAR>
 A;Cross-references: UNIPARC:UPI000005A06F; GB:AL513382; PIDN:CAD05383.1; PID:g16502146; C;Genetics:

A;Gene: STY0984
 C;Superfamily: competence protein ComEC

Query Match 85.0%; Score 34; DB 2; Length 754;
 Best Local Similarity 77.8%; Pred. No. 92;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 371 LLLPLQVAL 379

RESULT 8
 D97163
 cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: D97163
 R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: D97163
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-845 <KUR>
 A;Cross-references: UNIPROT:Q97H76; UNIPARC:UPI00000CA412; GB:AE001437; PIDN:AAK80095.1; A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC2137

Query Match 85.0%; Score 34; DB 2; Length 845;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQILL 9
 ||||| :||
 Db 670 LLLPLQILL 677

RESULT 9
 G65039
 hypothetical protein b2612 - Escherichia coli (strain K-12) C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C;Accession: G65039
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: G65039
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-136 <BLAT>
 A;Cross-references: UNIPARC:UPI000016ED74; GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAK A;Experimental source: strain K-12, substrain MG1655

Query Match 82.5%; Score 33; DB 2; Length 196;
 Best Local Similarity 77.8%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 123 LLLPLQILL 131

RESULT 10
 E70890
 hypothetical protein Rv1978 - Mycobacterium tuberculosis (strain H37Rv) C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: E70890
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: E70890
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-282 <COL>
A: Cross-references: UNIPROT: O53979; UNIPARC: UPI00001652BF; GB: AL123456; NID
A: Experimental source: strain H37Rv
C: Genetics:
A: Gene: RV1978

Query Match 82.5%; Score 33; DB 2; Length 282;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
||| ||| :||
Db 196 LLLPLQLL 204

RESULT 11
AB3334
daunorubicin resistance transmembrane protein [imported] - *Brucella melitensis* (strain 1
C: Species: *Brucella melitensis*
C: Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C: Accession: AB3334
R: DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A: Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A: Reference number: AD3252; PMID: 11756688
A: Accession: AB3334
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-370 <KUR>
A: Cross-references: UNIPROT: QBVHY9; UNIPROT: QBFX1; UNIPARC: UPI0000057D7A; GB: AE008917;
A: Experimental source: strain 16M
C: Genetics:
A: Gene: BMEI0656
A: Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 370;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQIL 8
: ||| ||| :||
Db 293 ILLPLQVL 300

RESULT 12
C81063
hypothetical protein EC83475 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C: Species: *Escherichia coli*
C: Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C: Accession: C91063
R: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gaaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A: Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A: Reference number: A99629; MUID: 21156231; PMID: 11258796
A: Accession: C91063
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-398 <HAY>
A: Cross-references: UNIPROT: QBX9C3; UNIPARC: UPI00001654C8; GB: BA000007; PIDN: BAB36898.1;
A: Experimental source: strain O157:H7, substrain R1MD 0509952

C: Genetics:
A: Gene: EC83475
C: Superfamily: yfjD protein

Query Match 82.5%; Score 33; DB 2; Length 398;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
||| ||| :||
Db 101 LLAPLQILM 109

RESULT 13
AC0834
probable membrane protein corB [imported] - *Salmonella enterica* subsp. *enterica* serovar 1
C: Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A: Note: this species has also been called *Salmonella typhi*
C: Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C: Accession: AC0834
R: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A: Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A: Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A: Reference number: AB0502; MUID: 21534947; PMID: 11677608
A: Accession: AC0834
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-413 <PAR>
A: Cross-references: UNIPARC: UPI000005A2E0; GB: AL513382; PIDN: CAD05858.1; PID: g16503833;
C: Genetics:
A: Gene: corB
C: Superfamily: hypothetical protein HI0107

Query Match 82.5%; Score 33; DB 2; Length 413;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
||| ||| :||
Db 116 LLAPLQILM 124

RESULT 14
C83103
hypothetical protein PA4338 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C: Species: *Pseudomonas aeruginosa*
C: Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C: Accession: C83103
R: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A: Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A: Reference number: AB2950; MUID: 20437337; PMID: 10984043
A: Accession: C83103
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-426 <STO>
A: Cross-references: UNIPROT: Q9HW63; UNIPARC: UPI00000C5CC9; GB: AE004850; GB: AE004091; NID:
A: Experimental source: strain PA01
C: Genetics:
A: Gene: PA4338

Query Match 82.5%; Score 33; DB 2; Length 426;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
||| ||| :||
Db 301 LLLPAQLLL 309

RESULT 15
A90083
hypothetical protein orf470 [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A90083
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Ren
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: A90083
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <DOU>
A:Cross-references: UNIPROT:Q9SEA5; UNIPARC:UPI0000092883; GB:AF165818; NID:g6690603; PI
C:Genetics:
A:Gene: orf470
A:Map position: 1
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 82.5%; Score 33; DB 2; Length 470;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 253 MLLPLEILI 261

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05_80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----------------|---------------------|
| 1 | 40 | 100.0 | 66 | Q6DTY1_HUMAN | Q6dtY1 homo sapien |
| 2 | 40 | 100.0 | 253 | 1 KLK7_HUMAN | P49862 homo sapien |
| 3 | 39 | 97.5 | 545 | 2 Q5N0S0_SYNP6 | Q5n0S0 synchococc |
| 4 | 38 | 95.0 | 73 | 2 Q8VCA9_MOUSE | Q8vca9 mus musculus |
| 5 | 38 | 95.0 | 104 | 2 Q8R5D6_MOUSE | Q8r5d6 mus musculus |
| 6 | 38 | 95.0 | 138 | 2 Q6PXE2_MOUSE | Q6pke2 mus musculus |
| 7 | 38 | 95.0 | 201 | 1 FK311_MOUSE | Q9dlm7 mus musculus |
| 8 | 38 | 95.0 | 246 | 2 Q585W6_9TRYP | Q585w6 trypanosoma |
| 9 | 38 | 95.0 | 361 | 1 INHA_TRITU | Q77755 trichosurus |
| 10 | 37 | 92.5 | 208 | 2 Q21527_CLEGA | Q21527 clethrionom |
| 11 | 36 | 90.0 | 146 | 2 Q9V2D5_PYRAB | Q9v2d5 pyrococcus |
| 12 | 36 | 90.0 | 205 | 2 Q65323_ORYSA | Q65323 oryza sativ |
| 13 | 35 | 87.5 | 181 | 2 Q6N896_RHOPA | Q6n896 rhodopseudo |
| 14 | 35 | 87.5 | 1064 | 2 Q41B17_GIBZE | Q41b17 gibberella |
| 15 | 35 | 87.5 | 1527 | 2 Q6PPA4_LEITA | Q6ppa4 leishmania |
| 16 | 34 | 85.0 | 96 | 2 Q5XFW5_RAT | Q5xfw5 rattus norv |
| 17 | 34 | 85.0 | 162 | 2 Q91T40_LSDV | Q91t40 lumpy skin |
| 18 | 34 | 85.0 | 162 | 2 Q91WZ4_LSDV | Q91wz4 lumpy skin |
| 19 | 34 | 85.0 | 205 | 2 Q5V730_HALMA | Q5v730 halocaula |
| 20 | 34 | 85.0 | 241 | 2 Q5V727_HALMA | Q5v727 halocaula |
| 21 | 34 | 85.0 | 251 | 2 Q5N5T6_SYNP6 | Q5n5t6 synchococc |
| 22 | 34 | 85.0 | 277 | 2 Q9HP13_HALSA | Q9hpi3 halobacteri |
| 23 | 34 | 85.0 | 369 | 1 SFTPD_BOVIN | P35246 bos taurus |
| 24 | 34 | 85.0 | 369 | 2 Q863A1_BOVIN | Q863a1 bos taurus |
| 25 | 34 | 85.0 | 371 | 1 CL46_BOVIN | Q8mhz9 bos taurus |
| 26 | 34 | 85.0 | 371 | 1 CONG_BOVIN | P23805 bos taurus |
| 27 | 34 | 85.0 | 371 | 2 Q58CU7_BOVIN | Q58cu7 bos taurus |
| 28 | 34 | 85.0 | 373 | 2 Q749Q7_GEOSL | Q749q7 geobacter s |
| 29 | 34 | 85.0 | 754 | 2 Q8Z802_SALTI | Q8z802 salmonella |
| 30 | 34 | 85.0 | 754 | 2 Q8ZQC3_SALTY | Q8zqc3 salmonella |
| 31 | 34 | 85.0 | 775 | 2 Q7N6C7_PHOLL | Q7n6c7 photorhabd |

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|----|----|------|-----|---|--------------|---------------------|
| 32 | 34 | 85.0 | 845 | 2 | Q97H76_CLOAB | Q97h76 clostridium |
| 33 | 33 | 82.5 | 68 | 2 | Q6KG65_9CAUD | Q6kg65 bacterioph |
| 34 | 33 | 82.5 | 109 | 2 | Q8BJK7_MOUSE | Q8bjk7 mus musculu |
| 35 | 33 | 82.5 | 189 | 2 | Q7M8B8_WOLSU | Q7m8b8 wolinnella s |
| 36 | 33 | 82.5 | 196 | 2 | Q9X620_SALTY | Q9x620 salmonella |
| 37 | 33 | 82.5 | 196 | 2 | Q9D226_MOUSE | Q9d226 mus musculu |
| 38 | 33 | 82.5 | 282 | 2 | Q53979_MYCTU | Q53979 mycobacteri |
| 39 | 33 | 82.5 | 282 | 2 | Q71Z68_MYCHO | Q71z68 mycobacteri |
| 40 | 33 | 82.5 | 294 | 2 | Q7D7M8_MYCTU | Q7d7m8 mycobacteri |
| 41 | 33 | 82.5 | 302 | 2 | Q6GNT6_XENLA | Q6gnt6 xenopus lae |
| 42 | 33 | 82.5 | 307 | 2 | Q4NVN1_9DELT | Q4nvn1 anaeromykob |
| 43 | 33 | 82.5 | 370 | 2 | Q8FZX1_BRUSU | Q8fzx1 bruceella su |
| 44 | 33 | 82.5 | 370 | 2 | Q8YHY9_BRUME | Q8yhy9 bruceella me |
| 45 | 33 | 82.5 | 374 | 2 | Q57CF5_BRUAB | Q57cf5 bruceella ab |

ALIGNMENTS

RESULT 1
Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T, Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646152; AAT66047.1; -; mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|----|---|--------------|
| QY | 1 | LLLPLQILL 9 |
| Db | 5 | LLLPLQILL 13 |

RESULT 2
KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
RT chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

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Query Match 100.0%; Score 40; DB 1; Length 253;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
 |||||
 DB 5 LLLPLQLLL 13

RESULT 3

QSNOS0 SYN6
 ID QSNOS0 SYN6 PRELIMINARY; PRT; 545 AA.
 AC QSNOS0;
 DT 01-FEB-2005 (TReMBLrel. 29, Created)
 DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Probable Na+/H+-exchanging protein.
 GN OrderedLocusNames=ncyl910.c;
 OS Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=269084;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCC6301;
 RA Sugita M.;
 RT "Complete genome structure of the unicellular cyanobacterium Anacystis
 nidulans 6301 (Synechococcus sp. PCC6301).";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP008231; BAD80100.1; -; Genomic DNA.
 DR GO; GO:0006950; P:response to stress; IEA.
 DR InterPro; IPR006153; Na_Hporter.
 DR InterPro; IPR006015; Usp.
 DR InterPro; IPR006016; UspA.
 DR Pfam; PF00999; Na_H Exchanger; 1.
 DR Pfam; PF00582; Usp_1.
 DR PRINTS; PR01438; UNRSLSLSTRESS.
 KW Complete proteome.
 SQ SEQUENCE 545 AA; 58143 MW; 2DB84E920CD7DEDC CRC64;

Query Match 97.5%; Score 39; DB 2; Length 545;
 Best Local Similarity 88.9%; Pred. No. 64;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
 |||||
 DB 193 LLLPLQLLL 201

RESULT 4

Q8VCA9 MOUSE
 ID Q8VCA9 MOUSE PRELIMINARY; PRT; 73 AA.
 AC Q8VCA9;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Fkbp11 protein.
 GN Name=Fkbp11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021345; AH21345.1; -; mRNA.
 DR MGI; MGI:1913370; Fkbp11.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 SQ SEQUENCE 73 AA; 7819 MW; 938F53399BF3C11 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 73;
 Best Local Similarity 88.9%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
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 DB 6 LLLPLQLLL 14

RESULT 5

Q8RSD6 MOUSE
 ID Q8RSD6 MOUSE PRELIMINARY; PRT; 104 AA.
 AC Q8RSD6;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Fkbp11 protein.
 GN Name=Fkbp11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022900; AAH22900.1; -; mRNA.

DR MGI; MGI:1913370; Fkbp11.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro; IPR001179; FKBP_PPIase.

DR Pfam; PF00254; FKBP_C; 1.

DR PROSITE; PS0059; FKBP_PPIase; 1.

SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 104;
 Best Local Similarity 88.9%; Pred. No. 21;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9

Db 6 LLLPLQLLL 14

RESULT 6

ID Q6PKX2_MOUSE PRELIMINARY; PRT; 138 AA.

AC Q6PKX2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Fkbp11 protein.

GN Name=Fkbp11;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old

RC virgin mouse. Taken by biopsy.

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hulyk S.W.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grumman J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old

RC virgin mouse. Taken by biopsy.

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC002311; AAH02311.1; -; mRNA.

DR MGI; MGI:1913370; Fkbp11.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro; IPR001179; FKBP_PPIase.

DR Pfam; PF00254; FKBP_C; 1.

DR PROSITE; PS0059; FKBP_PPIase; 1.

SQ SEQUENCE 138 AA; 15105 MW; C138B8B08FDDF59D CRC64;

Query Match 95.0%; Score 38; DB 2; Length 138;

Best Local Similarity 88.9%; Pred. No. 27;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9

Db 6 LLLPLQLLL 14

RESULT 7

FKB11_MOUSE

ID FKB11_MOUSE STANDARD; PRT; 201 AA.

AC Q9DJM7; O9CRB4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-MAY-2005 (Rel. 47, Last annotation update)

DE FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-

DE trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)

DE (FKBP-19).

GN Name=Fkbp11;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6J; TISSUE=Mammary gland;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carlini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -I- FUNCTION: PPIases accelerate the folding of proteins during
CC protein synthesis.
CC -I- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -I- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC -I- SIMILARITY: Contains 1 PPIase FKBP-type domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AK003331; BAB22719.1; -; mRNA.
DR EMBL; AK019132; BAB31559.1; -; mRNA.
DR EMBL; BC037596; AAH37596.1; -; mRNA.
DR HSSP; P20071; ITCO.
DR Ensembl; ENSMUSG0000003355; Mus musculus.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS0059; FKBP_PPIASE; 1.
KW Isomerase; Rotamase; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 201 FK506 binding protein 11.
FT DOMAIN 57 144 PPIase FKBP-type.
FT CONFLICT 53 53 S -> F (in Ref. 1; BAB31559).
FT CONFLICT 198 198 S -> R (in Ref. 1; BAB31559).
SQ SEQUENCE 201 AA; 22137 MW; 94D955C57264BD82 CRC64;

Query Match 95.0%; Score 38; DB 1; Length 201;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 6 LLLPLQLLL 14
|:|||||:
|:|||||:

RESULT 8
Q585W6_9TRYP PRELIMINARY; PRT; 246 AA.
AC Q585W6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=Tb927.6.3680;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,

RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA Haas B., Blandin G., El-Sayed N.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009259; AAX80785.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 27875 MW; 706DD83BA6BB46AB CRC64;

Query Match 95.0%; Score 38; DB 2; Length 246;
Best Local Similarity 88.9%; Pred. No. 47;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 163 LMLPLQLLL 171
|:|||||:
|:|||||:

RESULT 9
INHA_TRIVU STANDARD; PRT; 361 AA.
AC Q77755;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Inhibin alpha chain precursor.
GN Name=INHA;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
RA Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
RA Greenwood P.J., McNatty K.;
RT "cDNA sequence analysis, gene expression and protein localisation of
RT the inhibin alpha subunit of Australian brushtail possum (Trichosurus
RT vulpecula).";
RL J. Mol. Endocrinol. 21:141-152(1998).
CC -I- FUNCTION: Inhibins and activins inhibit and activate,
CC respectively, the secretion of follitropin by the pituitary gland.
CC Inhibins/activins are involved in regulating a number of diverse
CC functions such as hypothalamic and pituitary hormone secretion,
CC gonadal hormone secretion, germ cell development and maturation,
CC erythroid differentiation, insulin secretion, nerve cell survival,
CC embryonic axial development or bone growth, depending on their
CC subunit composition. Inhibins appear to oppose the functions of
CC activins.
CC -I- SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A
CC is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
CC beta-B.
CC -I- PTM: Proteolytic processing yields a number of bioactive forms,
CC consisting either solely of the mature alpha chain, of the most N-
CC terminal propeptide linked through a disulfide bond to the mature
CC alpha chain, or of the entire proprotein.
CC -I- SIMILARITY: Belongs to the TGF-beta family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

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CC EMBL; AF033340; AAC63945.1; -: mRNA.
DR GO; GO:0003576; Cetraxacellar region; ISS.
DR GO; GO:001706; F:activin inhibitor activity; ISS.
DR GO; GO:0005125; F:cytokine activity; ISS.
DR GO; GO:0008083; F:growth factor activity; ISS.
DR GO; GO:0005179; F:hormone activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007050; F:cell cycle arrest; ISS.
DR GO; GO:0030154; F:cell differentiation; ISS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0030218; P:erythrocyte differentiation; ISS.
DR GO; GO:0042541; P:hemoglobin biosynthesis; ISS.
DR GO; GO:0008917; P:induction of apoptosis; ISS.
DR GO; GO:0045578; P:negative regulation of B cell differentiation; ISS.
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
DR GO; GO:0046882; P:negative regulation of follicle-stimulating. .; ISS.
DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; ISS.
DR GO; GO:0045650; P:negative regulation of macrophage different. .; ISS.
DR GO; GO:0042326; P:negative regulation of phosphorylation; ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0001541; P:ovarian follicle development; ISS.
DR GO; GO:0046881; P:positive regulation of follicle-stimulating. .; ISS.
DR InterPro; IPR002405; Inhibin_alpha.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA.1; 1.
KW Glycoprotein; Growth_Factor; Hormone; Signal.
FT SIGNAL 1 21 By similarity.
FT PROPEP 22 64 By similarity.
FT PROPEP 65 230 Inhibin alpha N-terminal region (By
FT CHAIN 231 361 Inhibin alpha chain.
FT SITE 64 65 Cleavage (By similarity).
FT SITE 230 231 Cleavage (By similarity).
FT CARBOHYD 48 48 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc. .) (By similarity).
FT DISULFID 260 323 By similarity.
FT DISULFID 289 358 By similarity.
FT DISULFID 293 360 By similarity.
FT DISULFID 322 322 Interchain (By similarity).
SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDA87D CRC64;

Query Match 95.0%; Score 38; DB 1; Length 361;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 4 LLLPLQLL 12

RESULT 10
O21527 CLEGA PRELIMINARY; PRT; 208 AA.
AC O21527
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Clethrionomys gapperi (Southern red-backed vole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Arvicolinae; Clethrionomys.
OX NCBI_TaxID=56223;
RN [1]
```

```
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98152303; PubMed=9491603;
RA Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
RT "Molecular systematics and paleobiogeography of the South American
RL Mol. Biol. Evol. 15:35-49 (1998).
DR EMBL; U83808; AAB87168.1; -: Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; F:ATP synthesis coupled electron transport; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
DR InterPro; IPR003918; NADH_oxred4.
DR InterPro; IPR000260; Oxidored_q5_N.
DR Pfam; PF01059; Oxidored_q5_N; 1.
DR PRINTS; PR01437; NUOXDRDTASE4.
DR KW Mitochondrion.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 208;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 98 LLLPLQILL 106

RESULT 11
Q9V2D5 PYRAB PRELIMINARY; PRT; 146 AA.
AC Q9V2D5
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PYRAB01390; ORFNames=PAB00088;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RX DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi."
RL Mol. Microbiol. 47:1495-1512 (2003).
DR EMBL; AJ248283; CAB49063.1; -: Genomic_DNA.
DR PIR; H75201; H75201.
DR InterPro; IPR008537; DUF819.
DR Pfam; PF05684; DUF819; 1.
DR KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;

Query Match 90.0%; Score 36; DB 2; Length 146;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 67 LLLPLQIII 75

RESULT 12
Q65323 ORYSA PRELIMINARY; PRT; 205 AA.
AC Q65323
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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Endonuclease V protein-like.
GN Names=OSUNB0065C04.45;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT clone:OSJNB0065C04.45;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004744; BAD45874.1; -; Genomic_DNA.
DR Gramene; O65323; -;
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR007581; Endonuc V.
DR Pfam; PF04493; Endonuclease_5; 1.
DR Endonuclease.
KW SEQUENCE 205 AA; 22733 MW; 6FBFE7178FC9BEFF CRC64;

Query Match 90.0%; Score 36; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 96;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 176 ILLPLQLLL 184

RESULT 13
Q6NB96 RHOPA
ID Q6NB96 RHOPA PRELIMINARY; PRT; 181 AA.
AC Q6NB96;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RPA0932;
OS Rhodopsudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopsudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lanerding J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopsudomonas palustris."
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572595; CAE26376.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;

Query Match 87.5%; Score 35; DB 2; Length 181;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQLLL 9
DB 24 LLLPLQLLL 31

25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Endonuclease V protein-like.
GN Names=OSUNB0065C04.45;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT clone:OSJNB0065C04.45;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004744; BAD45874.1; -; Genomic_DNA.
DR Gramene; O65323; -;
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR007581; Endonuc V.
DR Pfam; PF04493; Endonuclease_5; 1.
DR Endonuclease.
KW SEQUENCE 205 AA; 22733 MW; 6FBFE7178FC9BEFF CRC64;

Query Match 90.0%; Score 36; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 96;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 176 ILLPLQLLL 184

RESULT 14
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AC Q4IB17;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG05591.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearliano K.,
RA Diaz J.S., Dodge S., Doolley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meidrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramaamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000229; EAA73727.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1064 AA; 117828 MW; 2174A5BE94DEB5F CRC64;

Query Match 87.5%; Score 35; DB 2; Length 1064;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 862 LLLPLNILL 870

Q6PPA4 LEITA
ID Q6PPA4 LEITA PRELIMINARY; PRT; 1527 AA.
AC Q6PPA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P-glycoprotein D.
GN Name=PGPD;
OS Leishmania tarentolae (Sauroleishmania tarentolae).
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
OC Lizard Leishmania.
OX NCBI_TaxID=5689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Leprohon P.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY589043; AAT02643.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0018887; F:ATPase activity; IEA.
 DR GO; GO:0043262; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR001140; ABC_TM_transp.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00929; ABC_TMIF; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 SQ SEQUENCE 1527 AA; 167945 MW; E942681FFC675AAE CRC64;

Query Match 87.5%; Score 35; DB 2; Length 1527;
 Best Local Similarity 77.8%; Pred. No. 1e+03;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLLPLQLL 9
 Db 424 LFLPLQVLL 432

Search completed: March 11, 2006, 00:38:42
 Job time : 99.3333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-33

Perfect score: 40

Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfileesl.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 40 | 100.0 | 9 | 2 | US-09-502-600-33 |
| 2 | 40 | 100.0 | 9 | 2 | US-09-918-243-33 |
| 3 | 40 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 4 | 40 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 5 | 40 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 6 | 40 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 7 | 40 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 8 | 40 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 9 | 40 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 10 | 40 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 11 | 38 | 95.0 | 812 | 2 | US-09-489-039A-12075 |
| 12 | 36 | 90.0 | 9 | 2 | US-09-502-600-35 |
| 13 | 36 | 90.0 | 9 | 2 | US-09-502-600-36 |
| 14 | 36 | 90.0 | 9 | 2 | US-09-918-243-35 |
| 15 | 36 | 90.0 | 9 | 2 | US-09-918-243-36 |
| 16 | 33 | 82.5 | 190 | 1 | US-08-339-152A-19 |
| 17 | 33 | 82.5 | 190 | 1 | US-08-007-999B-6 |
| 18 | 33 | 82.5 | 190 | 1 | US-08-689-276A-6 |
| 19 | 33 | 82.5 | 447 | 2 | US-09-252-991A-24312 |
| 20 | 33 | 82.5 | 634 | 1 | US-08-339-152A-17 |
| 21 | 33 | 82.5 | 653 | 1 | US-08-339-152A-16 |
| 22 | 33 | 82.5 | 653 | 1 | US-08-007-999B-3 |
| 23 | 33 | 82.5 | 653 | 1 | US-08-689-276A-3 |
| 24 | 32 | 80.0 | 21 | 2 | US-08-753-007A-24 |
| 25 | 32 | 80.0 | 21 | 2 | US-09-398-496-24 |
| 26 | 32 | 80.0 | 22 | 2 | US-08-977-378-22 |
| 27 | 32 | 80.0 | 102 | 2 | US-10-104-047-2266 |

Sequence 12, Appl
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Sequence 39889, A
Sequence 55106, A
Sequence 37, Appl
Sequence 8, Appl
Sequence 11785, A
Sequence 4, Appl
Sequence 12646, A
Sequence 7, Appl
Sequence 7, Appl
Sequence 1574, Ap
Sequence 4177, Ap
Sequence 3902, Ap
Sequence 21399, A
Sequence 42872, A

28 80.0 235 1 US-07-940-605A-12
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30 80.0 295 2 US-09-270-767-39889
31 80.0 295 2 US-09-270-767-55106
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33 80.0 376 2 US-08-751-512-8
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35 80.0 492 1 US-07-794-393-4
36 80.0 492 1 US-08-001-711-4
37 80.0 837 2 US-09-489-039A-12646
38 80.0 1306 2 US-08-989-299-7
39 80.0 1306 2 US-09-407-427-7
40 80.0 1306 2 US-09-635-501-7
41 77.5 91 2 US-09-605-703B-1574
42 77.5 129 2 US-09-513-999C-4177
43 77.5 134 2 US-09-621-976-3902
44 77.5 142 2 US-09-248-796A-21399
45 77.5 160 2 US-09-270-767-42872

ALIGNMENTS

RESULT 1
US-09-502-600-33
; Sequence 33, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 2
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match      100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
DB 5 LLLPLQILL 13

RESULT 6
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
ADDRESSEE: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
DB 5 LLLPLQILL 13

RESULT 7
US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
ADDRESSEE: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-853-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
DB 5 LLLPLQILL 13

RESULT 8
US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 317A Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: Genbank
/ CLONE: 532504
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 9
PCT-US96-04294-2
/ Sequence 2, Application PC/TUS9604294
/ GENERAL INFORMATION:
/ APPLICANT: Dixon, Eric P.
/ APPLICANT: Johnstone, Edward M.
/ APPLICANT: Little, Sheila P.
/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Eli Lilly and Company
/ STREET: Lilly Corporate Center
/ CITY: Indianapolis
/ STATE: Indiana
/ COUNTRY: United States of America
/ ZIP: 46285
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/04294
/ FILING DATE:
/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/416,257
/ FILING DATE: 04-APR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bialock, Donna K.
/ REGISTRATION NUMBER: 38,082
/ REFERENCE/DOCKET NUMBER: X9239
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 317-277-1090
/ TELEFAX: 317-276-3861
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US96-04294-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 10
US-09-949-016-7716
/ Sequence 7716, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7716
/ LENGTH: 265
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-7716

Query Match 100.0%; Score 40; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 17 LLLPLQILL 25

RESULT 11
US-09-489-039A-12075
/ Sequence 12075, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27

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; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12075
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075

Query Match      95.0%; Score 38; DB 2; Length 812;
Best Local Similarity 88.9%; Pred. No. 32;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LLLPLQLLL 9
Db      429 LLLPLQLLL 437
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      |||||:|

RESULT 12
US-09-502-600-35
; Sequence 35, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLLPLQLLL 9
Db      1 LLLPLQLLL 8
      |||||
      |||||

RESULT 13
US-09-502-600-36
; Sequence 36, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-502-600-36

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLLPLQLLL 9
Db      1 LLLPLQLLL 8
      |||||
      |||||

RESULT 14
US-09-918-243-35
; Sequence 35, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLLPLQLLL 9
Db      1 LLLPLQLLL 8
      |||||
      |||||

RESULT 15
US-09-918-243-36
; Sequence 36, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LLLPLQLLL 8
Db      2 LLLPLQLLL 9
      |||||
      |||||
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Search completed: March 11, 2006, 01:24:24
Job time : 21.2222 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*
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2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 40 | 100.0 | 9 | 3 | US-09-918-243-33 |
| 2 | 40 | 100.0 | 9 | 3 | US-09-905-083-33 |
| 3 | 40 | 100.0 | 9 | 3 | US-10-372-521-33 |
| 4 | 40 | 100.0 | 9 | 5 | US-10-831-075-33 |
| 5 | 40 | 100.0 | 136 | 5 | US-10-450-763-53737 |
| 6 | 40 | 100.0 | 198 | 4 | US-10-262-511-96 |
| 7 | 40 | 100.0 | 250 | 4 | US-10-262-511-92 |
| 8 | 40 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 9 | 40 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 10 | 40 | 100.0 | 253 | 4 | US-10-071-214-2 |
| 11 | 40 | 100.0 | 253 | 4 | US-10-071-214-48 |
| 12 | 40 | 100.0 | 253 | 4 | US-10-264-283-90 |
| 13 | 40 | 100.0 | 253 | 4 | US-10-295-027-498 |
| 14 | 40 | 100.0 | 253 | 4 | US-10-173-999-48 |
| 15 | 40 | 100.0 | 253 | 4 | US-10-408-765A-639 |
| 16 | 40 | 100.0 | 253 | 5 | US-10-643-795A-95 |
| 17 | 40 | 100.0 | 253 | 5 | US-10-948-518-95 |
| 18 | 40 | 100.0 | 253 | 5 | US-10-868-490A-1 |
| 19 | 40 | 100.0 | 257 | 4 | US-10-344-394-38 |
| 20 | 38 | 95.0 | 70 | 4 | US-10-424-599-207950 |
| 21 | 36 | 90.0 | 9 | 3 | US-09-918-243-35 |
| 22 | 36 | 90.0 | 9 | 3 | US-09-918-243-36 |
| 23 | 36 | 90.0 | 9 | 3 | US-09-905-083-35 |
| 24 | 36 | 90.0 | 9 | 3 | US-09-905-083-36 |
| 25 | 36 | 90.0 | 9 | 4 | US-10-372-521-35 |
| 26 | 36 | 90.0 | 9 | 4 | US-10-372-521-36 |
| 27 | 36 | 90.0 | 9 | 5 | US-10-831-075-35 |

28 36 90.0 187 5 US-10-831-075-36 Sequence 36, Appl
29 36 90.0 187 4 US-10-437-963-110905 Sequence 110905,
30 35 87.5 99 4 US-10-425-115-348070 Sequence 348070,
31 35 87.5 173 4 US-10-437-963-119305 Sequence 119305,
32 34 85.0 23 3 US-09-864-761-46097 A Sequence 46097, A
33 34 85.0 61 4 US-10-425-115-218429 Sequence 218429,
34 34 85.0 187 4 US-10-425-115-57128 Sequence 57128, A
35 34 85.0 201 3 US-09-956-622A-39 Sequence 39, Appl
36 34 85.0 229 4 US-10-425-115-227327 Sequence 227327,
37 34 85.0 369 5 US-10-820-155-60 Sequence 60, Appl
38 34 85.0 369 5 US-10-820-155-64 Sequence 64, Appl
39 34 85.0 369 5 US-10-820-155-74 Sequence 74, Appl
40 34 85.0 371 5 US-10-820-155-4 Sequence 3, Appl
41 34 85.0 371 5 US-10-820-155-4 Sequence 4, Appl
42 34 85.0 371 5 US-10-820-155-24 Sequence 24, Appl
43 34 85.0 371 5 US-10-820-155-54 Sequence 54, Appl
44 34 85.0 845 4 US-10-282-122A-51875 A Sequence 51875, A
45 33 82.5 46 4 US-10-424-599-265948 Sequence 265948,

ALIGNMENTS

RESULT 1
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 2
US-09-905-083-33
; Sequence 33, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-905-083-33

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
|||||
Db 1 LLLPLQILL 9

RESULT 3

US-10-372-521-33
; Sequence 33, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-10-372-521-33

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
|||||
Db 1 LLLPLQILL 9

RESULT 4

US-10-831-075-33
; Sequence 33, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-10-831-075-33

Query Match 100.0%; Score 40; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
|||||
Db 1 LLLPLQILL 9

RESULT 5

US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match 100.0%; Score 40; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
|||||
Db 11 LLLPLQILL 19

RESULT 6

US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.

APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 96
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 40; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 7
US-10-262-511-92
Sequence 92, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana

APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 92
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 2 LLLPLQILL 10

RESULT 8
US-09-888-615-98
Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
| | | | |
DB 5 LLLPLQILL 13

RESULT 9

US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/210,084

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PP-0252 US

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

; LENGTH: 253 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 532504

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-764-762-3

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
| | | | |
DB 5 LLLPLQILL 13

RESULT 10

US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:

; APPLICANT: HANSSON, Lennart

; APPLICANT: EGELRUD, Torbjorn

; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

; FILE REFERENCE: HANSSON=3A

; CURRENT APPLICATION NUMBER: US/10/071,214

; CURRENT FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: US 60/267,422

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: DK PA 2001 00218

; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 253

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-071-214-2

Query Match 100.0%; Score 40; DB 4; Length 253;

Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9

| | | | |

DB 5 LLLPLQILL 13

RESULT 11

US-10-071-214-48

; Sequence 48, Application US/10071214

; Publication No. US20030066099A1

; GENERAL INFORMATION:

; APPLICANT: HANSSON, Lennart

; APPLICANT: EGELRUD, Torbjorn

; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

; FILE REFERENCE: HANSSON=3A

; CURRENT APPLICATION NUMBER: US/10/071,214

; CURRENT FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: US 60/267,422

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: DK PA 2001 00218

; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 48

; LENGTH: 253

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from

; OTHER INFORMATION: homo sapiens.

US-10-071-214-48

Query Match 100.0%; Score 40; DB 4; Length 253;

Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9

| | | | |

DB 5 LLLPLQILL 13

RESULT 12

US-10-264-283-90

; Sequence 90, Application US/10264283

; Publication No. US2003014494A1

GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 13
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 14
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; FILE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 15
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 40; DB 4; Length 253;
 Best Local Similarity 100.0%; Fred. No. 36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLPLQILL 9
 |||||
 Db 5 LLLPLQILL 13

Search completed: March 11, 2006, 01:37:22
 Job time : 69.4444 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB_PUB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 40 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 2 | 40 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 3 | 40 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 4 | 40 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 5 | 34 | 85.0 | 71 | 7 | US-11-096-568A-27354 |
| 6 | 34 | 85.0 | 71 | 7 | US-11-096-568A-27391 |
| 7 | 34 | 85.0 | 85 | 7 | US-11-096-568A-27350 |
| 8 | 34 | 85.0 | 85 | 7 | US-11-096-568A-27390 |
| 9 | 33 | 82.5 | 125 | 7 | US-11-096-568A-23862 |
| 10 | 32 | 80.0 | 102 | 7 | US-11-072-512-2266 |
| 11 | 32 | 80.0 | 202 | 7 | US-11-098-686-10163 |
| 12 | 32 | 80.0 | 1302 | 6 | US-10-995-561-1024 |
| 13 | 31 | 77.5 | 278 | 6 | US-10-131-826A-136 |
| 14 | 31 | 77.5 | 278 | 6 | US-10-973-115B-136 |
| 15 | 31 | 77.5 | 461 | 6 | US-10-878-556A-162 |
| 16 | 31 | 77.5 | 463 | 6 | US-10-131-826A-360 |
| 17 | 31 | 77.5 | 463 | 6 | US-10-973-115B-360 |
| 18 | 31 | 77.5 | 463 | 7 | US-11-154-673-9 |
| 19 | 31 | 77.5 | 469 | 6 | US-10-821-234-1151 |
| 20 | 31 | 77.5 | 498 | 7 | US-11-051-720-1355 |
| 21 | 31 | 77.5 | 505 | 7 | US-11-051-720-1357 |
| 22 | 31 | 77.5 | 506 | 7 | US-11-154-673-2 |
| 23 | 31 | 77.5 | 519 | 7 | US-11-051-720-1350 |
| 24 | 31 | 77.5 | 541 | 7 | US-11-051-720-1351 |
| 25 | 31 | 77.5 | 544 | 7 | US-11-245-400-7 |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 26 | 31 | 77.5 | 544 | 7 | US-11-051-720-1352 | Sequence 1352, Ap |
| 27 | 31 | 77.5 | 550 | 7 | US-11-154-673-8 | Sequence 8, Appli |
| 28 | 31 | 77.5 | 588 | 7 | US-11-051-720-1356 | Sequence 1356, Ap |
| 29 | 31 | 77.5 | 593 | 7 | US-11-154-673-3 | Sequence 3, Appli |
| 30 | 31 | 77.5 | 597 | 7 | US-11-051-720-1354 | Sequence 1354, Ap |
| 31 | 31 | 77.5 | 619 | 7 | US-11-051-720-1353 | Sequence 1353, Ap |
| 32 | 31 | 77.5 | 625 | 7 | US-11-154-673-7 | Sequence 7, Appli |
| 33 | 31 | 77.5 | 650 | 7 | US-11-051-720-1439 | Sequence 1439, Ap |
| 34 | 31 | 77.5 | 673 | 6 | US-10-063-703-16 | Sequence 16, Appl |
| 35 | 31 | 77.5 | 673 | 7 | US-11-102-240-16 | Sequence 16, Appl |
| 36 | 31 | 77.5 | 758 | 7 | US-11-245-400-30 | Sequence 30, Appl |
| 37 | 31 | 77.5 | 1493 | 7 | US-11-183-136-26 | Sequence 26, Appl |
| 38 | 30 | 75.0 | 256 | 7 | US-11-072-512-3255 | Sequence 3255, Ap |
| 39 | 30 | 75.0 | 311 | 6 | US-10-793-626-2450 | Sequence 2450, Ap |
| 40 | 30 | 75.0 | 333 | 7 | US-11-181-234-5 | Sequence 5, Appli |
| 41 | 30 | 75.0 | 333 | 7 | US-11-181-234-7 | Sequence 7, Appli |
| 42 | 30 | 75.0 | 342 | 6 | US-10-793-626-2854 | Sequence 2854, Ap |
| 43 | 30 | 75.0 | 478 | 7 | US-11-092-353-4 | Sequence 4, Appli |
| 44 | 30 | 75.0 | 558 | 7 | US-11-096-568A-26217 | Sequence 26217, A |
| 45 | 29 | 72.5 | 146 | 7 | US-11-000-463-881 | Sequence 881, App |

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Human
; US-10-412-748-11

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
|----|---|--------------|
| QY | 1 | LLLPLQILL 9 |
| DB | 5 | LLLPLQILL 13 |

RESULT 2
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; TYPE: PRT

; ORGANISM: Human
US-10-412-748-14

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 3

US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A.
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 4

US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match 100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 5

US-11-096-568A-27354
; Sequence 27354, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27354
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354

Query Match 85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 5.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 8
Db 1 LLLPLQILL 8

RESULT 6

US-11-096-568A-27391
; Sequence 27391, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27391
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391

Query Match 85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 5.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 8
Db 1 LLLPLQILL 8

RESULT 7

US-11-096-568A-27353
; Sequence 27353, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.

```

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27353
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(85)
; OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353

Query Match      85.0%; Score 34; DB 7; Length 85;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQL 8
Db 15 MLLPLQL 22

RESULT 8
US-11-096-568A-27390
; Sequence 27390, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27390
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(85)
; OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390

Query Match      85.0%; Score 34; DB 7; Length 85;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQL 8
Db 15 MLLPLQL 22

RESULT 9
US-11-096-568A-23862
; Sequence 23862, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23862
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(125)
; OTHER INFORMATION: Ceres Seq. ID no. 12415965
US-11-096-568A-23862

Query Match      82.5%; Score 33; DB 7; Length 125;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQL 9
Db 82 LLLPLQL 90

RESULT 10
US-11-072-512-2266
; Sequence 2266, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2266
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2266

Query Match      80.0%; Score 32; DB 7; Length 102;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQL 9
Db 16 LLLPLQL 24

RESULT 11
US-11-098-686-10163
; Sequence 10163, Application US/11098686
; Publication No. US2006002496A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
```

```

; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10163
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10163

```

```

Query Match      80.0%; Score 32; DB 7; Length 202;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLLPLQILL 9
    ||||| :||
Db 146 LLLPLTILI 154

```

```

RESULT 12
US-10-995-561-1024
; Sequence 1024, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1024
; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1024

```

```

Query Match      80.0%; Score 32; DB 6; Length 1302;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLLPLQILL 9
    ||||| :||
Db 12 LLLPLPLL 20

```

```

RESULT 13
US-10-131-826A-136
; Sequence 136, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 136
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-136

```

```

Query Match      77.5%; Score 31; DB 6; Length 278;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LLLPLQILL 9
    ||||| :||
Db 13 LLLPLLLL 21

```

```

RESULT 14
US-10-973-115B-136
; Sequence 136, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678

```

; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 136
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-973-115B-136

Query Match 77.5%; Score 31; DB 6; Length 278;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
Db 13 LLLPLLLLL 21

RESULT 15
US-10-878-556A-162
; Sequence 162, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ncbl_human
; DATABASE ENTRY DATE: 1993-07-01
US-10-878-556A-162

Query Match 77.5%; Score 31; DB 6; Length 461;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
Db 11 LLLPLLLLL 19

Search completed: March 11, 2006, 01:38:40
Job time : 9 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLNERKWL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 47 | 100.0 | 9 | 4 AAE08239 | Aae08239 Human str |
| 2 | 47 | 100.0 | 9 | 8 ADR68795 | Adr68795 Human str |
| 3 | 47 | 100.0 | 97 | 6 ADA05740 | Ada05740 Human NOV |
| 4 | 47 | 100.0 | 97 | 8 ADN62904 | Adn62904 Human NOV |
| 5 | 47 | 100.0 | 136 | 4 ABG23378 | Abg23378 Novel hum |
| 6 | 47 | 100.0 | 181 | 6 ADA05738 | Ada05738 Human NOV |
| 7 | 47 | 100.0 | 181 | 8 ADN62902 | Adn62902 Human NOV |
| 8 | 47 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 9 | 47 | 100.0 | 198 | 8 ADN62900 | Adn62900 Human NOV |
| 10 | 47 | 100.0 | 224 | 6 ADA05744 | Ada05744 Human NOV |
| 11 | 47 | 100.0 | 224 | 8 ADN62908 | Adn62908 Human NOV |
| 12 | 47 | 100.0 | 224 | 9 ADV21100 | Adv21100 Human str |
| 13 | 47 | 100.0 | 225 | 4 AAB98502 | Aab98502 Human Str |
| 14 | 47 | 100.0 | 247 | 6 ADA05742 | Ada05742 Human NOV |
| 15 | 47 | 100.0 | 247 | 8 ADN62906 | Adn62906 Human NOV |
| 16 | 47 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 17 | 47 | 100.0 | 250 | 8 ADN62896 | Adn62896 Human NOV |
| 18 | 47 | 100.0 | 252 | 6 ADA05734 | Ada05734 Human NOV |
| 19 | 47 | 100.0 | 252 | 8 ADN62898 | Adn62898 Human NOV |
| 20 | 47 | 100.0 | 253 | 2 AAR67888 | Aar67888 Human str |
| 21 | 47 | 100.0 | 253 | 2 AAW05383 | Aaw05383 Human amy |
| 22 | 47 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 23 | 47 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 24 | 47 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |

| | | | | | |
|----|----|-------|-----|------------|--------------------|
| 25 | 47 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 26 | 47 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 27 | 47 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |
| 28 | 47 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 29 | 47 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 30 | 47 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/an |
| 31 | 47 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 32 | 47 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antipsori |
| 33 | 47 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 34 | 47 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 35 | 47 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 36 | 47 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |
| 37 | 43 | 91.5 | 9 | 4 AAE08245 | Aae08245 Human str |
| 38 | 43 | 91.5 | 9 | 4 AAE08255 | Aae08255 Human str |
| 39 | 43 | 91.5 | 9 | 8 ADR68801 | Adr68801 Human str |
| 40 | 43 | 91.5 | 9 | 8 ADR68811 | Adr68811 Human str |
| 41 | 40 | 85.1 | 243 | 5 ABB84419 | Abb84419 Bovine SC |
| 42 | 40 | 85.1 | 249 | 5 ABB84420 | Abb84420 Porcine S |
| 43 | 39 | 83.0 | 212 | 2 AAY28590 | Aay28590 Human Fac |
| 44 | 39 | 83.0 | 228 | 7 AAE39994 | Aae39994 Human adi |
| 45 | 39 | 83.0 | 228 | 8 ADN04134 | Adn04134 Antipsori |

ALIGNMENTS

RESULT 1
AAE08239
ID AAE08239 standard; peptide; 9 AA.
XX AAE08239;
AC AAE08239;
XX
DT 01-NOV-2001 (first entry)
DE Human stratum corneum chymotrypsin enzyme peptide #3 (residues 58-66).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX (UYAR-) UNIV ARKANSAS.
XX O'brien TJ;
XX WPI; 2001-514676/56.
XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX Claim 25; Page 103; 127pp; English.
XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate CC and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 1 VLVNERWVL 9

RESULT 2

ADR68795
ID ADR68795 standard; peptide; 9 AA.

XX AC ADR68795;

XX DT 02-DEC-2004 (first entry)

XX DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:34.

XX KW serine protease; stratum corneum chymotrytic enzyme; SCCE;

XX KW immune response; ovarian cancer; lung cancer; prostate cancer;

XX KW pancreatic cancer; colon cancer.

XX OS Homo sapiens.

XX PN WO2004075723-A2.

XX PD 10-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US005134.

XX PR 21-FEB-2003; 2003US-00372521.

XX PA (UYAR-) UNIV ARKANSAS.

XX PI O'Brien TJ, Cannon MJ, Santin A;

XX DR WPI; 2004-653294/63.

XX PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.

XX PS Claim 5; SEQ ID NO 34; 117pp; English.

XX CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 1 VLVNERWVL 9

RESULT 3

ADA05740

ID ADA05740 standard; protein; 97 AA.

XX AC ADA05740;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV18e protein SEQ ID NO:100.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-032749P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 17-MAY-2002; 2002US-0381042P.

XX PR 28-MAY-2002; 2002US-0381642P.

XX PR 29-MAY-2002; 2002US-0383656P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Sytek KA, Edinger SR, Ellerman K, Malvankar UM;
PI Ott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eissen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

XX DR N-PSDB; ADA05739.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing,

XX PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
XX PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
XX PT pharmacogenomics.

XX PS Claim 1; Page 171; 586pp; English.

CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipaeamic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 97 AA;
 Query Match 100.0%; Score 47; DB 6; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLVNERWVL 9
 DB 39 VLVNERWVL 47
 |||||
 RESULT 4
 ADN62904
 ID ADN62904 standard; protein; 97 AA.
 AC
 XX
 AC ADN62904;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18e.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 XX 26-FEB-2004.
 PD
 XX 01-OCT-2002; 2002US-00262511.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 12-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (EAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGE E M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 WPI; 2004-213931/20.
 DR N-PSDB; ADN62903.
 DR
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,

PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 100; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 97 AA;
Query Match 100.0%; Score 47; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
QY 1 VLVNERWVL 9
DB 39 VLVNERWVL 47
RESULT 5
ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
KW
XX Homo sapiens.
OS
XX WO200175067-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US008631.
PF
XX 31-MAR-2000; 2000US-00540217.
PR
XX 23-AUG-2000; 2000US-00649167.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR

DR N-PSDB; AAS87565.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in:
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 136 AA;
Query Match 100.0%; Score 47; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLVNERWVL 9
DB 64 VLVNERWVL 72
RESULT 6
ADA05738
ID ADA05738 standard; protein; 181 AA.
XX
AC ADA05738;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18d protein SEQ ID NO:98.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
XX WO2003029424-A2.
PN
XX 10-APR-2003.
PD
XX 02-OCT-2002; 2002WO-US031373.
PF
XX 02-OCT-2001; 2001US-0326483P.
PR
XX 05-OCT-2001; 2001US-032743P.
PR
XX 05-OCT-2001; 2001US-0327449P.
PR
XX 09-OCT-2001; 2001US-0327917P.
PR
XX 09-OCT-2001; 2001US-0328029P.
PR
XX 09-OCT-2001; 2001US-0328044P.
PR

PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328449P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehusen BD, Anderson DM, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2003-381626/36.
DR N-PSDB; ADA05737.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 171; 586pp; English.
XX
XX The present invention describes NOVX proteins, where x can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antileptemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 181 AA;
SQ
Query Match 100.0%; Score 47; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLVNERWVL 9
Db 39 VLVNERWVL 47
|||||||
RESULT 7
ADN62902
ID ADN62902 standard; protein; 181 AA.
XX
XX AC ADN62902;
DT 01-JUL-2004 (first entry)
XX
XX Human NOV18d.
XX
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX OS Homo sapiens.
XX
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I. PA

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPVT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGRE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP1/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX
DR WPI; 2004-213931/20.
DR N-PSDB; ADN62901.
XX
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
XX
PS Claim 1; SEQ ID NO 98; 395pp; English.
XX
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient with
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent.
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

SQ Sequence 181 AA;

Query Match 100.0%; Score 47; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

OY 1 VLVNERWVL 9
Db 39 VLVNERWVL 47
|||||||

RESULT 8

ADA05736
ID ADA05736 standard; protein; 198 AA.

XX
AC ADA05736;

DT 06-NOV-2003 (first entry)

DE Human NOV18c protein SEQ ID NO:96.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329144P.

PR 17-OCT-2001; 2001US-0330142P.

PR 18-OCT-2001; 2001US-0330309P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339266P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 17-APR-2002; 2002US-0373260P.

PR 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373817P.

PR 19-APR-2002; 2002US-0373826P.

PR 19-APR-2002; 2002US-0373884P.

PR 22-APR-2002; 2002US-0374977P.

PR 16-MAY-2002; 2002US-0381037P.

PR 16-MAY-2002; 2002US-0381038P.

PR 16-MAY-2002; 2002US-0381042P.

PR 17-MAY-2002; 2002US-0381642P.

PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.

PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

XX

PA

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spyček KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05735.
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 170; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipase activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC present invention.
XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 47; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66

RESULT 9
ADN62900
ID ADN62900 standard; protein; 198 AA.
XX
AC ADN62900;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18c.
XX

KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-033266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374377P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 29-JUN-2002; 2002US-0391335P.
XX
XX (SMIT//) SMITHSON G.
XX (MILL//) MILLET I.
XX (PEYM//) PEYMAN J A.
XX (KEKU//) KEKUDA R.
XX (JUGU//) JU J.
XX (LILL//) LI L.
XX (GUOX//) GUO X.
XX (PATT//) PATTURAJAN M.
XX (SPYT//) SPYTEK K A.
XX (EDIN//) EDINGER S R.
XX (ELLE//) ELLERMAN K.
XX (NALY//) MALLYANKAR U M.
XX (ORTT//) ORT T.
XX (GORM//) GORMAN L.
XX (ZERH//) ZERHUSEN B D.
XX (ANDE//) ANDERSON D W.
XX (ZHON//) ZHONG M.
XX (CATT//) CATTERTON E.
XX (JIWW//) JI W.
XX (MILL//) MILLER C E.
XX (RAST//) RASTELLI L.
XX (STON//) STONE D J.
XX (PENA//) PENA C E A.
XX (SHEN//) SHENOY S G.
XX (SHIM//) SHIMKETS R A.
XX (ROTH//) ROTHENBERG M E.
XX (LEAC//) LEACH M D.
XX (AGEE//) AGE M L.
XX (BERG//) BERGHs C.

PA (DIPI/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR WPI: 2004-213931/20.
DR N-PSDB; ADM62899.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 96; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient with
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 47; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNRRWVL 9
|||
DB 58 VLVNRRWVL 66

RESULT 10
ADA05744
ID ADA05744 standard; protein; 224 AA.
XX
AC ADA05744;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18g protein SEQ ID NO:104.
XX
XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; antilipaemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 22-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381039P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2003-381626/36.
XX N-PSDB; ADA05743.
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 172; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to

CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 224 AA;

Query Match 100.0%; Score 47; DB 6; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
 DB 44 VLVNERWVL 52
 |||||

RESULT 11
 ADN62908
 ID ADN62908 standard; protein; 224 AA.
 XX
 AC ADN62908;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18g.
 DE
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 01-OCT-2002; 2002US-00262511.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.

PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 17-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJG/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWJ/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPIO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhuseen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 WPI; 2004-213931/20.
 DR N-PSDB; ADN62907.
 DR
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 104; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our

CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent
 CC disease and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 224 AA;

Query Match 100.0%; Score 47; DB 8; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 VLVNERWVL 9
 |||||
 Db 44 VLVNERWVL 52

RESULT 12

ADV21100
 ID ADV21100 standard; protein; 224 AA.

AC ADV21100;

XX 24-FEB-2005 (first entry)

XX Human stratum corneum chymotrypsin protein.

DE Protein purification; PS133 protein; serine protease; prostate disease;
 KW andrology; genitourinary disease; prostatic cancer; cytostatic;
 KW protein therapy; chymotrypsin; enzyme.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Domain 26..42 /note = Catalytically functional motif

FT Domain 83..87 /note = Catalytically functional motif

FT Domain 174..179 /note = Catalytically functional motif

XX US2004241646-A1.

XX 02-DEC-2004.

XX 20-FEB-2001; 2001US-00789210.

XX 06-OCT-1997; 97US-00944483.

XX (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GRAN/) GRANADOS E.

PA (KLAS/) KLAS M R.

PA (RUSSEL/) RUSSELL J C.

PA (STEW/) STEWART K D.

PA (STRO/) STROUPE S D.
 XX Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;
 PI Russell JC, Stewart KD, Stroupe SD;
 XX WPI; 2005-011614/01.
 DR GENBANK; L33404.
 XX New isolated polypeptides, useful for detecting, diagnosing, staging,
 PT monitoring, prognosticating, preventing or treating, or determining
 PT predisposition to diseases or conditions of the prostate such as prostate
 PT cancer.
 XX Example 1; SEQ ID NO 33; 96pp; English.
 PS The invention relates to PS133 protein, a member of the human serine
 CC protease family and its corresponding nucleic acid sequence. PS133
 CC polypeptide is useful for detecting, diagnosing, staging, monitoring,
 CC prognosticating, preventing or treating or determining predisposition to
 CC diseases or conditions of the prostate such as prostatic cancer. The
 CC present sequence is the human stratum corneum chymotrypsin protein. This
 CC sequence is used to align with PS133 consensus protein.
 XX
 SQ Sequence 224 AA;

Query Match 100.0%; Score 47; DB 9; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 VLVNERWVL 9
 |||||
 Db 29 VLVNERWVL 37

RESULT 13

AAB98502
 ID AAB98502 standard; protein; 225 AA.

XX AAB98502;

XX 03-AUG-2001 (first entry)

XX Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.

XX Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;

XX tumour antigen-derived gene 15; serine protease;

XX Stratum Corneum Chymotryptic Enzyme; SCCE.

XX Homo sapiens.

XX WO200129056-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000WO-US029095.

XX 20-OCT-1999; 99US-00421213.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ, Tanimoto H;

XX WPI; 2001-381031/40.

XX Novel extracellular serine protease, termed tumor antigen-derived gene 15
 PT protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
 PT treatment, prevention of cancer, particularly breast, ovarian cancer.

XX Example 10; Fig 1; 130pp; English.

XX The present invention relates to human tumour antigen-derived gene 15
 CC (TADG-15) protein and coding sequence (see AAB98500). TADG-
 CC 15 is an extracellular serine protease. It was found that TADG-15 is over

CC -expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20
CC residues that lack TADG-15 protease activity are useful for vaccinating
CC an individual against TADG-15, having, suspected of having or at risk of
CC getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic
CC or therapeutic target in cancer. The present sequence was used in a
CC sequence homology alignment with the catalytic domain of TADG-15
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 47; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 30 VLVNERWVL 38

RESULT 14
ADA05742
ID ADA05742 standard; protein; 247 AA.

XX
AC ADA05742;
XX
DT 06-NOV-2003 (first entry)

DE Human NOV18f protein SEQ ID NO:102.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 09-OCT-2001; 2001US-0327449P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

XX 09-OCT-2001; 2001US-0328044P.

XX 09-OCT-2001; 2001US-0328056P.

XX 12-OCT-2001; 2001US-0328849P.

XX 15-OCT-2001; 2001US-0329414P.

XX 17-OCT-2001; 2001US-0330142P.

XX 18-OCT-2001; 2001US-0330309P.

XX 22-OCT-2001; 2001US-0341058P.

XX 24-OCT-2001; 2001US-0339266P.

XX 24-OCT-2001; 2001US-0343629P.

XX 29-OCT-2001; 2001US-0349575P.

XX 01-NOV-2001; 2001US-0346357P.

XX 17-APR-2002; 2002US-0373260P.

XX 19-APR-2002; 2002US-0373815P.

XX

PA (CURA-) CURAGEN CORP.

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ott T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

DR N-PSDB; ADA05741.

XX

PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

XX Claim 1; Page 172; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

XX Sequence 247 AA;

Query Match 100.0%; Score 47; DB 6; Length 247;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9

DB 44 VLVNERWVL 52

RESULT 15

ADN62906

ID ADN62906 standard; protein; 247 AA.

XX AC ADN62906;

XX

DT 01-JUL-2004 (first entry)

XX DE Human NOV18f.
XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX OS Homo sapiens.
XX US2004038223-A1.
XX 26-FEB-2004.
XX 01-OCT-2002; 2002US-00262511.
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 09-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 09-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG W.
PA (CATT/) CATTERTON E.
PA (JIWV/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.

PA (LEAC/) LEACH M D.
PA (AGEE/) AGE E M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong W, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghe C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62905.
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX Claim 1; SEQ ID NO 102; 395pp; English.
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 247 AA;

Query Match 100.0%; Score 47; DB 8; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWYL 9
| | | | | | | | | |
Db 44 VLVNERWYL 52

Search completed: March 11, 2006, 00:24:13
Job time : 86.6667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-34

Perfect score: 47

Sequence: 1 VLVNERWVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 47 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 39 | 83.0 | 246 | 1 DBHU | complement factor |
| 3 | 38 | 80.9 | 232 | 1 KQPG | tissue kallikrein |
| 4 | 38 | 80.9 | 260 | 2 I56559 | neuropsin - mouse |
| 5 | 38 | 80.9 | 417 | 2 T25594 | hypothetical prote |
| 6 | 37 | 78.7 | 250 | 2 T01779 | trypsin (EC 3.4.21 |
| 7 | 37 | 78.7 | 250 | 2 S31384 | trypsin (EC 3.4.21 |
| 8 | 37 | 78.7 | 258 | 1 S44184 | chymotrypsin (EC 3 |
| 9 | 37 | 78.7 | 259 | 1 S49129 | chymotrypsin (EC 3 |
| 10 | 37 | 78.7 | 1421 | 2 T05892 | hypothetical prote |
| 11 | 36 | 76.6 | 72 | 2 F82825 | hypothetical prote |
| 12 | 36 | 76.6 | 258 | 2 A45161 | serine proteinase |
| 13 | 36 | 76.6 | 426 | 2 D42519 | A20R protein - vac |
| 14 | 36 | 76.6 | 426 | 2 T37408 | probable 49.1K pro |
| 15 | 36 | 76.6 | 426 | 2 C72166 | A22R protein - var |
| 16 | 36 | 76.6 | 426 | 2 T28563 | hypothetical prote |
| 17 | 36 | 76.6 | 426 | 2 C36850 | A21R protein - var |
| 18 | 36 | 76.6 | 516 | 2 T47075 | hypothetical prote |
| 19 | 35 | 74.5 | 178 | 2 T25570 | hypothetical prote |
| 20 | 35 | 74.5 | 231 | 2 S31778 | trypsin (EC 3.4.21 |
| 21 | 35 | 74.5 | 242 | 2 S31776 | trypsin (EC 3.4.21 |
| 22 | 35 | 74.5 | 242 | 2 S31775 | trypsin (EC 3.4.21 |
| 23 | 35 | 74.5 | 242 | 2 S49489 | trypsin (EC 3.4.21 |
| 24 | 35 | 74.5 | 247 | 1 A25852 | trypsin (EC 3.4.21 |
| 25 | 35 | 74.5 | 257 | 1 JC2479 | venombin B (EC 3.4 |
| 26 | 35 | 74.5 | 258 | 2 G02959 | haptoglobin - rhes |
| 27 | 35 | 74.5 | 258 | 2 I36945 | haptoglobin Hp - c |
| 28 | 35 | 74.5 | 258 | 2 I36947 | haptoglobin Hpp - |
| 29 | 35 | 74.5 | 274 | 2 I47078 | coagulation factor |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 35 | 74.5 | 274 | 2 E70472 | ribosomal protein |
| 31 | 35 | 74.5 | 282 | 2 A83757 | hypothetical prote |
| 32 | 35 | 74.5 | 329 | 1 HPDG | haptoglobin precu |
| 33 | 35 | 74.5 | 345 | 2 I36941 | haptoglobin - chim |
| 34 | 35 | 74.5 | 346 | 2 I36942 | haptoglobin - chim |
| 35 | 35 | 74.5 | 347 | 1 HPHU1 | haptoglobin precu |
| 36 | 35 | 74.5 | 347 | 2 G00006 | haptoglobin - blac |
| 37 | 35 | 74.5 | 348 | 1 HPHUR | haptoglobin-relate |
| 38 | 35 | 74.5 | 349 | 2 I36944 | haptoglobin - chim |
| 39 | 35 | 74.5 | 406 | 1 HPHU2 | haptoglobin precu |
| 40 | 35 | 74.5 | 410 | 2 T46034 | branched-chain-ami |
| 41 | 35 | 74.5 | 416 | 1 KFBO | coagulation factor |
| 42 | 35 | 74.5 | 421 | 1 S11674 | acrosin (EC 3.4.21 |
| 43 | 35 | 74.5 | 453 | 2 G96895 | hypothetical prote |
| 44 | 35 | 74.5 | 505 | 2 C86443 | unknown protein [i |
| 45 | 35 | 74.5 | 539 | 2 S54045 | probable membrane |

ALIGNMENTS

RESULT 1

A53968

serine proteinase SCCE precursor - human

N;Alternate names: stratum corneum chymotryptic enzyme

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C;Accession: A53968

R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.

J. Biol. Chem. 269, 19420-19426, 1994

A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym.

A;Reference number: A53968; MUID:94308225; PMID:8034709

A;Accession: A53968

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-253 <HAN>

A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:7

C;Genetics:

A;Gene: GDB:PRSS6; SCCE

A;Cross-references: GDB:377730

A;Map position: 7q35-7q35

C;Superfamily: trypsin; trypsin; trypsin homology

F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9

DB 58 VLVNERWVL 66

RESULT 2

DBHU

complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)

N;Alternate names: adipisin; C3 convertase activator

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C;Accession: A40197; A00936; A60571; S66645

R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;

J. Biol. Chem. 267, 9210-9213, 1992

A;Title: Human adipisin is identical to complement factor D and is expressed at high level

A;Reference number: A40197; MUID:92250520; PMID:1374388

A;Accession: A40197

A;Molecule type: mRNA

A;Residues: 1-246 <WHI>

A;Cross-references: UNIPROT:P00746; UNIPARC:UPI0000172AE4; GB:M94526

R;Niemann, M.A.; Bhow, A.S.; Bennett, J.C.; Volanakis, J.E.

Biochemistry 23, 2482-2486, 1984

A;Title: Amino acid sequence of human D of the alternative complement pathway.

A;Reference number: A00936; MUID:85000441; PMID:6383466

A;Accession: A00936

A:Molecule type: protein
A:Residues: 19-44, 'G', 46-51, 'O', 53-75, 'TH', 78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235, '
A:Cross-references: UNIPARC:UPI0000172AE5
A:Note: a few residues were assigned from the previously published sequence of Reid et al
R: Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya
Mol. Immunol. 27, 637-644, 1990
A:Title: Molecular and functional identification and purification of complement component
A:Reference number: A60571; MUID: 90370044; PMID: 2395435
A:Accession: A60571
A:Molecule type: protein
A:Residues: 19-20, 'XX', 23-27, 'XX', 30-31, 'XX', 34, 'X', 36-40 <MIY>
A:Cross-references: UNIPARC:UPI0000172AE6
R: Balke, N.; Holtkamp, U.; Hoerl, W.H.; Teschesche, H.
FEBS Lett. 371, 300-302, 1995
A:Title: Inhibition of degradation of human polymorphonuclear leukocytes by complement
A:Reference number: S66645; MUID: 96013156; PMID: 7556615
A:Accession: S66645
A:Status: preliminary
A:Molecule type: protein
A:Residues: 19-44, 'C', 46-48 <BAL>
A:Cross-references: UNIPARC:UPI0000172AE7
C:Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
C:Genetics:
A:Gene: GDB:DF
A:Cross-references: GDB:132645; OMIM:134350
A:Map position: Xpter-Xqter
C:Superfamily: trypsin; trypsin homology
C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-246/Product: complement factor D (fragment) #status experimental <MAT>
F:19-241/Domain: trypsin homology <TRY>
F:44-60, 141-207, 172-188, 197-222/disulfide bonds: #status predicted
F:59, 105, 201/Active site: His, Asp, Ser #status predicted

Query Match 83.0%; Score 39; DB 1; Length 246;
Best Local Similarity 88.9%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 47 VLVNERWVL 55
||| :|||

RESULT 3
KQPG
tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
N: Alternate names: glandular kallikrein; kininogenin
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
A:Accession: A00938; A92895
R: Teschesche, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, M.;
Adv. Exp. Med. Biol. 120, 245-260, 1979
A:Title: The primary structure of porcine glandular kallikreins.
A:Reference number: A90015
A:Accession: A00938
A:Molecule type: protein
A:Residues: 1-49, 'GWL', 53-134, 'D', 136-156, 'H', 158, 'B', 160-224, 'B', 226-232 <TSC>
A:Cross-references: UNIPARC:UPI0000172AB9
A:Note: the residue identified as 225-Asx is bound to carbohydrate; therefore, we have s
R: Bode, W.; Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunik, H.
J. Mol. Biol. 164, 237-282, 1983
A:Title: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein A,
C: structure and its comparison with bovine trypsin.
A:Reference number: A92895; MUID: 83189107; PMID: 6551452
A:Contents: X-ray crystallography, 2 angstroms
A:Accession: A92895
A:Molecule type: protein
A:Residues: 1-224, 'B', 226-232 <BOD>
A:Cross-references: UNIPARC:UPI0000172ABA
C:Comment: The protein consists of two chains, A and B, held together by disulfide bonds
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; pancreas; serine proteinase

F:1-224/Domain: trypsin homology <TRY>
F:1-80/Product: tissue kallikrein chain A #status experimental <MPTA>
F:79-82/Region: autocatalytic loop
F:91-232/Product: tissue kallikrein chain B #status experimental <MPTB>
F:144, 26-42, 121-190, 155-169, 180-205/disulfide bonds: #status experimental
F:41, 89, 184/Active site: His, Asp, Ser #status experimental
F:78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:225/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 80.9%; Score 38; DB 1; Length 232;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 29 VLVNERWVL 37
||| :|||

RESULT 4
I56559
neurospain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56559
R: Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishin
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease gene
A:Reference number: I56559; MUID: 95348817; PMID: 7623137
A:Accession: I56559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: UNIPROT:Q61955; UNIPARC:UPI00000292C5; GB:D30785; NID:G1648847; PIDN:
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match 80.9%; Score 38; DB 2; Length 260;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 61 VLVNERWVL 69
||| :|||

RESULT 5
T25594
hypotheical protein C32E8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25594
R: Gattung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid C32E8.
A:Reference number: Z20056
A:Accession: T25594
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <GAT>
A:Cross-references: UNIPROT:P91123; UNIPARC:UPI000017B7F4; EMBL:U88308; PIDN:AA842324.1;
A:Experimental source: strain Bristol N2; clone C32E8
C:Genetics:
A:Gene: CESP:C32E8.6
A:Map position: 1
A:Introns: 22/3; 51/2; 92/1; 297/1; 354/1

Query Match 80.9%; Score 38; DB 2; Length 417;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERW 7
DB 219 VLVNERW 225
||| :|||

```

A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anophe
A;Reference number: S35412
A;Accession: S49130
A;Molecule type: DNA
A;Residues: 1-165, 'R', 167-193, 'FPD', 197-258 <MU2>
A;Cross-references: UNIPARC:UPI000016B7D4; EMBL:Z18888; NID:G509416; PIDN:CAA79326.1; PI
C;Genetics:
A;Introns: 78/2; 209/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: activation peptide #status predicted <PRO>
F;33-258/Product: chymotrypsin 2 #status predicted <MAT>
F;33-250/Domain: trypsin homology <TRY>
F;59-75,182-198,208-232/Disulfide bonds: #status experimental
F;74,119,212/Active site: His, Asp, Ser #status predicted

Query Match 78.7%; Score 37; DB 1; Length 258;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
DB 63 LLNDRWVL 70

RESULT 9
S49129
chymotrypsin (EC 3.4.21.1) 1 precursor - African malaria mosquito
N;Alternate names: chymotrypsin-like proteinase ANCHYM1
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S49129; S44185
R;Mueller, H.
submitted to the EMBL Data Library, November 1992
A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anophe
A;Reference number: S35412
A;Accession: S49129
A;Molecule type: mRNA
A;Residues: 1-259 <MUE>
A;Cross-references: UNIPROT:Q27289; UNIPARC:UPI0000128651; EMBL:Z18887; NID:G509414; PIDN
A;Experimental source: strain Suakoko
R;Mueller, H.M.; Catteruccia, F.; Crisanti, A.
submitted to the EMBL Data Library, April 1994
A;Description: An Anopheles gambiae locus containing the sequences of two closely relat
A;Reference number: S44184
A;Accession: S44185
A;Molecule type: DNA
A;Residues: 1-259 <MU2>
A;Cross-references: UNIPARC:UPI0000128651; EMBL:Z32645; NID:G474026; PIDN:CAA83568.1; PI
A;Experimental source: strain Suakoko
C;Genetics:
A;Introns: 78/2; 209/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: Hydrolase; protein digestion; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: activation peptide #status predicted <PRO>
F;33-259/Product: chymotrypsin 1 #status predicted <MAT>
F;33-250/Domain: trypsin homology <TRY>
F;59-75,182-198,208-232/Disulfide bonds: #status experimental
F;74,119,212/Active site: His, Asp, Ser #status predicted

Query Match 78.7%; Score 37; DB 1; Length 259;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
DB 63 LLNDRWVL 70

RESULT 10
T05892
chymotrypsin (EC 3.4.21.1) 2 precursor - African malaria mosquito
N;Alternate names: chymotrypsin-like proteinase ANCHYM2
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S49130
R;Mueller, H.M.; Catteruccia, F.; Crisanti, A.
submitted to the EMBL Data Library, April 1994
A;Description: An Anopheles gambiae locus containing the sequences of two closely relat
A;Reference number: S44184
A;Accession: S44184
A;Molecule type: DNA
A;Residues: 1-258 <MUE>
A;Cross-references: UNIPROT:Q17025; UNIPARC:UPI0000128657; EMBL:Z32645; NID:G474026; PID
R;Mueller, H.
submitted to the EMBL Data Library, November 1992

```

hypothetical protein F6H11.110 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999
C:Accession: T05892
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15456
A:Accession: T05892
A:Molecule type: DNA
A:Residues: 1-1421 <BEV>
A:Cross-references: UNIPARC:UPI000016DB25; EMBL:AL021684
A:Experimental source: cultivar Columbia; BAC clone F6H11
C:Genetics:
A:Map position: 5
A:Introns: 72/3; 142/3; 227/2; 344/3; 372/3; 941/2; 1016/3; 1038/3; 1055/1; 1095/2; 1155
A:Note: F6H11.110

Query Match 78.7%; Score 37; DB 2; Length 1421;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||:|:|:
Db 1208 VLANKRWVI 1216

RESULT 11
F82825
hypothetical protein XF0279 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82825
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82825
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <SIM>
A:Cross-references: UNIPROT:O9PGL9; UNIPARC:UPI00000C2364; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.F.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Prohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Nenck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0279

Query Match 76.6%; Score 36; DB 2; Length 72;
Best Local Similarity 62.5%; Pred. No. 7.5;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWV 8
:|:|:|:
Db 50 ILWNERWL 57

RESULT 12
A45161
serine proteinase (EC 3.4.21.-) RNK-Met-1 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: A45161
R:Smyth, M.J.; Wiltrout, T.; Trapani, J.A.; Ottaway, K.S.; Sowder, R.; Henderson, L.E.; P
J. Biol. Chem. 267, 24418-24425, 1992
A:Title: Purification and cloning of a novel serine protease, RNK-Met-1, from the granule
A:Reference number: A45161; MUID:93077530; PMID:1447189
A:Accession: A45161
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-258 <SMY>
A:Cross-references: UNIPROT:Q03238; UNIPARC:UPI000012BA73; GB:L05175; NID:92066691; PIDN:
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:21-245/Domain: trypsin homology <TRY>

Query Match 76.6%; Score 36; DB 2; Length 258;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||:|:|:
Db 49 VLVHOKRWL 57

RESULT 13
D42519
A20R protein - vaccinia virus (strain Copenhagen)
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C:Accession: D42519
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: D42519
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <JOH>
A:Cross-references: UNIPROT:P20995; UNIPARC:UPI0000138054
C:Superfamily: vaccinia virus probable 49.1K protein

Query Match 76.6%; Score 36; DB 2; Length 426;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||:|:|:
Db 130 VLLNRRWIM 138

RESULT 14
T37408
probable 49.1K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T37408
R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strai
A:Reference number: Z20877
A:Accession: T37408
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <ANT>
A:Cross-references: UNIPROT:O57228; UNIPARC:UPI00000EC2CA; EMBL:U94848; PIDN:AAB96523.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA132R
C:Superfamily: vaccinia virus probable 49.1K protein

Query Match 76.6%; Score 36; DB 2; Length 426;
Best Local Similarity 55.6%; Pred. No. 49;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:
Db 130 VLLNNEWIM 138

RESULT 15
C72166
A22R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: C72166
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: C72166
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <SHC>
A:Cross-references: UNIPROT:Q89166; UNIPARC:UPI0000061D50; GB:Y16780; NID:G5830555; PIDN
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: A22R
C:Superfamily: vaccinia virus probable 49.1X protein

Query Match 76.6%; Score 36; DB 2; Length 426;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:
Db 130 VLLNNEWIM 138

Search completed: March 11, 2006, 00:40:49
Job time : 15.1111 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|----------------|---------------------|
| 1 | 47 | 100.0 | 253 | 1 KLK7_HUMAN | P49862 homo sapien |
| 2 | 40 | 85.1 | 455 | 2 Q9FFR7_ARATH | Q9ffr7 arabidopsis |
| 3 | 39 | 83.0 | 100 | 2 Q9MTV8_BOVIN | Q9myv8 bos taurus |
| 4 | 39 | 83.0 | 235 | 2 Q4K9V0_PSEF5 | Q4k9v0 pseudomonas |
| 5 | 39 | 83.0 | 249 | 2 Q8JFQ7_GADMO | Q8jfq7 gadus morhu |
| 6 | 39 | 83.0 | 254 | 2 Q5M8G2_XENTR | Q5m8g2 xenopus tro |
| 7 | 39 | 83.0 | 690 | 2 Q5F3N3_CHICK | Q5f3n3 gallus gall |
| 8 | 38 | 80.9 | 223 | 2 Q9XY58_CTEFE | Q9xy58 ctenucephal |
| 9 | 38 | 80.9 | 234 | 2 Q7SZE2_AKCA | Q7sze2 agkistrodon |
| 10 | 38 | 80.9 | 235 | 2 Q66PG8_FUGRU | Q66pg8 fugu rubrip |
| 11 | 38 | 80.9 | 246 | 1 KLK_PIG | P00752 sus scrofa |
| 12 | 38 | 80.9 | 252 | 2 Q5M508_XENTR | Q5m508 xenopus tro |
| 13 | 38 | 80.9 | 260 | 1 NRPN_MOUSE | Q61955 mus musculus |
| 14 | 38 | 80.9 | 260 | 1 NRPN_RAT | Q88780 rattus norv |
| 15 | 38 | 80.9 | 262 | 2 Q7ZOG5_9DIPT | Q7z0g5 phlebotomus |
| 16 | 38 | 80.9 | 313 | 2 Q8T3B8_CABEL | Q8t3b8 caenorhabdi |
| 17 | 38 | 80.9 | 377 | 2 Q9SNY8_SOLTU | Q9sny8 solanum tub |
| 18 | 38 | 80.9 | 418 | 2 Q9SNY9_SOLTU | Q9sny9 solanum tub |
| 19 | 38 | 80.9 | 461 | 2 P91123_CABEL | P91123 caenorhabdi |
| 20 | 38 | 80.9 | 791 | 2 Q7NUH8_CHRVO | Q7nuh8 chromobacte |
| 21 | 37 | 78.7 | 60 | 2 Q4RC62_TETNG | Q4rc62 tetraodon n |
| 22 | 37 | 78.7 | 184 | 2 Q67PW1_SYMTX | Q67pw1 symbiobacte |
| 23 | 37 | 78.7 | 229 | 2 Q5QX46_IDILO | Q5qx46 idiomarina |
| 24 | 37 | 78.7 | 233 | 2 Q9PT51_AKCHA | Q9pt51 agkistrodon |
| 25 | 37 | 78.7 | 234 | 2 Q8UUD1_AKCA | Q8uu1 agkistrodon |
| 26 | 37 | 78.7 | 243 | 2 Q9VEM7_DROME | Q9vem7 drosophila |
| 27 | 37 | 78.7 | 249 | 2 Q9W6K0_9PERC | Q9w6k0 notothenia |
| 28 | 37 | 78.7 | 249 | 2 Q92046_DISMA | Q92046 disostichu |
| 29 | 37 | 78.7 | 249 | 2 Q788V0_DISMA | Q788v0 disostichu |
| 30 | 37 | 78.7 | 250 | 1 TRYF_PLEPL | P35034 pleuronecte |
| 31 | 37 | 78.7 | 250 | 2 Q93265_PSEAM | Q93265 pseudopleur |

| | | | | | | |
|----|----|------|-----|---|--------------|---------------------|
| 32 | 37 | 78.7 | 254 | 2 | Q97098_ANOQA | Q97098 anopheles a |
| 33 | 37 | 78.7 | 255 | 2 | Q97100_ANODA | Q97100 anopheles d |
| 34 | 37 | 78.7 | 257 | 1 | VSP4_TRIMU | Q91510 trimeresuru |
| 35 | 37 | 78.7 | 257 | 1 | VSP5_TRIMU | Q91511 trimeresuru |
| 36 | 37 | 78.7 | 257 | 1 | VSP7_TRIMU | Q9d984 trimeresuru |
| 37 | 37 | 78.7 | 257 | 1 | VSPC_TRIGA | Q13062 trimeresuru |
| 38 | 37 | 78.7 | 257 | 2 | Q9PT13_AKHB | Q9pt13 agkistrodon |
| 39 | 37 | 78.7 | 257 | 2 | Q9YUJ9_AGRHP | Q9yuj9 agkistrodon |
| 40 | 37 | 78.7 | 257 | 2 | Q71QJ0_TRIST | Q71qj0 trimeresuru |
| 41 | 37 | 78.7 | 257 | 2 | Q71QI7_TRIST | Q71qi7 trimeresuru |
| 42 | 37 | 78.7 | 257 | 2 | Q71QI5_TRIST | Q71qi5 trimeresuru |
| 43 | 37 | 78.7 | 258 | 1 | CTR2_ANOQA | Q17025 anopheles g |
| 44 | 37 | 78.7 | 258 | 2 | Q9XY53_CTEFE | Q9xy53 ctenucephal |
| 45 | 37 | 78.7 | 258 | 2 | Q7SZE1_SSAUR | Q7szel glyodyius sa |

ALIGNMENTS

RESULT 1
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stromqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
RT chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=Keratinocyte;
RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
RA Yousef G.M., Scorialas A., Magklara A., Soosaipillai A.,
RA Diamandis E.P.;
RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
RT enzyme is a new member of the human kallikrein gene family - Genomic
RT characterization, mapping, tissue expression and hormonal
RT regulation.";
RL Gene 254:119-128(2000).
RN [3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=1054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepker B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
RA Wallbrandt P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
RT mice; a model for chronic itchy dermatitis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
RP AND TISSUE SPECIFICITY.
RC TISSUE=Ovarian carcinoma;

XX MEDLINE=22623266; PubMed=12738725;
RA Dong Y., Kaushal A., Brattesand M., Nicklin J., Clements J.A.;
RT "Differential splicing of KLKS and KLK7 in epithelial ovarian cancer
produces novel variants with potential as cancer biomarkers.";
RL Clin. Cancer Res. 9:1710-1720(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutherford Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=95314630; PubMed=7794273;
RA Skyt A., Stromqvist M., Egelrud T.;
RT "Primary substrate specificity of recombinant human stratum corneum
chymotryptic enzyme.";
RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
structures in the cornified layer of the skin in the continuous
shedding of cells from the skin surface. Specific for amino acid
residues with aromatic side chains in the P1 position. SCCE
cleaves insulin B chain at 4-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-
Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the
activation of precursors to inflammatory cytokines.
CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
also observed at the apical membrane and in cytoplasm at the
invasive front.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=P49862-1; Sequences=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=P49862-2; Sequences=VSP_013581;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
expressed by keratinocytes in the epidermis. Also expressed in the
brain, mammary gland, cerebellum, spinal cord and kidney. Lower
levels in salivary glands, uterus, thymus, thyroid, placenta,
trachea and testis. Up-regulated in ovarian carcinoma, especially
late-stage serous carcinoma, compared with normal ovaries and
benign adenomas (at the protein level).
CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
cell line.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC DR EMBL; L33404; AAC37551.1; -; mRNA.
CC EMBL; AF166330; AAD49718.1; -; Genomic_DNA.

DR EMBL; AF243527; AAG33360.1; -; Genomic_DNA.
DR EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
DR EMBL; AF411214; AAN03662.1; -; mRNA.
DR EMBL; AF411215; AAN03663.1; -; mRNA.
DR EMBL; BC032005; AAH32005.1; -; mRNA.
DR PIR; A53968; A53968.
DR HSP; P00760; 1EZX.
DR MEROPS; S01.300; -.
DR Ensembl; ENSG00000169035; Homo sapiens.
DR HGNC; HGNC:16368; KLK7.
DR H-InvDB; HIX0015373; -.
DR MIM; 604438; -.
DR GO; GO:0008236; P:serine-type peptidase activity; TAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR InterPro; IPR001354; Peptidase_S1_S6.
DR Pfam; PF0089; Trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 22
FT PROPEP 23 29 Activation peptide.
FT CHAIN 30 253 Kallikrein 7.
FT DOMAIN 30 250 Peptidase S1.
FT ACT_SITE 70 70 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 205 205 Charge relay system (By similarity).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTID=VSP_013581.
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;
SQ
Query Match 100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66
RESULT 2
Q9FFR7 ARATH
ID Q9FFR7 ARATH PRELIMINARY; PRT; 455 AA.
AC Q9FFR7
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK23.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
P1 clones.";
RT P1 clones."

```

RL DNA Res. 4:215-230(1997).
DR EMBL; AB005233; BAB1469.1; -; Genomic_DNA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
SQ SEQUENCE 455 AA; 52305 MW; 763F5D5278D22F13 CRC64;

Query Match      85.1%; Score 40; DB 2; Length 455;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
Db      104 IINERWVL 111
          :|:|||||

RESULT 3
O9MYV8_BOVIN PRELIMINARY;      PRT; 100 AA.
AC O9MYV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Haptoglobin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oviduct;
RA Lavery K.S., Gabler C., Killian G.J.;
RL Submitted [JAN-2000] to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271156; CAC00531.1; -; mRNA.
DR HSP; P00751; 1DLR.
DR MEROPS; S01.972; -.
DR GO; GO:0008233; F:Peptidase activity; IEA.
DR GO; GO:0004295; F:Trypsin activity; IEA.
DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
FT NON_TER 1
FT NON_TER 100
FT NON_TER 100
SQ SEQUENCE 100 AA; 11239 MW; FFF6A5A843CED9 CRC64;

Query Match      83.0%; Score 39; DB 2; Length 100;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
Db      22 LINERWLL 29
          |:|||||:|

RESULT 4
O4KV0_PSEFS PRELIMINARY;      PRT; 235 AA.
AC O4KV0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Arginine-tRNA-protein transferase-related protein.
GN ORFNames=PF13883;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]_TaxID=220664;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;

RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY93147.1; -; Genomic_DNA.
KW Transferase.
SQ SEQUENCE 235 AA; 27624 MW; 75C5203A8254CCAF CRC64;

Query Match      83.0%; Score 39; DB 2; Length 235;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      225 LLVNRWVI 233
          :|:|||||:

RESULT 5
O8JFQ7_GADMO PRELIMINARY;      PRT; 249 AA.
AC O8JFQ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Trypsinogen Y precursor (Fragment).
DE Name=tryp1 gene;
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]_TaxID=8049;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pyloric caecum;
RA Gudmundsdottir A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ459311; CAD30563.1; -; mRNA.
DR HSP; P00746; 1FDP.
DR MEROPS; S01.124; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Signal.
FT SIGNAL 1 15 Potential.
FT CHAIN 23 >249 trypsinogen Y.
FT NON_TER 249
FT NON_TER 249
SQ SEQUENCE 249 AA; 27400 MW; 8F898462CDBEFC9 CRC64;

Query Match      83.0%; Score 39; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLVNERWVL 9
Db 50 VLVNDQWVL 58

RESULT 6
Q5M8G2_XENTR PRELIMINARY; PRT; 254 AA.
AC Q5M8G2;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE LOC496767 protein (Fragment).
GN Name=LOC496767;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]_TaxID=8364;
RP NUCLEOTIDE SEQUENCE.
RC TISSU=Whole body;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSU=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088038; AAH88038.1; -; mRNA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:00030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001314; Peptidase_S1.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00020; TRYP_SPC; 1.
DR PROSITE; PS00134; TRYP_SIN_DOM; 1.
FT NON_TER 1
SQ SEQUENCE 254 AA; 27526 MW; 642AFC41A467C38 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 254;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
Db 53 LINEKWVL 60

RESULT 7
Q5F3N3_CHICK PRELIMINARY; PRT; 690 AA.
AC Q5F3N3;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.11k6;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSU=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851617; CAH65251.1; -; mRNA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB_Ca.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS05923; SUSHI; 2.
DR PROSITE; PS50240; TRYP_SIN_DOM; 1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
KW Hypothetical protein.
SQ SEQUENCE 690 AA; 77326 MW; E85A9C65A1D97E7B CRC64;

Query Match 83.0%; Score 39; DB 2; Length 690;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 465 VLISERWVM 473

RESULT 8
Q9XY58_CTEFE PRELIMINARY; PRT; 223 AA.
AC Q9XY58;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Chymotrypsin-like serine protease (Fragment).
GN Name=SP-4;
OS Ctenocephalides felis (Cat flea).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;
OC Ctenocephalides.
OX NCBI_TaxID=7515;
RN [1]
```

RP NUCLEOTIDE SEQUENCE.
 RA Gaines P.J., Sampson C.M., Rushlow K.E., Stiegler G.L.;
 RT "Cloning of a family of serine protease genes from the cat flea
 RL Ctenocephalides felis";
 DR EMBL; AF053916; AAD21836.1; -, mRNA.
 DR HSSP; P00761; IEP.
 DR MEROPS; S01.166; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1_S6.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Protease.
 FT NON_TER 1 1
 SQ SEQUENCE 223 AA; 24844 MW; C34BBE9455DD7DE9 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 223;
 Best Local Similarity 75.0%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LVNERWVL 9
 DB 35 ILNERWVL 42
 RESULT 9
 QTSZ2 AGKA
 ID QTSZ2 AGKA PRELIMINARY; PRT; 234 AA.
 AC QTSZ2;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Thrombin-like enzyme defibrase (Fragment).
 OS Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=35671;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Snake venom gland;
 RA Sun D.-J., Yang T.-S.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204242; AAP20637.1; -, mRNA.
 DR HSSP; Q91516; IBQY.
 DR SMR; Q7SZE2; 1-234.
 DR MEROPS; S01.347; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 234 AA; 25351 MW; 0124C1485525F560 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 234;

Best Local Similarity 87.5%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LVNERWVL 9
 DB 30 LVNEEWVL 37
 RESULT 10
 Q66PG8 FUGRU
 ID Q66PG8 FUGRU PRELIMINARY; PRT; 235 AA.
 AC Q66PG8;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Trypsinogen (Fragment).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Roach J.C.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY661446; AAU06121.1; -, Genomic DNA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 235 AA; 26025 MW; 489D3617C943CC5A CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 235;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLNERWVL 9
 DB 36 VLINKQWVL 44
 RESULT 11
 KLK_PIG
 ID KLK_PIG STANDARD; PRT; 246 AA.
 AC P00752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Glandular kallikrein precursor (EC 3.4.21.35) (Tissue kallikrein).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP PROTEIN SEQUENCE OF 1-15 AND 95-102.
 RX MEDLINE=89230643; PubMed=3246048;
 RA Kamada M., Aoki K., Ikeita M., Kizuki K., Moriya H., Kamo M.,
 RA Tsugita A.;
 RT "Generation of alpha- and beta-kallikreins from porcine pancreatic
 RT prokallikrein by the action of trypsin."
 RL Chem. Pharm. Bull. 36:4891-4899 (1988).
 RN [2]

RP PROTEIN SEQUENCE OF 8-87 AND 95-246.
 RC TISSUE=Pancreas;
 RA Tschesche H., Mair G., Codec G., Fiedler P., Ehret W., Hirschauer C.,
 RA Lemon M., Fritz H., Schmidt-Kastner G., Kutzbach C.;
 RT "The primary structure of porcine glandular kallikreins.";
 RL Adv. Exp. Med. Biol. 120:245-260(1979).
 RN [3]
 RP PROTEIN SEQUENCE OF 8-87; 95-127 AND 176-246.
 RC TISSUE=Pancreas;
 RA Ehret W.;
 RT "The primary structure of the kallikrein from porcine pancreas.";
 RL Thesis (1976), University of Munich, Germany.
 RN [4]
 RP PROTEIN SEQUENCE OF 84-98.
 RX MEDLINE=90336040; PubMed=2379280;
 RA Kamada M., Ikeita M., Kurahashi T., Aoki K., Kizuki K., Moriya H.,
 RA Sweeley C.C., Kamo M., Taugita A.;
 RT "Generation of a different type of beta-kallikrein from porcine
 RT pancreatic alpha-kallikrein by the action of chymotrypsin --
 RT observation of proteolytic processing occurring around 'kallikrein
 RT autolysis loop' region.";
 RL Chem. Pharm. Bull. 38:1053-1057(1990).
 RN [5]
 RP PROTEIN SEQUENCE OF 128-175.
 RC TISSUE=Pancreas;
 RA Ehret W.;
 RT "Investigation of the sequence of amino acid residues 127 to 174 of
 RT the kallikrein from porcine pancreas.";
 RL Thesis (1978), University of Munich, Germany.
 RN [6]
 RP REVIEW.
 RX MEDLINE=82194877; PubMed=7043199;
 RA Fiedler P., Fink E., Tschesche H., Fritz H.;
 RA "Porcine glandular kallikreins.";
 RL Meth. Enzymol. 80:493-533(1981).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS), AND SEQUENCE REVISION.
 RX MEDLINE=83189107; PubMed=6581452;
 RA Bode W., Chen Z., Bartels K., Kutzbach C., Schmidt-Kastner G.,
 RA Bartunik H.;
 RT "Refined 2-A X-ray crystal structure of porcine pancreatic kallikrein
 RT A, a specific trypsin-like serine proteinase. Crystallization,
 RT structure determination, crystallographic refinement, structure and
 RT its comparison with bovine trypsin.";
 RL J. Mol. Biol. 164:237-282(1983).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH BOVINE
 RP PANCREATIC TRYPSIN INHIBITOR.
 RX MEDLINE=83189108; PubMed=6188842;
 RA Chen Z., Bode W.;
 RT "Refined 2.5 A X-ray crystal structure of the complex formed by
 RT porcine kallikrein A and the bovine pancreatic trypsin inhibitor.
 RT Crystallization, Patterson search, structure determination,
 RT refinement, structure and comparison with its components and with the
 RT bovine trypsin-pancreatic trypsin inhibitor complex.";
 RL J. Mol. Biol. 164:283-311(1983).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH HIRUSTASIN.
 RX MEDLINE=97184690; PubMed=9032072; DOI=10.1016/S0969-2126(97)00183-4;
 RA Mittl P.R.E., di Marco S., Fendrich G., Pohlrig G., Heim J.,
 RA Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.;
 RT "A new structural class of serine protease inhibitors revealed by the
 RT structure of the hirustasin-kallikrein complex.";
 RL Structure 5:253-264(1997).
 RN [10]
 RP ERRATUM.
 RA Mittl P.R.E., di Marco S., Fendrich G., Pohlrig G., Heim J.,
 RA Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.;
 RL Structure 5:585-585(1997).
 RN [11]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=89062455; PubMed=3196708;
 RA Tomiya N., Yamaguchi T., Awaya J., Kurono M., Endo S., Arata Y.,
 RA Takahashi N., Ishihara H., Mori M., Tejima S.;
 RT "Structural analyses of asparagine-linked oligosaccharides of porcine
 RT pancreatic kallikrein.";
 RL Biochemistry 27:7146-7154(1988).
 CC -!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in
 CC in kininogen to release Lys-bradykinin.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
 CC Met-|-Xaa or Leu-|-Xaa.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -!- CAUTION: Native porcine kallikrein is a monomer. Chains of the
 CC pancreatic beta-kallikrein are heterogeneous artifacts of
 CC proteolytic degradation during isolation.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 CC PDB; 1HIA; X-ray; A/X=8-87, B/Y=95-246.
 DR PDB; 2KAI; X-ray; A=8-87, B=95-246.
 DR PDB; 2PKA; X-ray; A/X=8-87, B/Y=95-246.
 DR SMR; P00752; 8-245.
 DR MEROPS; S01.160; -.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
 KW Pancreas; Protease; Serine protease; Zymogen.
 FT PROPEP 1 7
 FT CHAIN 8 246 Glandular kallikrein.
 FT DOMAIN 8 243 Peptidase S1.
 FT REGION 85 104 Kallikrein (autolysis) loop.
 FT ACT_SITE 48 48 Charge relay system.
 FT ACT_SITE 103 103 Charge relay system.
 FT ACT_SITE 198 198 Charge relay system.
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 239 239 N-linked (GlcNAc...) (Potential).
 FT DISULFID 14 158
 FT DISULFID 33 49
 FT DISULFID 135 204
 FT DISULFID 169 183
 FT DISULFID 194 219
 FT STRAND 9 9
 FT STRAND 12 13
 FT STRAND 16 17
 FT TURN 20 21
 FT TURN 22 27
 FT STRAND 28 29
 FT TURN 28 29
 FT STRAND 30 39
 FT TURN 40 41
 FT STRAND 42 45
 FT HELIX 47 49
 FT STRAND 55 58
 FT STRAND 62 62
 FT STRAND 63 64
 FT TURN 71 80
 FT STRAND 82 86
 FT TURN 101 102
 FT STRAND 105 109
 FT STRAND 116 116
 FT TURN 117 118
 FT STRAND 119 119

FT TURN 131 132
 FT STRAND 134 139
 FT STRAND 155 155
 FT STRAND 157 164
 FT TURN 166 166
 FT TURN 167 170
 FT TURN 171 172
 FT TURN 179 180
 FT STRAND 181 185
 FT TURN 187 188
 FT STRAND 192 192
 FT TURN 195 196
 FT TURN 198 199
 FT STRAND 201 204
 FT TURN 205 206
 FT STRAND 207 214
 FT TURN 219 220
 FT TURN 222 223
 FT STRAND 226 230
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 FT HELIX 235 244
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Query Match 80.9%; Score 38; DB 1; Length 246;

Best Local Similarity 77.8%; Pred. No. 76;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
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 Db 36 VLVNPKWVL 44

RESULT 12

Q5M908 XENTR
 ID Q5M908_XENTR PRELIMINARY; PRT; 252 AA.
 AC Q5M908
 DT 01-FEB-2005 (TREMELrel. 29, Created)
 DT 01-FEB-2005 (TREMELrel. 29, Last sequence update)
 DE LOC496635 protein (Fragment).
 GN Names=LOC496635;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 OC NCBI_TaxID=8364;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;

RA Klein S., Gerhard D.S.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC087753; AAH87753.1; -, mRNA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS02440; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 FT NON TER 1
 SQ SEQUENCE 252 AA; 27288 MW; DD68633914557564 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 252;

Best Local Similarity 77.8%; Pred. No. 78;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
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 Db 48 VLVNEWWVL 56

RESULT 13

NRPN_MOUSE
 ID NRPN_MOUSE STANDARD; PRT; 260 AA.
 AC Q61955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Neuropsin precursor (EC 3.4.21.-) (NP (kallikrein 8)).
 GN Names=Klk8; Synonyms=Nrpn, Press19;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c; TISSUE=Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
 RT "Expression and activity-dependent changes of a novel limbic-serine
 protease gene in the hippocampus.";
 RL J. Neurosci. 15:5088-5097(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 RT "Cloning and assignment of mouse neuropsin gene, Press19 to chromosome
 7B4.";
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan M., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Groomwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS
RP SPECTROMETRY.
RC STRAIN=BALE/C; TISSUE=Brain;
RX MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka T., Midorikawa R., Kanachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neuropsin, a plasicity-
RT related serine protease.";
RL J. Biol. Chem. 273:11189-11196(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neuropsin, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224(1999).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
CC fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
CC fluoride.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
CC mouse brain and is localized at highest concentration in pyramidal
CC neurons of the hippocampal CA1-3 subfields.
CC -!- MASS SPECTROMETRY: MW=26613; METHOD=WALDI; RANGE=29-260;
CC NOTE=Ref.4.
CC -!- MASS SPECTROMETRY: MW=26229; METHOD=WALDI; RANGE=33-260;
CC NOTE=Ref.4.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC EMBL; D30785; BAA06451.1; -; mRNA.
CC EMBL; AB032202; BAA92435.1; -; Genomic DNA.
CC EMBL; BC055895; AAH55895.1; -; mRNA.
CC PIR; I56559; I56559.
CC PDB; INPW; X-ray; A/B=33-257.
CC MEROPS; S01.244; -.
CC Ensembl; ENSMUSG0000064023; Mus musculus.
CC MGI; MGI:892018; K1k8.
CC InterPro; IPR001254; Peptidase_S1_S6.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00889; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SRR; 1.
KW 3D-structure: Direct protein sequencing; Glycoprotein; Hydrolase;
KW Processase; Serine processase; Signal; Zymogen.
FT SIGNAL 1 28
FT PROPEP 29 32
FT CHAIN 33 260 Neuropsin.
FT DOMAIN 33 257 Peptidase S1.

Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlcNAc...) (Potential).

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260 AA; 28524 MW; BESF6F6BE37CD60E CRC64;

FT ACT_SITE

FT ACT_SITE

FT ACT_SITE

FT CARBOHYD

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FT DISULFID

FT DISULFID

FT DISULFID

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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fischer; TISSUE=Brain;
RX MEDLINE=98399725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lache R.;
RT "Serine proteases in rodent hippocampus";
RL J. Biol. Chem. 273:23004-23011(1998).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin (By similarity).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to hippocampus.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AJ005641; CAA06643.1; -; mRNA.
DR HSSP: O61955; INPM.
DR SMR: O88780; 33-256.
DR MEROPS: S01.244; -.
DR Ensembl: ENSRNOG0000018580; Rattus norvegicus.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 28 Potential.
FT PROPEP 29 32 By similarity.
FT CHAIN 33 260 Neuropilin.
FT DOMAIN 33 257 Peptidase S1.
FT ACT_SITE 73 73 Charge relay system (By similarity).
FT ACT_SITE 120 120 Charge relay system (By similarity).
FT ACT_SITE 212 212 Charge relay system (By similarity).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT DISULFID 39 173 By similarity.
FT DISULFID 58 74 By similarity.
FT DISULFID 145 246 By similarity.
FT DISULFID 152 218 By similarity.
FT DISULFID 184 198 By similarity.
FT DISULFID 208 233 By similarity.
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 260;
Best Local Similarity 77.8%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 61 VLVGDRWVL 69

RESULT 15
ID Q720G5_9D1PT PRELIMINARY; PRT; 262 AA.
AC Q720G5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chymotrypsin.

GN Name=chym1;
OS Phlebotomus papatasi.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Phlebotomus; Phlebotomus.
OX NCBI_TaxID=29031;
RN [1]_TaxID=29031;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Midgut;
RA Ramalho-Ortigao M., Kamhawi S., Rowton E., Sacks D.L., Ribeiro J.M.,
RA Valenzuela J.G.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY128106; AAM96938.1; -; mRNA.
DR HSSP: PI8291; IF18.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 262 AA; 28863 MW; 31F11012206A65D4 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
DB 57 ILNERWVL 64

Search completed: March 11, 2006, 00:38:45
Job time : 98.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 47 | 100.0 | 9 | 2 US-09-918-243-34 | Sequence 34, Appl |
| 3 | 47 | 100.0 | 154 | 2 US-09-261-416-7 | Sequence 7, Appl |
| 4 | 47 | 100.0 | 224 | 2 US-08-944-483-33 | Sequence 33, Appl |
| 5 | 47 | 100.0 | 225 | 1 US-08-557-146-12 | Sequence 12, Appl |
| 6 | 47 | 100.0 | 225 | 1 US-09-027-337-4 | Sequence 4, Appl |
| 7 | 47 | 100.0 | 225 | 1 US-09-154-344-12 | Sequence 12, Appl |
| 8 | 47 | 100.0 | 225 | 2 US-09-644-600-4 | Sequence 4, Appl |
| 9 | 47 | 100.0 | 225 | 2 US-09-654-600A-4 | Sequence 4, Appl |
| 10 | 47 | 100.0 | 253 | 1 US-08-557-146-2 | Sequence 2, Appl |
| 11 | 47 | 100.0 | 253 | 1 US-08-824-874-3 | Sequence 3, Appl |
| 12 | 47 | 100.0 | 253 | 1 US-09-154-344-2 | Sequence 2, Appl |
| 13 | 47 | 100.0 | 253 | 2 US-08-930-188-2 | Sequence 2, Appl |
| 14 | 47 | 100.0 | 253 | 2 US-09-210-084-3 | Sequence 3, Appl |
| 15 | 47 | 100.0 | 253 | 2 US-09-764-762-3 | Sequence 3, Appl |
| 16 | 47 | 100.0 | 253 | 4 PCT-US96-04294-2 | Sequence 2, Appl |
| 17 | 47 | 100.0 | 265 | 2 US-09-949-016-7716 | Sequence 7716, Ap |
| 18 | 43 | 91.5 | 9 | 2 US-09-502-600-40 | Sequence 40, Appl |
| 19 | 43 | 91.5 | 9 | 2 US-09-502-600-50 | Sequence 50, Appl |
| 20 | 43 | 91.5 | 9 | 2 US-09-918-243-40 | Sequence 40, Appl |
| 21 | 43 | 91.5 | 9 | 2 US-09-918-243-50 | Sequence 50, Appl |
| 22 | 39 | 83.0 | 228 | 2 US-08-944-483-44 | Sequence 44, Appl |
| 23 | 39 | 83.0 | 228 | 2 US-10-202-676-6 | Sequence 6, Appl |
| 24 | 39 | 83.0 | 253 | 6 5223425-8 | Patent No. 5223425 |
| 25 | 38 | 80.9 | 64 | 1 US-08-485-455D-75 | Sequence 75, Appl |
| 26 | 38 | 80.9 | 64 | 1 US-08-482-130C-75 | Sequence 75, Appl |
| 27 | 38 | 80.9 | 64 | 1 US-08-484-211C-75 | Sequence 75, Appl |

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29 38 80.9 64 2 US-08-906-616-75 Sequence 75, Appl
30 38 80.9 64 2 US-08-817-795-75 Sequence 75, Appl
31 38 80.9 64 2 US-08-485-443B-75 Sequence 75, Appl
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34 38 80.9 64 2 US-09-012-692-75 Sequence 75, Appl
35 38 80.9 64 2 US-08-906-613-75 Sequence 75, Appl
36 38 80.9 64 4 PCT-US95-14442A-75 Sequence 75, Appl
37 38 80.9 223 1 US-08-485-455D-17 Sequence 17, Appl
38 38 80.9 223 1 US-08-482-130C-17 Sequence 17, Appl
39 38 80.9 223 1 US-08-484-211C-17 Sequence 17, Appl
40 38 80.9 223 2 US-08-817-795-17 Sequence 17, Appl
41 38 80.9 223 2 US-08-485-443B-17 Sequence 17, Appl
42 38 80.9 223 4 PCT-US95-14442A-17 Sequence 17, Appl
43 38 80.9 224 2 US-08-906-769-17 Sequence 17, Appl
44 38 80.9 224 2 US-08-906-616-17 Sequence 17, Appl
45 38 80.9 224 2 US-08-639-075A-17 Sequence 17, Appl

```

ALIGNMENTS

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RESULT 1
US-09-502-600-34
; Sequence 34, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-502-600-34

```

```

Query Match 100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 VLVNERWVL 9
|||
Db 1 VLVNERWVL 9

```

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RESULT 2
US-09-918-243-34
; Sequence 34, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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/
/ FEATURE:
/ NAME/KEY: CHAIN
/ OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-918-243-34

Query Match      100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 3
US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TAGD-12: A No. 6291663el Transmembrane Serine Protease
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
; OTHER INFORMATION: domain in TAGD-12
US-09-261-416-7

Query Match      100.0%; Score 47; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 4 VLVNERWVL 12

RESULT 4
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; City: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

/
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/944,483
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Becker, Cheryl L.
/ REGISTRATION NUMBER: 35,441
/ REFERENCE/DOCKET NUMBER: 6183.US.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847/935-1729
/ TELEFAX: 847/938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 224 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match      100.0%; Score 47; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 29 VLVNERWVL 37

RESULT 5
US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match      100.0%; Score 47; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 6
US-09-027-337-4
; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
; OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Query Match      100.0%; Score 47; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 7
US-09-154-344-12
; Sequence 12, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-09-154-344-12

Query Match      100.0%; Score 47; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 8
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4

Query Match      100.0%; Score 47; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 9
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
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09/027.337
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4

Query Match 100.0%; Score 47; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 10
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66

RESULT 11
US-08-824-874-3

; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match 100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66

RESULT 12
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 58 VLVNERWVL 66

RESULT 13
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 58 VLVNERWVL 66

RESULT 14
US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 58 VLVNERWVL 66

RESULT 15
US-09-764-762-3

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; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66

Search completed: March 11, 2006, 01:24:25
Job time : 22.2222 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-34

Perfect score: 47

Sequence: 1 VLVNERWVL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 47 | 100.0 | 9 | 3 | US-09-918-243-34 |
| 2 | 47 | 100.0 | 9 | 3 | US-09-905-083-34 |
| 3 | 47 | 100.0 | 9 | 4 | US-10-372-521-34 |
| 4 | 47 | 100.0 | 9 | 5 | US-10-831-075-34 |
| 5 | 47 | 100.0 | 97 | 4 | US-10-372-521-40 |
| 6 | 47 | 100.0 | 136 | 5 | US-10-450-763-53737 |
| 7 | 47 | 100.0 | 181 | 4 | US-10-262-511-98 |
| 8 | 47 | 100.0 | 198 | 4 | US-10-262-511-96 |
| 9 | 47 | 100.0 | 224 | 3 | US-09-789-210-33 |
| 10 | 47 | 100.0 | 224 | 4 | US-10-262-511-104 |
| 11 | 47 | 100.0 | 225 | 4 | US-10-600-187-4 |
| 12 | 47 | 100.0 | 247 | 4 | US-10-262-511-102 |
| 13 | 47 | 100.0 | 250 | 4 | US-10-262-511-92 |
| 14 | 47 | 100.0 | 222 | 4 | US-10-262-511-94 |
| 15 | 47 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 16 | 47 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 17 | 47 | 100.0 | 253 | 4 | US-10-071-214-2 |
| 18 | 47 | 100.0 | 253 | 4 | US-10-071-214-48 |
| 19 | 47 | 100.0 | 253 | 4 | US-10-264-283-90 |
| 20 | 47 | 100.0 | 253 | 4 | US-10-395-027-498 |
| 21 | 47 | 100.0 | 253 | 4 | US-10-173-999-48 |
| 22 | 47 | 100.0 | 253 | 4 | US-10-408-765A-639 |
| 23 | 47 | 100.0 | 253 | 5 | US-10-643-795A-95 |
| 24 | 47 | 100.0 | 253 | 5 | US-10-948-518-95 |
| 25 | 47 | 100.0 | 253 | 5 | US-10-868-490A-1 |
| 26 | 47 | 100.0 | 257 | 4 | US-10-344-394-38 |
| 27 | 43 | 91.5 | 9 | 3 | US-09-918-243-40 |

28 43 91.5 9 3 US-09-918-243-50 Sequence 50, Appl
29 43 91.5 9 3 US-09-905-083-40 Sequence 40, Appl
30 43 91.5 9 3 US-09-905-083-50 Sequence 50, Appl
31 43 91.5 9 4 US-10-372-521-40 Sequence 40, Appl
32 43 91.5 9 4 US-10-372-521-50 Sequence 50, Appl
33 43 91.5 9 5 US-10-831-075-40 Sequence 40, Appl
34 43 91.5 9 5 US-10-831-075-50 Sequence 50, Appl
35 40 85.1 243 4 US-10-071-214-46 Sequence 46, Appl
36 40 85.1 249 4 US-10-071-214-47 Sequence 47, Appl
37 39 83.0 228 3 US-09-789-210-44 Sequence 44, Appl
38 39 83.0 228 5 US-10-202-676-6 Sequence 6, Appl
39 39 83.0 228 5 US-10-756-149-5803 Sequence 5803, Appl
40 38 80.9 81 4 US-10-045-367A-7 Sequence 7, Appl
41 38 80.9 81 4 US-10-170-789-57 Sequence 57, Appl
42 38 80.9 225 4 US-10-072-012-611 Sequence 611, Appl
43 38 80.9 259 4 US-10-072-012-222 Sequence 222, Appl
44 38 80.9 260 3 US-09-796-294-8 Sequence 8, Appl
45 38 80.9 260 4 US-10-461-787-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-918-243-34
; Sequence 34, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-918-243-34

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||
Db 1 VLVNERWVL 9

RESULT 2
US-09-905-083-34
; Sequence 34, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-905-083-34
Query Match      100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 3
US-10-372-521-34
; Sequence 34, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-10-372-521-34
Query Match      100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 4
US-10-831-075-34
; Sequence 34, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-10-831-075-34
Query Match      100.0%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 5
US-10-262-511-100
; Sequence 100, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 100
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-262-511-100

Query Match 100.0%; Score 47; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 39 VLVNERWVL 47

RESULT 6

US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match 100.0%; Score 47; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.1; DB 5; Length 136;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 64 VLVNERWVL 72

RESULT 7

US-10-262-511-98
; Sequence 98, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana

; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSequid version 0.1
; SEQ ID NO 98
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-98

Query Match 100.0%; Score 47; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 39 VLVNERWVL 47

RESULT 8
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.

APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 96
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 47; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 58 VLVNERWVL 66
|||||

RESULT 9
US-09-789-210-33
Sequence 33, Application US/09789210
Publication No. US20040241646A1
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
COLPITS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.

STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,210
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,483
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match 100.0%; Score 47; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 29 VLVNERWVL 37
|||||

RESULT 10
US-10-262-511-104
Sequence 104, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei

APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 104
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-104

Query Match 100.0%; Score 47; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 44 VLVNERWVL 52

RESULT 11
US-10-600-187-4
Sequence 4, Application US/10600187
Publication No. US20040086910A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotsoshi
TITLE OF INVENTION: TAGC-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/10/600,187
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/654,600A
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
NUMBER OF SEQ ID NOS: 98

SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: SCCE
US-10-600-187-4

Query Match 100.0%; Score 47; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 12
US-10-262-511-102
Sequence 102, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19

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, PRIOR APPLICATION NUMBER: 60/327,435
, PRIOR FILING DATE: 2001-10-05
, Remaining Prior Application data removed - See File Wrapper or PALM.
, NUMBER OF SEQ ID NOS: 439
, SOFTWARE: CuraSeqList version 0.1
, SEQ ID NO 102
, LENGTH: 247
, TYPE: PRT
, ORGANISM: Homo sapiens
US-10-262-511-102

Query Match      100.0%; Score 47; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 44 VLVNERWVL 52

RESULT 13
US-10-262-511-92
, Sequence 92, Application US/10262511
, Publication No. US20040038223A1
, GENERAL INFORMATION:
, APPLICANT: Smithson, Glenda
, APPLICANT: Millet, Isabelle
, APPLICANT: Peyman, John A.
, APPLICANT: Kekuda, Ramesh
, APPLICANT: Ju, Jingfang
, APPLICANT: Li, Li
, APPLICANT: Guo, Xiaojia (Sasha)
, APPLICANT: Patturajan, Meera
, APPLICANT: Spytek, Kimberly A.
, APPLICANT: Edinger, Shlomit R.
, APPLICANT: Ellerman, Karen
, APPLICANT: Malyankar, Uriel M.
, APPLICANT: Ort, Tatiana
, APPLICANT: Gorman, Linda
, APPLICANT: Zerhusen, Bryan D.
, APPLICANT: Anderson, David W.
, APPLICANT: Zhong, Mei
, APPLICANT: Catterton, Elina
, APPLICANT: Ji, Weizhen
, APPLICANT: Miller, Charles E.
, APPLICANT: Rastelli, Luca
, APPLICANT: Stone, David J.
, APPLICANT: Pena, Carol E. A.
, APPLICANT: Shenoy, Suresh G.
, APPLICANT: Shinkets, Richard A.
, APPLICANT: Rothenberg, Mark E.
, APPLICANT: Leach, Martin D.
, APPLICANT: Agee, Michele L.
, APPLICANT: Berghs, Constance
, TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
, FILE REFERENCE: 21402-462C
, CURRENT APPLICATION NUMBER: US/10/262,511
, CURRENT FILING DATE: 2003-05-28
, PRIOR APPLICATION NUMBER: 60/326,483
, PRIOR FILING DATE: 2001-10-02
, PRIOR APPLICATION NUMBER: 60/373,815
, PRIOR FILING DATE: 2002-04-19
, PRIOR APPLICATION NUMBER: 60/327,917
, PRIOR FILING DATE: 2001-10-09
, PRIOR APPLICATION NUMBER: 60/381,642
, PRIOR FILING DATE: 2002-05-17
, PRIOR APPLICATION NUMBER: 60/328,029
, PRIOR FILING DATE: 2002-10-09
, PRIOR APPLICATION NUMBER: 60/381,038
, PRIOR FILING DATE: 2002-05-16
, PRIOR APPLICATION NUMBER: 60/328,056
, PRIOR FILING DATE: 2001-10-09
, PRIOR APPLICATION NUMBER: 60/373,260
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, PRIOR FILING DATE: 2002-04-17
, PRIOR APPLICATION NUMBER: 60/373,826
, PRIOR FILING DATE: 2002-04-19
, PRIOR APPLICATION NUMBER: 60/327,435
, PRIOR FILING DATE: 2001-10-05
, Remaining Prior Application data removed - See File Wrapper or PALM.
, NUMBER OF SEQ ID NOS: 439
, SOFTWARE: CuraSeqList version 0.1
, SEQ ID NO 92
, LENGTH: 250
, TYPE: PRT
, ORGANISM: Homo sapiens
US-10-262-511-92

Query Match      100.0%; Score 47; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 55 VLVNERWVL 63

RESULT 14
US-10-262-511-94
, Sequence 94, Application US/10262511
, Publication No. US20040038223A1
, GENERAL INFORMATION:
, APPLICANT: Smithson, Glennda
, APPLICANT: Millet, Isabelle
, APPLICANT: Peyman, John A.
, APPLICANT: Kekuda, Ramesh
, APPLICANT: Ju, Jingfang
, APPLICANT: Li, Li
, APPLICANT: Guo, Xiaojia (Sasha)
, APPLICANT: Patturajan, Meera
, APPLICANT: Spytek, Kimberly A.
, APPLICANT: Edinger, Shlomit R.
, APPLICANT: Ellerman, Karen
, APPLICANT: Malyankar, Uriel M.
, APPLICANT: Ort, Tatiana
, APPLICANT: Gorman, Linda
, APPLICANT: Zerhusen, Bryan D.
, APPLICANT: Anderson, David W.
, APPLICANT: Zhong, Mei
, APPLICANT: Catterton, Elina
, APPLICANT: Ji, Weizhen
, APPLICANT: Miller, Charles E.
, APPLICANT: Rastelli, Luca
, APPLICANT: Stone, David J.
, APPLICANT: Pena, Carol E. A.
, APPLICANT: Shenoy, Suresh G.
, APPLICANT: Shinkets, Richard A.
, APPLICANT: Rothenberg, Mark E.
, APPLICANT: Leach, Martin D.
, APPLICANT: Agee, Michele L.
, APPLICANT: Berghs, Constance
, TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
, FILE REFERENCE: 21402-462C
, CURRENT APPLICATION NUMBER: US/10/262,511
, CURRENT FILING DATE: 2003-05-28
, PRIOR APPLICATION NUMBER: 60/326,483
, PRIOR FILING DATE: 2001-10-02
, PRIOR APPLICATION NUMBER: 60/373,815
, PRIOR FILING DATE: 2002-04-19
, PRIOR APPLICATION NUMBER: 60/327,917
, PRIOR FILING DATE: 2001-10-09
, PRIOR APPLICATION NUMBER: 60/381,642
, PRIOR FILING DATE: 2002-05-17
, PRIOR APPLICATION NUMBER: 60/328,029
, PRIOR FILING DATE: 2002-10-09
, PRIOR APPLICATION NUMBER: 60/381,038
, PRIOR FILING DATE: 2002-05-16
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; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 94
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-94

Query Match      100.0%; Score 47; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
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Db      57 VLVNERWVL 65

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RESULT 15
US-09-888-615-98
; Sequence 98, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

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Query Match      100.0%; Score 47; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
        |||||
Db      58 VLVNERWVL 66

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Search completed: March 11, 2006, 01:37:23
Job time : 70.4444 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pbp.*
 - 2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pbp.*
 - 3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pbp.*
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 - 8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 47 | 100.0 | 48 | 6 | US-10-412-748-21 |
| 2 | 47 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 3 | 47 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 4 | 47 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 5 | 47 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 6 | 38 | 80.9 | 81 | 7 | US-11-151-601-39 |
| 7 | 37 | 78.7 | 359 | 7 | US-11-037-243-114 |
| 8 | 36 | 76.6 | 345 | 7 | US-11-174-816-44 |
| 9 | 36 | 76.6 | 345 | 7 | US-11-174-816-59 |
| 10 | 36 | 76.6 | 345 | 7 | US-11-174-819-13 |
| 11 | 36 | 76.6 | 345 | 7 | US-11-174-819-78 |
| 12 | 36 | 76.6 | 1128 | 7 | US-11-037-243-97 |
| 13 | 35 | 74.5 | 236 | 6 | US-10-821-234-1274 |
| 14 | 35 | 74.5 | 239 | 7 | US-11-043-788-140 |
| 15 | 35 | 74.5 | 307 | 7 | US-11-043-788-141 |
| 16 | 35 | 74.5 | 347 | 7 | US-11-043-788-133 |
| 17 | 35 | 74.5 | 347 | 7 | US-11-043-788-137 |
| 18 | 35 | 74.5 | 348 | 7 | US-11-177-506-40 |
| 19 | 35 | 74.5 | 365 | 7 | US-11-096-568A-16466 |
| 20 | 35 | 74.5 | 366 | 7 | US-11-043-788-139 |
| 21 | 35 | 74.5 | 403 | 7 | US-11-096-568A-16465 |
| 22 | 35 | 74.5 | 406 | 7 | US-11-043-788-131 |
| 23 | 35 | 74.5 | 406 | 7 | US-11-043-788-132 |
| 24 | 35 | 74.5 | 406 | 7 | US-11-189-120-6 |
| 25 | 35 | 74.5 | 406 | 7 | US-11-177-506-39 |

| | | | | | | |
|----|----|------|-----|---|----------------------|-------------------|
| 26 | 35 | 74.5 | 445 | 7 | US-11-096-568A-16464 | Sequence 16464, A |
| 27 | 35 | 74.5 | 688 | 6 | US-10-821-234-1533 | Sequence 1533, Ap |
| 28 | 35 | 74.5 | 688 | 7 | US-11-169-041-149 | Sequence 149, App |
| 29 | 34 | 72.3 | 38 | 7 | US-11-129-861-11 | Sequence 11, Appl |
| 30 | 34 | 72.3 | 315 | 7 | US-11-096-568A-23072 | Sequence 23072, A |
| 31 | 34 | 72.3 | 331 | 7 | US-11-096-568A-23071 | Sequence 23071, A |
| 32 | 34 | 72.3 | 343 | 7 | US-11-080-991-86 | Sequence 86, Appl |
| 33 | 34 | 72.3 | 343 | 7 | US-11-019-711-130 | Sequence 130, App |
| 34 | 34 | 72.3 | 344 | 7 | US-11-174-816-47 | Sequence 47, Appl |
| 35 | 34 | 72.3 | 344 | 7 | US-11-174-816-62 | Sequence 62, Appl |
| 36 | 34 | 72.3 | 344 | 7 | US-11-174-819-32 | Sequence 32, Appl |
| 37 | 34 | 72.3 | 344 | 7 | US-11-174-819-81 | Sequence 81, Appl |
| 38 | 34 | 72.3 | 389 | 7 | US-11-087-099-4063 | Sequence 4063, Ap |
| 39 | 34 | 72.3 | 393 | 6 | US-10-821-234-1043 | Sequence 1043, Ap |
| 40 | 34 | 72.3 | 413 | 7 | US-11-096-568A-23070 | Sequence 23070, A |
| 41 | 34 | 72.3 | 415 | 7 | US-11-166-028-1 | Sequence 1, Appli |
| 42 | 34 | 72.3 | 462 | 7 | US-11-183-205-10 | Sequence 10, Appl |
| 43 | 34 | 72.3 | 516 | 7 | US-11-080-991-2 | Sequence 2, Appli |
| 44 | 34 | 72.3 | 687 | 7 | US-11-074-176-260 | Sequence 260, App |
| 45 | 34 | 72.3 | 696 | 7 | US-11-029-003-8 | Sequence 8, Appli |

ALIGNMENTS

RESULT 1
US-10-412-748-21
; Sequence 21, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-21

Query Match 100.0%; Score 47; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.024; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 VLVNERWVL 9
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Db 34 VLVNERWVL 42

RESULT 2
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66
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RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66
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RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66
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RESULT 5
US-10-412-748-18
; Sequence 18, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-18

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66
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RESULT 6
US-11-151-601-39
; Sequence 39, Application US/11151601
; Publication No. US20060003413A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Welch, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; FILE REFERENCE: MPI00-054P1RCPIOMNIDV1M
; CURRENT APPLICATION NUMBER: US/11/151,601
; CURRENT FILING DATE: 2005-06-13
; PRIOR APPLICATION NUMBER: US 10/170,789
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-11-151-601-39

Query Match      80.9%; Score 38; DB 7; Length 81;
Best Local Similarity 75.0%; Pred. No. 1.8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
      |:|:|:|
Db      5 LINEQWVL 12

RESULT 7
US-11-037-243-114
; Sequence 114, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-114

Query Match      78.7%; Score 37; DB 7; Length 359;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
      |||:|:|
Db      122 LVRRWVL 129

RESULT 8
US-11-174-816-44
; Sequence 44, Application US/11174816
; Publication No. US20060009441A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
; FILE REFERENCE: 22645
; CURRENT APPLICATION NUMBER: US/11/174,816
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 04103261.6
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mTAAR6
US-11-174-819-13

Query Match      76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
      |:|:|:|
Db      192 VVVNQWVL 200

RESULT 9
US-11-174-816-59
; Sequence 59, Application US/11174816
; Publication No. US20060009441A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
; FILE REFERENCE: 22645
; CURRENT APPLICATION NUMBER: US/11/174,816
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 04103261.6
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-174-816-59

Query Match      76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
      |:|:|:|
Db      192 VVVNQWVL 200

RESULT 10
US-11-174-819-13
; Sequence 13, Application US/11174819
; Publication No. US20060008880A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 22646
; CURRENT APPLICATION NUMBER: US/11/174,819
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 04103262.4
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mTAAR6
US-11-174-819-13

Query Match      76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 VLVNERWVL 9
|:|:|:|
Db 192 VVYNQWVL 200

RESULT 11
; Sequence 78, Application US/11174819
; Publication No. US20060008880A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTAR
; TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 22646
; CURRENT APPLICATION NUMBER: US/11/174,819
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: EP 04103262.4
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 78
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-174-819-78

Query Match 76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:|
Db 192 VVYNQWVL 200

RESULT 12
US-11-037-243-97
; Sequence 97, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 1128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-97

Query Match 76.6%; Score 36; DB 7; Length 1128;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:|
Db 925 VLVNERWVL 933

RESULT 13
US-10-821-234-1274
; Sequence 1274, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1274
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1274

Query Match 74.5%; Score 35; DB 6; Length 236;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:|
Db 37 VLVNERWVL 45

RESULT 14
US-11-043-788-140
; Sequence 140, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEROF FOR DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 140
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-140

Query Match 74.5%; Score 35; DB 7; Length 299;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
|:|:|:|
Db 84 LINEQWVL 91

RESULT 15
US-11-043-788-141
; Sequence 141, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEROF FOR DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 141
; LENGTH: 307

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-141

Query Match 74.5%; Score 35; DB 7; Length 307;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
|:|:|:
Db 92 LINEQWLL 99

Search completed: March 11, 2006, 01:38:41
Job time : 9 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LPLQLILL 9

Scoring table: BLOSUM62
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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
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4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 40 | 100.0 | 9 | 4 AAE08240 | Aae08240 Human str |
| 2 | 40 | 100.0 | 9 | 8 ADR68796 | Adr68796 Human str |
| 3 | 40 | 100.0 | 136 | 4 ABG23378 | Abg23378 Novel hum |
| 4 | 40 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 5 | 40 | 100.0 | 198 | 8 ADN62900 | Adn62900 Human NOV |
| 6 | 40 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 7 | 40 | 100.0 | 250 | 8 ADN62896 | Adn62896 Human NOV |
| 8 | 40 | 100.0 | 253 | 2 AAR67888 | Arr67888 Human str |
| 9 | 40 | 100.0 | 253 | 2 AAW05383 | Raw05383 Human amy |
| 10 | 40 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 11 | 40 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 12 | 40 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 13 | 40 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 14 | 40 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 15 | 40 | 100.0 | 253 | 6 ABR58471 | AbR58471 Human str |
| 16 | 40 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 17 | 40 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 18 | 40 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/tu |
| 19 | 40 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tan |
| 20 | 40 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antiporin |
| 21 | 40 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 22 | 40 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 23 | 40 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 24 | 40 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |

ALIGNMENTS

RESULT 1
AAE08240
ID AAE08240 standard; peptide; 9 AA.
XX
AC AAE08240;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #5 (residues 6-14).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
(UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
PS Claim 25; Page 103; 127pp; English.
XX
CC The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used CC to treat a cancer selected from ovarian, breast, lung, colon, prostate CC and other cancers in which SCCE is overexpressed. The present sequence is CC human SCCE peptide
XX
SQ Sequence 9 AA;

25 38 95.0 142 4 AAB63580 Aab63580 Human gas
26 38 95.0 156 4 AAB63578 Aab63578 Human gas
27 38 95.0 159 4 AAB63582 Aab63582 Human gas
28 36 90.0 9 4 AAE08238 Aae08238 Human str
29 36 90.0 9 8 ADR68794 Adr68794 Human str
30 36 90.0 845 6 ABU23951 AbU23951 Protein e
31 36 90.0 868 8 ADS21222 Ads21222 Bacterial
32 35 87.5 23 4 ABB43858 ABB43858 Peptide #
33 35 87.5 23 4 AAM37771 Aam37771 Peptide #
34 35 87.5 23 4 AAM64837 Aam64837 Human bra
35 35 87.5 23 4 ABG59233 Abg59233 Human liv
36 35 87.5 23 5 ABG46617 Abg46617 Human pep
37 35 87.5 480 2 AAW98431 Aaw98431 H. pylori
38 35 87.5 637 8 ADY22442 Ady22442 Plant ful
39 34 85.0 70 2 AAY36291 Aay36291 Human sec
40 34 85.0 70 6 ADA11692 Ada11692 Human nov
41 34 85.0 73 2 AAW89030 Aaw89030 Polypepti
42 34 85.0 73 4 ABB51130 Abb51130 Human sec
43 34 85.0 73 7 ABO45387 Abo45387 Novel hum
44 34 85.0 73 7 ABO26867 Abo26867 Protein a
45 34 85.0 86 4 AAO08397 Aao08397 Human pol

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
| | | | |
Db 1 LPLQLILL 9

RESULT 2
ADR68796
ID ADR68796 standard; peptide; 9 AA.
AC ADR68796;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:35.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/63.
XX
PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Claim 5; SEQ ID NO 35; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
| | | | |
Db 1 LPLQLILL 9

RESULT 3
ABG23378

ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AA587565.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG0377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 136 AA;

Query Match 100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
| | | | |
Db 12 LPLQLILL 20

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX

ADA05736;
 06-NOV-2003 (first entry)
 Human NOV18c protein SEQ ID NO:96.
 human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 immunomodulator; cytostatic; nootropic; neuroprotective;
 antiparkinsonian; antilipaeamic; gene therapy; human disease;
 metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 immune disorder; haematopoietic disorder; dyslipidaemia.
 Homo sapiens.
 WO2003029424-A2.
 10-APR-2003.
 02-OCT-2002; 2002WO-US031373.
 02-OCT-2001; 2001US-0326483P.
 05-OCT-2001; 2001US-0327435P.
 05-OCT-2001; 2001US-0327449P.
 09-OCT-2001; 2001US-0327917P.
 09-OCT-2001; 2001US-0328029P.
 09-OCT-2001; 2001US-0328044P.
 09-OCT-2001; 2001US-0328056P.
 12-OCT-2001; 2001US-0328849P.
 15-OCT-2001; 2001US-0329414P.
 17-OCT-2001; 2001US-0330142P.
 18-OCT-2001; 2001US-0330309P.
 22-OCT-2001; 2001US-0341058P.
 24-OCT-2001; 2001US-0339266P.
 24-OCT-2001; 2001US-0343629P.
 29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
 16-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383566P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 01-OCT-2002; 2002US-00262511.
 (CURA-) CURAGEN CORP.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ort T, Gorman L, Zerkow BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen AV, Gangolli EA, Rieger DK, Spaderna SK;
 WPI; 2003-381626/36.
 N-PSDB; ADA05735.
 New NOVX polypeptides and nucleic acids, useful for diagnosing,
 preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 pharmacogenomics.
 Claim 1; Page 170; 586pp; English.
 The present invention describes NOVX proteins, where X can be 1 to 55
 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

described above and a carrier; (2) a kit comprising, in one or more
 containers, the composition described above; (3) an isolated nucleic acid
 molecule which encodes a NOVX protein of the invention; (4) a vector
 comprising the nucleic acid molecule described above; (5) a cell
 comprising the above vector; (6) an antibody that immunospecifically
 binds to the polypeptide described above; (7) methods for determining the
 presence or amount of the above polypeptide or nucleic acid molecule in a
 sample; (8) methods for determining the presence of or predisposition to
 a disease associated with altered levels of expression of the above
 polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 method of identifying an agent that binds to the polypeptide described
 above; (10) a method for identifying a potential therapeutic agent for
 use in treating a pathology that is related to an aberrant expression or
 aberrant physiological interactions of the polypeptide; (11) a method of
 screening for a modulator of activity or of latency or predisposition to
 a pathology associated with the polypeptide; (12) a method for modulating
 the activity of the polypeptide described above; (13) methods of treating
 or preventing a pathology associated with the above polypeptide in a
 mammal; and (14) a method for producing the above polypeptide. NOVX
 sequences have antidiabetic, anorectic, antibacterial, virucide,
 immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 and antilipaeamic activities, and can be used in gene therapy. The
 polypeptide is useful in manufacturing a medicament for treating a
 syndrome associated with a human disease. The polypeptide or the nucleic
 acid molecule may be used to diagnose, treat or prevent metabolic
 disorders such as diabetes or obesity, infections, cachexia, cancer,
 neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 disease, immune disorders, haematopoietic disorders and various
 dyslipidaemias. The nucleic acids can also be used as hybridisation
 probes, in chromosome mapping, tissue typing, preventive medicine and
 pharmacogenomics. The present sequence represents a human NOVX from the
 present invention.
 Sequence 198 AA;
 Query Match 100.0%; Score 40; DB 6; Length 198;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLILL 9
 Db 6 LLPLQLILL 14
 RESULT 5
 ADN62900
 ID ADN62900 standard; protein; 198 AA.
 AC ADN62900;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18c.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 01-OCT-2002; 2002US-00262511.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (WILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KERU/) KERUDA R.
 PA (JUGJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTI/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWU/) JI W.
 PA (MILL/) MILLER C E.
 PA (RASI/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIP/) DIPPIO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malvankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2004-213931/20.
 DR N-PSDB; ADN62899.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 40; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 DB 6 LLPLQLLLL 14
 RESULT 6
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX
 AC ADA05732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18a protein SEQ ID NO:92.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 OS Homo sapiens.
 XX
 XX WO2003029424-A2.
 PN
 XX 10-APR-2003.
 PD
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.

09-OCT-2001; 2001US-0328056P.
12-OCT-2001; 2001US-0328849P.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-00262511.
(CURA-) CURAGEN CORP.
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ott T, Gorman L, Zerkhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
WPI: 2003-381626/36.
N-PSDB; ADA05731.
New NOVX polypeptides and nucleic acids, useful for diagnosing,
preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
cancer or dyslipidemia, and in chromosome mapping, tissue typing or
pharmacogenomics.
Claim 1; Page 169-170; 586pp; English.
The present invention describes NOVX proteins, where X can be 1 to 55
(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of treating
or preventing a pathology associated with the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
and antilipidemic activities, and can be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
syndrome associated with a human disease. The polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
disorders such as diabetes or obesity, infections, cachexia, cancer,
neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 40; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPQLILL 9
DB 3 LLPQLILL 11
RESULT 7
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX AC
XX ADN62896;
XX DT 01-JUL-2004 (first entry)
XX DE Human NOV18a.
XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX OS Homo sapiens.
XX PN US2004038223-A1.
XX PD 26-FEB-2004.
XX PF 01-OCT-2002; 2002US-00262511.
XX PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWV/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP1/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR WPI; 2004-213931/20.
DR N-PSDB; ADN62895.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 92; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 40; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQILL 9
Db 3 LLPLQILL 11
RESULT 8
AAR67888
ID AAR67888 standard; protein; 253 AA.
XX
AC AAR67888;
XX
DT 25-MAR-2003 (revised)
DT 09-AUG-1995 (first entry)
XX
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE) .
XX
KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX
OS Homo sapiens.
XX
PN WO9500651-A1.
XX
PD 05-JAN-1995.
XX
PF 20-JUN-1994; 94WO-IB000166.
XX
PR 18-JUN-1993; 93DK-00000725.
XX
PA (SYMB-) SYMBICOM AB.
XX
PI Egelrud T, Hansson L;
XX
DR WPI; 1995-052088/07.
DR N-PSDB; AAQ81203.
XX
PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
PT related vectors, transformed cells and polypeptides, useful for treating
PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.
XX
PS Disclosure; Page 97; 137pp; English.
XX
CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callosities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammal, insect, plant, or microorganism
CC transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQILL 9
Db 6 LLPLQILL 14
RESULT 9

```

AAW05383
ID AAW05383 standard; protein; 253 AA.
XX
AC AAW05383;
XX
DT 31-DEC-1996 (first entry)
XX
DE Human amyloid precursor protein protease.
XX
KW Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN W09631122-A1.
XX
PD 10-OCT-1996.
XX
PF 02-APR-1996; 96WO-US004294.
XX
PR 04-APR-1995; 95US-00416257.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Dixon EP, Johnstone EM, Little SP;
XX
DR WPI; 1996-464694/46.
XX
DR N-PSDB; AAT39783.
XX
PT New isolated human amyloid precursor protein protease - used to develop
PT prod. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.
XX
PS Claim 1; Page 44-45; 55pp; English.
XX
CC Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obtd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells. It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQLILL 9
Db 6 LLPLQLILL 14
RESULT 10
ID ABB84421
XX ABB84421 standard; peptide; 253 AA.
XX
AC ABB84421;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein N-terminal fragment SEQ ID 48.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
PN W0200262135-A2.

15-AUG-2002.
08-FEB-2002; 2002WO-IB001300.
09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
XX
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
PI Egelrud T, Hansson L;
XX
DR WPI; 2002-643380/69.
XX
PT Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
PS Example 6; Page 37; 74pp; English.
XX
CC This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the N-terminal
CC fragment of the human stratum corneum chymotryptic enzyme, SCCE
CC synonymous with human kallikrein 7 (KLK7), used in the development of the
CC transgenic mammals described in the invention
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQLILL 9
Db 6 LLPLQLILL 14
RESULT 11
ID ABB84406
XX ABB84406 standard; protein; 253 AA.
XX
AC ABB84406;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.

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KW WO200262135-A2.
 PN 15-AUG-2002.
 PD 08-FEB-2002; 2002WO-IB001300.
 PF 09-FEB-2001; 2001CA-02332655.
 PR 09-FEB-2001; 2001DK-00000218.
 XX (EGBL/) EGBLRUD T.
 PA (HANS/) HANSSON L.
 PI Egelrud T, Hansson L;
 XX WPI; 2002-643380/69.
 DR N-PSDB; ABQ76226.
 XX Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 XX Claim 10; Page 58-59; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide
 CC sequence comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous scce
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathological condition, for development or testing of a
 CC cosmetic or a pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC compound or composition effective for the prevention or treatment of
 CC inflammatory skin diseases selected from diseases consisting of epidermal
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful
 CC as a model for further studies of itch mechanisms and the testing of
 CC potential compounds and compositions for relieve of various skin diseases
 CC where itch is a component. This sequence represents the human stratum
 CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
 CC with human kallikrein 7 (KLK7) and is used in the development of the
 CC transgenic mammals described in the invention
 XX Sequence 253 AA;
 SQ
 Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 Db 6 LLPLQLLLL 14
 RESULT 12
 AAU82740
 ID AAU82740 standard; protein; 253 AA.
 XX AAU82740;
 AC
 XX 23-APR-2002 (first entry)
 DT Amino acid sequence of novel human protease #39.
 DE Human; protease; cancer; immune-related disorder; cardiovascular disease;
 XX neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 XX

KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 KW ocular disease; cytostatic; enzyme.
 XX Homo sapiens.
 OS WO200200860-A2.
 PN 03-JAN-2002.
 PD 26-JUN-2001; 2001WO-US020171.
 XX 26-JUN-2000; 2000US-0214047P.
 PF (SUGE-) SUGEN INC.
 PR Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
 XX Charydzak G;
 PI WPI; 2002-139913/18.
 DR N-PSDB; ABK31782.
 XX Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related diseases
 PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 PT disorders.
 XX Claim 6; Fig 2N; 313pp; English.
 XX The present invention relates to the isolation of novel human proteases,
 CC and the nucleic acids encoding them. The sequences of the invention are
 CC useful for treating diseases and disorders such as cancers (e.g. breast,
 CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
 CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
 CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
 CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
 CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
 CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
 CC disorders, cognition disorders, hypotension, hypertension, psychotic
 CC disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease) and dyskinesias. The nucleic acids and polypeptides are also
 CC useful for treating viral infections caused by human immunodeficiency
 CC virus (HIV), and non-viral infections such as ocular disease (e.g.
 CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
 CC human proteases of the invention
 XX Sequence 253 AA;
 SQ
 Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 Db 6 LLPLQLLLL 14
 RESULT 13
 ABU07440
 ID ABU07440 standard; protein; 253 AA.
 XX ABU07440;
 AC
 XX 28-JAN-2003 (first entry)
 DT Protein differentially regulated in prostate cancer #43.
 DE Prostate cancer; gene expression; differential regulation;
 XX molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX Homo sapiens.
 OS

PN WO200281638-A2.
 XX 17-OCT-2002.
 PD 08-APR-2002; 2002WO-US010824.
 PF 06-APR-2001; 2001US-0281731P.
 XX 06-APR-2001; 2001US-0281732P.
 PR (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX Sun Z, Jay G;
 XX WPI; 2003-058520/05.
 DR N-PSDB; ABX10343.
 XX Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX Claim 1; Page 293-294; 416pp; English.
 XX The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX Sequence 253 AA;
 SQ
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLL 9
 Db 6 LLPLQLLL 14
 RESULT 14
 ABU07471
 ID ABU07471 standard; protein; 253 AA.
 XX
 AC ABU07471;

XX 28-JAN-2003 (first entry)
 XX Protein differentially regulated in prostate cancer #74.
 DE Prostate cancer; gene expression; differential regulation;
 XX molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 KW
 XX Homo sapiens.
 OS
 XX WO200281638-A2.
 PN
 XX 17-OCT-2002.
 PD
 XX 08-APR-2002; 2002WO-US010824.
 PF
 XX 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.
 PA Sun Z, Jay G;
 XX WPI; 2003-058520/05.
 DR N-PSDB; ABX10375.
 XX Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX Claim 1; Page 351; 416pp; English.
 XX The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX Sequence 253 AA;
 SQ
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
| | | | |
Db 6 LLPLQILL 14

RESULT 15

ABR58471

ID ABR58471 standard; protein; 253 AA.

XX AC ABR58471;

XX XX

XX DT 07-JUL-2003 (first entry)

XX XX

XX DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.

XX XX

XX KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.

XX XX

XX OS Homo sapiens.

XX XX

XX PN WO2003029468-A1.

XX XX

XX PD 10-APR-2003.

XX XX

XX PF 02-OCT-2002; 2002WO-US031467.

XX XX

XX PR 02-OCT-2001; 2001US-0327135P.

XX PR

XX 30-MAY-2002; 2002US-0384531P.

XX XX

XX PA (CORI-) CORIXA CORP.

XX XX

XX PI Algate PA, Mannion J;

XX XX

XX DR WPI; 2003-372001/35.

XX XX

XX PT New polynucleotide and polypeptide useful for diagnosing and/or treating

XX PT

XX cancer, particularly ovarian cancer, and as a vaccine.

XX XX

XX PS Claim 2; Page 157-158; 169pp; English.

XX XX

XX CC The invention relates to a novel isolated polynucleotide. The

XX CC

XX polynucleotides of the invention have cytostatic activity, and may have a

XX CC

XX use in gene therapy, and in a vaccine. The composition and methods are

XX CC

XX useful in diagnosing and/or treating cancer, particularly ovarian cancer.

XX CC

XX The composition may also be used as a vaccine to prevent cancer. The

XX CC

XX present sequence is used in the exemplification of the invention

XX XX

SQ Sequence 253 AA;

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
| | | | |
Db 6 LLPLQILL 14

Search completed: March 11, 2006, 00:24:14
Job time : 87.6667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPLQLLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: piri:*
2: piri2:*
3: piri3:*
4: piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 40 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 36 | 90.0 | 845 | 2 D97163 | cation transport p |
| 3 | 35 | 87.5 | 493 | 2 A71875 | hypothetical prote |
| 4 | 35 | 87.5 | 496 | 2 B64838 | conserved hypothet |
| 5 | 34 | 85.0 | 266 | 2 JC7300 | tax-responsive ele |
| 6 | 34 | 85.0 | 267 | 2 JC4857 | hepatocarcinogenes |
| 7 | 34 | 85.0 | 369 | 2 S33603 | surfactant protein |
| 8 | 34 | 85.0 | 371 | 1 JN0450 | conglutinin precur |
| 9 | 34 | 85.0 | 371 | 2 I45878 | conglutinin - bovi |
| 10 | 34 | 85.0 | 429 | 2 T17215 | hypothetical prote |
| 11 | 34 | 85.0 | 539 | 2 H82994 | probable permease |
| 12 | 34 | 85.0 | 1092 | 2 T12520 | hypothetical prote |
| 13 | 34 | 85.0 | 1236 | 2 T50904 | Mg protoporphyryn |
| 14 | 33 | 82.5 | 146 | 2 H75201 | hypothetical prote |
| 15 | 33 | 82.5 | 277 | 2 H84314 | cytochrome a3 con |
| 16 | 33 | 82.5 | 282 | 2 E70890 | hypothetical prote |
| 17 | 33 | 82.5 | 294 | 2 A25970 | transcription acti |
| 18 | 33 | 82.5 | 294 | 2 E82257 | cholera toxin tran |
| 19 | 33 | 82.5 | 653 | 2 A46362 | amyloid precursor- |
| 20 | 32 | 80.0 | 245 | 2 E75440 | hypothetical prote |
| 21 | 32 | 80.0 | 253 | 2 AF1535 | transport protein |
| 22 | 32 | 80.0 | 286 | 2 JQ0708 | lipopolysaccharide |
| 23 | 32 | 80.0 | 394 | 1 B43750 | chloramphenicol re |
| 24 | 32 | 80.0 | 394 | 2 B85535 | probable transport |
| 25 | 32 | 80.0 | 394 | 2 F90684 | probable transport |
| 26 | 32 | 80.0 | 412 | 2 A57468 | P-selectin glycopr |
| 27 | 32 | 80.0 | 491 | 2 JC6197 | stromelysin 3 (EC |
| 28 | 32 | 80.0 | 492 | 2 A44399 | stromelysin 3 (EC |
| 29 | 32 | 80.0 | 543 | 2 A12088 | Na+/H+-exchanging |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 32 | 80.0 | 1041 | 2 T29010 | hypothetical prote |
| 31 | 32 | 80.0 | 1306 | 1 A31759 | peptidyl-dipeptida |
| 32 | 32 | 80.0 | 1485 | 2 S23756 | CfTR protein - Afr |
| 33 | 31 | 77.5 | 157 | 2 A83214 | probable transcrip |
| 34 | 31 | 77.5 | 189 | 2 T43766 | hypothetical prote |
| 35 | 31 | 77.5 | 196 | 2 G65039 | hypothetical prote |
| 36 | 31 | 77.5 | 209 | 2 A54984 | Enf-1 protein prec |
| 37 | 31 | 77.5 | 213 | 2 JE0322 | ephA2 - human |
| 38 | 31 | 77.5 | 303 | 2 C84914 | hypothetical prote |
| 39 | 31 | 77.5 | 306 | 2 H86811 | sugar ABC transpor |
| 40 | 31 | 77.5 | 327 | 1 A41720 | acid phosphatase (|
| 41 | 31 | 77.5 | 328 | 1 A41927 | insulin-like growt |
| 42 | 31 | 77.5 | 370 | 2 AB3334 | daunorubicin resis |
| 43 | 31 | 77.5 | 372 | 2 A98157 | probable permease |
| 44 | 31 | 77.5 | 372 | 2 AH3130 | ABC transporter, m |
| 45 | 31 | 77.5 | 388 | 2 T26360 | hypothetical prote |

ALIGNMENTS

RESULT 1

A53968
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hanson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:1
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9
|||
DB 6 LLPLQLLLL 14

RESULT 2

D97163
cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97163
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-845 <KUR>

A;Cross-references: UNIPROT:Q97H76; UNIPARC:UPI000000CA412; GB:AE001437; PIDN:AAK80095.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2137

```

Query Match      90.0%; Score 36; DB 2; Length 845;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 670 LLPLQIILL 678

RESULT 3
A71875
hypothetical protein jhp0880 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: A71875
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923382
A:Accession: A71875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <ARN>
A:Cross-references: UNIPROT:Q9ZK05; UNIPARC:UPI00000D7271; GB:AE001518; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0880

Query Match      87.5%; Score 35; DB 2; Length 493;
Best Local Similarity 88.9%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 254 LLPLSILL 262

RESULT 4
B64638
conserved hypothetical integral membrane protein HP0946 - Helicobacter pylori (strain 26
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: B64638
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64638
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-496 <TOM>
A:Cross-references: UNIPROT:Q25600; UNIPARC:UPI00000D30BA; GB:AE000604; GB:AE000511; NID
C:Genetics:
A:Start codon: GTG

Query Match      87.5%; Score 35; DB 2; Length 496;
Best Local Similarity 88.9%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 254 LLPLSILL 262

RESULT 5
JC7300
tax-responsive element-binding protein 5 - mouse
C:Species: Mus musculus (house mouse)

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```

C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
A:Accession: JC7300
R:Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatau, K.
DNA Res. 7, 187-193, 2000
A:Title: Isolation and characterization of the gene encoding mouse tax-responsive element
A:Reference number: JC7300
A:Accession: JC7300
A:Molecule type: mRNA
A:Residues: 1-266 <MAS>
A:Cross-references: UNIPROT:Q9ESS3; UNIPARC:UPI00000E73B0; DDBJ:AB036745
C:Genetics:
A:Gene: treb5
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor

Query Match      85.0%; Score 34; DB 2; Length 266;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 187 LLPLQIILL 195

RESULT 6
JC4857
hepatocarcinogenesis-related transcription factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4857
R:Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
Biochem. Biophys. Res. Commun. 224, 746-751, 1996
A:Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREB1
A:Reference number: JC4857
A:Accession: JC4857
A:Molecule type: mRNA
A:Residues: 1-267 <KIS>
A:Cross-references: UNIPROT:Q9R1S4; UNIPARC:UPI00000E80AD
C:Comment: This is a basic-leucine zipper type transcription factor involved in hepatocel
C:Genetics:
A:Gene: htf
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor
F:58-98/Domain: fos/jun DNA-binding domain homology <FJD>
F:89-126/Region: leucine zipper motif

Query Match      85.0%; Score 34; DB 2; Length 267;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 188 LLPLQIILL 196

RESULT 7
S33603
surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S33603
R:Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A:Title: Structural similarity between bovine conglutinin and bovine lung surfactant prot
A:Reference number: S33603; MUID:93170856; PMID:8436402
A:Accession: S33603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-369 <LIM>
A:Cross-references: UNIPARC:UPI0000177932
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-367/Domain: C-type lectin homology <LCH>

```

Query Match 85.0%; Score 34; DB 2; Length 369;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 LLPLQILL 9
 |||| :|||
 Db 3 LLPLSVLL 11

RESULT 8
 JN0450
 conglutinin precursor - bovine
 N;Alternate names: C3b-binding protein
 N;Contains: conglutinin-N
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: JN0450; JC2396; S33235; A23740; S36879; S35044; I46010; A29416; S34054
 R;Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
 Biochem. Biophys. Res. Commun. 191, 335-342, 1993
 A;Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
 A;Reference number: JN0450; MUID:93213261; PMID:8460993
 A;Accession: JN0450
 A;Molecule type: mRNA
 A;Residues: 1-371 <SUZ>
 A;Cross-references: UNIPROT:P23805; UNIPARC:UPI0000127EB3; DDBJ:D14085; NID:g285643; PIR
 A;Experimental source: liver
 R;Kawasaki, N.; Itoh, N.; Kawasaki, T.
 Biochem. Biophys. Res. Commun. 198, 597-604, 1994
 A;Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamm
 A;Reference number: JC2396; MUID:94128104; PMID:8297370
 A;Accession: JC2396
 A;Molecule type: mRNA
 A;Residues: 1-371 <KA2>
 A;Cross-references: UNIPARC:UPI0000127EB3
 A;Note: The authors translated the codon GAT for residues 250 and 270 as Glu
 R;Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
 Biochem. J. 292, 157-162, 1993
 A;Title: The cDNA cloning of conglutinin and identification of liver as a primary site o
 A;Reference number: S33235; MUID:93277452; PMID:7684896
 A;Accession: S33235
 A;Molecule type: mRNA
 A;Residues: 1-172, 'H', 174-217, 'A', 219-271, 'V', 273-371 <LUJ>
 A;Cross-references: UNIPARC:UPI000016C2E3; EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PI
 A;Experimental source: liver
 R;Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarma, T.B.
 J. Biol. Chem. 266, 2715-2723, 1991
 A;Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin f
 A;Reference number: A23740; MUID:91131556; PMID:1993651
 A;Accession: A23740
 A;Molecule type: protein
 A;Residues: 21-209, 'S', 211-371 <LEE>
 A;Cross-references: UNIPARC:UPI000014DF2A
 R;Kawasaki, N.; Yokota, Y.; Kawasaki, T.
 Arch. Biochem. Biophys. 305, 533-540, 1993
 A;Title: Differentiation of conglutination activity and sugar-binding activity of conglu
 A;Reference number: S36879; MUID:93384312; PMID:8373191
 A;Accession: S36879
 A;Molecule type: protein
 A;Residues: 21-54; 75-86, 'X', 88-89, 'X', 91, 'X', 93-94; 208-209, 'X', 211-227 <KAW>
 A;Cross-references: UNIPARC:UPI00001741A3; UNIPARC:UPI00001741A4; UNIPARC:UPI00001741A5
 A;Experimental source: serum
 R;Lu, J.; Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
 Eur. J. Biochem. 215, 793-799, 1993
 A;Title: Structural similarity between lung surfactant protein D and conglutinin. Two di
 A;Reference number: S35044; MUID:93358905; PMID:8354286
 A;Accession: S35044
 A;Molecule type: protein
 A;Residues: 75-86, 'X', 88-89, 'X', 91, 'I', <LUJ>
 A;Cross-references: UNIPARC:UPI00001741A6
 A;Experimental source: lung
 R;Young, N.M.; Leon, M.A.
 Biochem. Biophys. Res. Commun. 143, 645-651, 1987
 A;Title: The carbohydrate specificity of conglutinin and its homology to proteins in the

A;Reference number: A29416; MUID:87184551; PMID:3566740
 A;Contents: annotation
 R;Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
 Biochem. J. 293, 15-19, 1993
 A;Title: Research Communication. Localization of the receptor-binding site in the collect
 A;Reference number: S34054; MUID:93319501; PMID:8328957
 A;Contents: annotation
 R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry,
 J. Immunol. 153, 173-180, 1994
 A;Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to
 A;Reference number: I46010; MUID:94267222; PMID:8207234
 A;Accession: I46010
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-371 <LIO>
 A;Cross-references: UNIPARC:UPI0000127EB3; EMBL:U06860; NID:g507183; PIDN:AAB60624.1; PIR
 C;Comment: This protein mediates the agglutination of erythrocytes with antibody and com
 C;Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamin
 C;Genetics:
 A;Gene: CGN1
 A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 C;Keywords: calcium binding; glycoprotein; hydroxyllysine; hydroxyproline
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-371/Product: conglutinin #status predicted <MAT>
 F;46-214/Region: collagen-like
 F;75-371/Product: conglutinin-N #status predicted <MA2>
 F;248-369/Domain: C-type lectin homology <LCH>
 F;63, 87, 99, 135, 141, 159, 162, 198, 210/Binding site: carbohydrate (lys) (covalent) #status p
 F;63, 87, 99, 135, 141, 159, 162, 198, 210/Modified site: 5-hydroxyllysine (lys) #status experim
 F;78, 96, 108, 111, 129, 132, 147, 153, 171, 195/Modified site: 4-hydroxyproline (pro) #status exp
 F;337/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 85.0%; Score 34; DB 1; Length 371;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
 |||| :|||
 Db 3 LLPLSVLL 11

RESULT 9
 I45878
 conglutinin - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
 C;Accession: I45878
 R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry,
 Gene 141, 277-281, 1994
 A;Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of
 A;Reference number: I45878; MUID:94215917; PMID:8163202
 A;Accession: I45878
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-371 <LIO>
 A;Cross-references: UNIPROT:P23805; UNIPARC:UPI000016C2E0; GB:L18871; NID:g495012; PIDN:
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 F;248-369/Domain: C-type lectin homology <LCH>

Query Match 85.0%; Score 34; DB 2; Length 371;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
 |||| :|||
 Db 3 LLPLSVLL 11

RESULT 10
 T1215
 hypothetical protein DKFP434H2235.1 - human
 C;Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17215
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723
A:Accession: T17215
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-429 <POU>
A:Cross-references: UNIPARC:UPI000000D884; EMBL:AL117404
A:Experimental source: adult testis; clone DKFZp434H2235
C:Genetics:
A:Note: DKFZp434H2235.1

Query Match 85.0%; Score 34; DB 2; Length 429;

Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQIILL 9
|||:||||
DB 381 LPLQLLLL 388

RESULT 11

H82994
Probable permease of ABC iron transporter PA5216 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: H82994

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen

A:Reference number: AB2950; MUID:20437337; PMID:10984043

A:Accession: H82994

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-539 <STO>

A:Cross-references: UNIPROT:Q9HTX4; UNIPARC:UPI000000CF5A; GB:AE004934; GB:AE004091; NID

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA5216

C:Superfamily: sfuB protein

Query Match 85.0%; Score 34; DB 2; Length 539;

Best Local Similarity 77.8%; Pred. No. 64;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
|||:||||
DB 21 LLPLSVLLL 29

RESULT 12

T12520

hypothetical protein DKFZp434G173.1 - human

C:Species: Homo sapiens (man)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: T12520

R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z17524

A:Accession: T12520

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1092 <WAM>

A:Cross-references: UNIPARC:UPI00000711F2; EMBL:AL080133

A:Experimental source: adult testis; clone DKFZp434G173

C:Genetics:

A:Note: DKFZp434G173.1

Query Match 85.0%; Score 34; DB 2; Length 1092;

Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQIILL 9
|||:||||
DB 1044 LPLQLLLL 1051

RESULT 13

T50904

Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus

C:Species: Rubrivivax gelatinosus

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: T50904

R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

submitted to the EMBL Data Library, November 1999

A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynth

A:Reference number: Z25270

A:Accession: T50904

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-1236 <NAG>

A:Cross-references: UNIPROT:Q9JPA4; UNIPARC:UPI00000B2528; EMBL:AB034704; PIDN:BA094057.1

A:Experimental source: strain IL144

C:Genetics:

A:Gene: bchH

C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 85.0%; Score 34; DB 2; Length 1236;

Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
|||:||||
DB 946 LLPLQIKLL 954

RESULT 14

H75201

hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: H75201

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc

A:Reference number: A75001

A:Accession: H75201

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <KAW>

A:Cross-references: UNIPROT:Q9V2D5; UNIPARC:UPI0000063243; GB:AJ248283; GB:AL096836; NID:

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB0088

C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

Query Match 82.5%; Score 33; DB 2; Length 146;

Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
|||:||||
DB 68 LLPLQIIIV 76

RESULT 15

H84314

cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84314

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: H84314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <STO>
A;Cross-references: UNIPROT:Q9HPI3; UNIPARC:UPI0000063931; GB:AE004437; NID:gl0581096; E
C;Genetics:
A;Gene: ccp

Query Match 82.5%; Score 33; DB 2; Length 277;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLPQLLL 8
Db 98 LLPQLVIL 105
|||||::|

Search completed: March 11, 2006, 00:40:50
Job time : 15.1111 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LPLQLILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 40 | 100.0 | 66 | 2 | Q6DYL1_HUMAN |
| 2 | 40 | 100.0 | 253 | 1 | P49862_homo sapien |
| 3 | 38 | 95.0 | 73 | 2 | Q8VCA9_MOUSE |
| 4 | 38 | 95.0 | 104 | 2 | Q8R5D6_mus musculus |
| 5 | 38 | 95.0 | 138 | 2 | Q6PKE2_MOUSE |
| 6 | 38 | 95.0 | 201 | 1 | FKB11_MOUSE |
| 7 | 38 | 95.0 | 361 | 1 | INHA_TRITU |
| 8 | 37 | 92.5 | 552 | 2 | Q75B55_ASHGO |
| 9 | 36 | 90.0 | 71 | 2 | Q4XN42_PLACH |
| 10 | 36 | 90.0 | 79 | 2 | Q8VB59_WSSV |
| 11 | 36 | 90.0 | 637 | 2 | Q7RO54_PLAYO |
| 12 | 36 | 90.0 | 845 | 2 | Q97H76_CLOBAB |
| 13 | 36 | 90.0 | 887 | 2 | Q6FMG7_LACAC |
| 14 | 35 | 87.5 | 181 | 2 | Q6NB96_RHOPA |
| 15 | 35 | 87.5 | 183 | 2 | Q8MZZ0_HELAU |
| 16 | 35 | 87.5 | 208 | 2 | Q21527_CLEGA |
| 17 | 35 | 87.5 | 233 | 2 | Q8IMF1_DROME |
| 18 | 35 | 87.5 | 433 | 2 | Q9ZKQ5_HELPJ |
| 19 | 35 | 87.5 | 496 | 2 | Q25600_HELPJ |
| 20 | 35 | 87.5 | 545 | 2 | Q5N0S0_SYNPF |
| 21 | 35 | 87.5 | 1620 | 2 | Q622J8_ORYSA |
| 22 | 34 | 85.0 | 96 | 2 | Q5XFW5_RAT |
| 23 | 34 | 85.0 | 182 | 2 | Q8MZV6_SPOLT |
| 24 | 34 | 85.0 | 182 | 2 | Q8MXZ7_PLOIN |
| 25 | 34 | 85.0 | 182 | 2 | Q8MZV6_NAMBR |
| 26 | 34 | 85.0 | 182 | 2 | Q8MZZ6_CYPDO |
| 27 | 34 | 85.0 | 205 | 2 | Q653Z3_ORYSA |
| 28 | 34 | 85.0 | 242 | 2 | Q7VHT6_HELPJ |
| 29 | 34 | 85.0 | 243 | 2 | Q4QC15_LEIMA |
| 30 | 34 | 85.0 | 245 | 2 | Q50KZ3_CALJA |
| 31 | 34 | 85.0 | 246 | 2 | Q50KZ9_homo sapien |

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|----|----|------|-----|---|--------------|
| 32 | 34 | 85.0 | 246 | 2 | Q585W6_TRYYP |
| 33 | 34 | 85.0 | 246 | 2 | Q50KZ2_CEBAP |
| 34 | 34 | 85.0 | 246 | 2 | Q50KZ4_MACWU |
| 35 | 34 | 85.0 | 246 | 2 | Q50KZ5_HYLAG |
| 36 | 34 | 85.0 | 246 | 2 | Q50KZ6_PONPY |
| 37 | 34 | 85.0 | 262 | 2 | Q8BMM1_MOUSE |
| 38 | 34 | 85.0 | 267 | 1 | XBPI_MOUSE |
| 39 | 34 | 85.0 | 267 | 1 | XBPI_RAT |
| 40 | 34 | 85.0 | 283 | 2 | Q8KI47_MOUSE |
| 41 | 34 | 85.0 | 331 | 2 | Q7XI51_ORYSA |
| 42 | 34 | 85.0 | 338 | 2 | Q6US81_SPOLI |
| 43 | 34 | 85.0 | 369 | 1 | SFTPD_BOVIN |
| 44 | 34 | 85.0 | 369 | 2 | Q863AI_BOVIN |
| 45 | 34 | 85.0 | 371 | 1 | CL46_BOVIN |

ALIGNMENTS

RESULT 1
Q6DYL1_HUMAN PRELIMINARY; PRT; 66 AA.

AC Q6DYL1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY646152; AN766047.1; -; mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 4,9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
|||
Db 6 LPLQLILL 14

RESULT 2
KLK7_HUMAN STANDARD; PRT; 253 AA.

ID KLK7_HUMAN
AC P49862; Q8NSN9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroengvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

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Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 3
Q8VCA9 MOUSE
ID Q8VCA9_MOUSE PRELIMINARY; PRT; 73 AA.
AC Q8VCA9_2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSSP; P18203; 1FKL.
DR MGI; MGI:191370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PP1ase.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS50059; FKBP_PP1ase; 1.
SQ SEQUENCE 73 AA; 7819 MW; 93E8F5399BF3C11 CRC64;

Query Match      95.0%; Score 38; DB 2; Length 73;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 7 LLPLQLILL 15

RESULT 4
Q8RSD6 MOUSE
ID Q8RSD6_MOUSE PRELIMINARY; PRT; 104 AA.
AC Q8RSD6_2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021345; AAH21345.1; -; mRNA.
DR MGI; MGI:191370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match      95.0%; Score 38; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 7 LLPLQLILL 15

RESULT 5
Q8PKE2 MOUSE
ID Q8PKE2_MOUSE PRELIMINARY; PRT; 138 AA.
AC Q8PKE2_2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

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DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSSP; P18203; 1FKL.
DR MGI; MGI:191370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PP1ase.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS50059; FKBP_PP1ase; 1.
SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match      95.0%; Score 38; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 7 LLPLQLILL 15

RESULT 5
Q8PKE2 MOUSE
ID Q8PKE2_MOUSE PRELIMINARY; PRT; 138 AA.
AC Q8PKE2_2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RA Strausberg R.J.
RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002311; AAH02311.1; -; mRNA.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C1_PPIase.
DR PROSITE; PS5059; FKBP_PPIase; 1.
SQ SEQUENCE 138 AA; 15105 MW; C138B8B08FDDF59D CRC64;

Query Match 95.0%; Score 38; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9
Db |||||:|
7 LLPLQLLLL 15

RESULT 6
FKB11 MOUSE STANDARD; PRT; 201 AA.
AC Q9DIM7; O9CRE4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
DE trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
DE (FKBP-19).
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

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DR PROSITE; PS50059; FKBP_PP1ASE; 1.
 KW isomerase; Rotamase; Signal. Potential.
 FT SIGNAL 1 27
 FT CHAIN 28 201 FK506 binding protein 11.
 FT DOMAIN 57 144 P1ase FKBP-type.
 FT CONFLICT 53 53 S -> F (in Ref. 1; BAB31559).
 FT CONFLICT 198 198 S -> R (in Ref. 1; BAB31559).
 SQ SEQUENCE 201 AA; 21237 MW; 94D955C57264BD82 CRC64;

Query Match 95.0%; Score 38; DB 1; Length 201;
 Best Local Similarity 88.9%; Pred. No. 36;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9
 DB 7 LLPLQLLLL 15

RESULT 7
 INHA_TRIVU STANDARD; PRT; 361 AA.
 AC 07755;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Inhibin alpha chain precursor.
 GN Name=INHA;
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
 RA Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tiedall D.J.,
 Greenwood P.J., McNatty K.;
 RT cDNA sequence analysis, Gene expression and protein localisation of
 the inhibin alpha subunit of Australian brushtail possum (Trichosurus
 vulpecula).
 RL J. Mol. Endocrinol. 21:141-152(1998).
 CC -!- FUNCTION: Inhibins and activins inhibit and activate,
 respectively, the secretion of follitropin by the pituitary gland.
 CC Inhibins/activins are involved in regulating a number of diverse
 CC functions such as hypothalamic and pituitary hormone secretion,
 CC gonadal hormone secretion, germ cell development and maturation,
 CC erythroid differentiation, insulin secretion, nerve cell survival,
 CC embryonic axial development or bone growth, depending on their
 CC subunit composition. Inhibins appear to oppose the functions of
 CC activins.
 CC -!- SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A
 CC is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
 CC beta-B.
 CC -!- PTM: Proteolytic processing yields a number of bioactive forms,
 CC consisting either solely of the mature alpha chain, of the most N-
 CC terminal propeptide linked through a disulfide bond to the mature
 CC alpha chain, or of the entire proprotein.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF033340; AAC63945.1; -; mRNA.
 DR GO; GO:0005376; C:extracellular region; ISS.
 DR GO; GO:0017106; F:activin inhibitor activity; ISS.
 DR GO; GO:0005125; F:cytokine activity; ISS.
 DR GO; GO:0008083; F:growth factor activity; ISS.
 DR GO; GO:0005179; F:hormone activity; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0007050; P:cell cycle arrest; ISS.
 DR GO; GO:0030154; P:cell differentiation; ISS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; ISS.
 DR GO; GO:0007267; P:cell-cell signaling; ISS.
 DR GO; GO:0030218; P:erythrocyte differentiation; ISS.
 DR GO; GO:0042541; P:hemoglobin biosynthesis; ISS.
 DR GO; GO:0006917; P:induction of apoptosis; ISS.
 DR GO; GO:0045578; P:negative regulation of cell cycle; ISS.
 DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
 DR GO; GO:0046882; P:negative regulation of follicle-stimulating. . ; ISS.
 DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. . ; ISS.
 DR GO; GO:0045650; P:negative regulation of macrophage different. . ; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR GO; GO:0001541; P:ovarian follicle development; ISS.
 DR GO; GO:0046881; P:positive regulation of follicle-stimulating. . ; ISS.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein; Growth factor; Hormone; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 64
 FT PROPEP 65 230
 FT CHAIN 231 361
 FT SITE 64 65
 FT SITE 230 231
 FT CARBOHYD 48 48
 FT CARBOHYD 144 144
 FT CARBOHYD 266 266
 FT DISULFID 260 323
 FT DISULFID 289 358
 FT DISULFID 293 360
 FT DISULFID 322 360
 SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDAA87D CRC64;

Query Match 95.0%; Score 38; DB 1; Length 361;
 Best Local Similarity 88.9%; Pred. No. 63;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9
 DB 5 LLPLQLLLL 13

RESULT 8
 Q75E55_ASHGO
 ID Q75E55_ASHGO PRELIMINARY; PRT; 552 AA.
 AC Q75E55;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ABL185Cp.
 GN Name=ABL185C;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 Mohr C., Pöhlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome.";
 RL Science 304:304-307(2004).
 DR EMBL; AE016815; AAS50586.1; -; Genomic_DNA.
 DR AGD; ABL185C; -;
 DR InterPro; IPR005599; Alg9_trans.

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DR InterPro: IPR001202; WW_Rsp5_WWP.
DR Pfam: PF03901; Glyco_transf_22; 1.
DR PROSITE: PS01159; WW_DOMAIN_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 552 AA; 62708 MW; 62A8842023DEEA04 CRC64;
  Query Match          92.5%; Score 37; DB 2; Length 552;
  Best Local Similarity 77.8%; Pred. No. 1.5e+02;
  Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPLQLILL 9
Db 67 LMPQLVLL 75

RESULT 9
QAXN42 PLACH PRELIMINARY; PRT; 71 AA.
AC QAXN42.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC108599.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jance C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01004512; CAH81670.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8015 MW; 5176BF698D94CAC2 CRC64;
  Query Match          90.0%; Score 36; DB 2; Length 71;
  Best Local Similarity 100.0%; Pred. No. 32;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LPLQLILL 9
Db 7 LPLQLILL 14

RESULT 10
Q8VB59 WSSV PRELIMINARY; PRT; 79 AA.
AC Q8VB59;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Wsv132 (WSSV187).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21548311; PubMed=11689662;
RX DOI=10.1128/JVI.75.23.11811-11820.2001;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
  J. Virol. 75:11811-11820(2001).
  [2]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
  RA Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
  Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
  RT "Identification and characterization of a shrimp white spot syndrome
  RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
  RT cellular-type thymidine kinase and thymidylate kinase.";
  RL Virology 277:100-110(2000).
  [3]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
  RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
  Lo C.F., Kou G.H.;
  RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
  RT spot syndrome virus and characterization of the motif important for
  RT targeting VP35 to the nuclei of transfected insect cells.";
  RL Virology 293:44-53(2002).
  [4]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX PubMed=12202227; DOI=10.1006/viro.2002.1480;
  RA Tzeng H.F., Chang Z.F., Peng S.E., Wang C.H., Lin J.Y., Kou G.H.,
  Lo C.F.;
  RT "Chimeric polypeptide of thymidine kinase and thymidylate kinase of
  RT shrimp white spot syndrome virus: thymidine kinase activity of the
  RT recombinant protein expressed in a baculovirus/insect cell system.";
  RL Virology 299:248-255(2002).
  [5]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX PubMed=12359454; DOI=10.1006/viro.2002.1536;
  RA Chen L.L., Huang H.C., Huang C.J., Peng S.E., Chen Y.G., Lin S.J.,
  Chen W.Y., Dai C.F., Yu H.T., Wang C.H., Lo C.F., Kou G.H.;
  RT "Transcriptional analysis of the DNA polymerase gene of shrimp white
  RT spot syndrome virus.";
  RL Virology 301:136-147(2002).
  [6]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX PubMed=12504569; DOI=10.1006/viro.2002.1696;
  RA Lin S.T., Chang Y.S., Wang H.C., Tzeng H.F., Chang Z.F., Lin J.Y.,
  Wang C.H., Lo C.F., Kou G.H.;
  RT "Ribonucleotide reductase of shrimp white spot syndrome virus (WSSV):
  RT expression and enzymatic activity in a baculovirus/insect cell system
  RT and WSSV-infected shrimp.";
  RL Virology 304:282-290(2002).
  [7]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX PubMed=15452257; DOI=10.1128/JVI.78.20.11360-11370.2004;
  RA Tsai J.M., Wang H.C., Leu J.H., Hsiao H.H., Wang A.H., Kou G.H.,
  Lo C.F.;
  RT "Genomic and proteomic analysis of thirty-nine structural proteins of
  RT shrimp white spot syndrome virus.";
  RL J. Virol. 78:11360-11370(2004).
  [8]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RX PubMed=15596810; DOI=10.1128/JVI.79.1.140-149.2005;
  RA Leu J.H., Tsai J.M., Wang H.C., Wang A.H., Wang C.H., Kou G.H.,
  Lo C.F.;
  RT "The unique stacked rings in the nucleocapsid of the white spot
  RT syndrome virus virion are formed by the major structural protein
  RT VP664, the largest viral structural protein ever found.";
  RL J. Virol. 79:140-149(2005).
  [9]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=Taiwan;
  RA Lo C.F., Kou G.-H.;

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF333136.1; -; Genomic DNA.
 DR EMBL; AF440570; AAL89055.1; -; Genomic DNA.
 SQ SEQUENCE 79 AA; 9287 MW; 800910C7FFA0EC7E CRC64;

Query Match 90.0%; Score 36; DB 2; Length 79;
 Best Local Similarity 77.8%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
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 Db 34 LPLQLILL 42

RESULT 11
 Q7RQ54 PLAYO
 ID Q7RQ54 PLAYO PRELIMINARY; PRT; 637 AA.
 AC Q7RQ54
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE MCN3/saliva family, putative.
 GN Name=PY01249;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22555706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlson J.M., Angluoia S.V., Suh B.B., Kooij T.W., Perte M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

DR EMBL; AABL01000328; EAA20540.1; -; Genomic DNA.
 DR GO; GO:0016020; C-membrane; IEA.
 DR InterPro; IPR004316; Mtn3_slv.
 DR PANTHER; PTHR10791; Mtn3_slv; 1.
 DR Pfam; PF03083; Mtn3_slv; 2.
 SQ SEQUENCE 637 AA; 70992 MW; BC506320B2AE1FE5 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 637;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLILL 9
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 Db 7 LPLQLILL 14

RESULT 12
 Q97H76 CLOAB
 ID Q97H76 CLOAB PRELIMINARY; PRT; 845 AA.
 AC Q97H76
 DT 01-OCT-2001 (T-EMBLrel. 18, Created)
 DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Cation transport P-type ATPase.
 GN OrderedLocusNames=CAZ2137;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007714; AAK80095.1; -; Genomic DNA.
 DR PIR; D97163; D97163.
 DR HSSP; P04191; 1SU4.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0015662; F-ATPase activity, coupled to transmembrane m. .; IEA.
 DR GO; GO:0003824; F-catalytic activity; IEA.
 DR GO; GO:0016820; F-hydrolase activity, acting on acid anhydrid. .; IEA.
 DR GO; GO:0006812; P-cation transport; IEA.
 DR GO; GO:0008152; P-metabolism; IEA.
 DR GO; GO:0015992; P-proton transport; IEA.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006068; Cation_ATPase_C.
 DR InterPro; IPR004014; Cation_ATPase_N.
 DR InterPro; IPR005834; Dehal_Like_hydro.
 DR InterPro; IPR008250; E1-E2_ATPase_reg.
 DR InterPro; IPR000695; H_ATPase.
 DR Pfam; PF00689; Cation_ATPase_C; 1.
 DR Pfam; PF00690; Cation_ATPase_N; 1.
 DR Pfam; PF00122; E1-E2_ATPase; 1.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00120; HATPASE.
 DR TIGRFAMs; TIGR01494; ATPase_P-type; 3.
 DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 845 AA; 93779 MW; 401293AA1PF9D757 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 845;
 Best Local Similarity 77.8%; Pred. No. 3.6e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
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 Db 670 LPLQLILL 678

RESULT 13
 Q5FMG7 LACAC
 ID Q5FMG7 LACAC PRELIMINARY; PRT; 887 AA.
 AC Q5FMG7
 DT 10-MAY-2005 (T-EMBLrel. 30, Created)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
 DE Cation transporter P-ATPase (EC 3.6.1.-).
 GN OrderedLocusNames=LBA0212;
 OS Lactobacillus acidophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1579;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCFM;
 RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
 RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
 RA Buck B.L., McAuliffe O., Southern N., Dobson A., Duong T., Callanan M.,
 RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
 RT "Complete genome sequence of the probiotic lactic acid bacterium
 Lactobacillus acidophilus NCFM.";

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RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
DR EMBL; CP000033; AAV42107.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .; IEA.
DR GO; GO:0015440; F:magnesium-importing ATPase activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0015693; P:magnesium ion transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR006415; ATPase-IIIB_Mg.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal-like_hydro.
DR InterPro; IPR000695; H_ATPase.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolyase; 1.
DR PRINTS; PR00119; HATPASE.
DR PRINTS; PR00120; HATPASE.
DR TIGRFAMs; TIGR01524; ATPase-IIIB_Mg; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 1.
DR PROSITE; PS00154; ATPASE_E1-E2; UNKNOWN_1.
KW Complete proteome; Hydrolyase.
SQ SEQUENCE 887 AA; 99091 MW; 9071A032A09BE9CE CRC64;

Query Match 90.0%; Score 36; DB 2; Length 887;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPQLILL 9
Db 708 LLPQLILL 716
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RESULT 14
Q6NB96 RHOPA
ID Q6NB96 RHOPA PRELIMINARY; PRT; 181 AA.
AC Q6NB96;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RP0932;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Maltatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Peres C.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572595; CAE26376.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;

Query Match 87.5%; Score 35; DB 2; Length 181;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPQLILL 8
Db 24 LLPQLILL 31
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RESULT 15
Q8MZZO HELAU
ID Q8MZZO HELAU PRELIMINARY; PRT; 183 AA.
AC Q8MZZO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acyl-CoA desaturase HaasPPAE (Fragment).
OS Helicoverpa assulta (Oriental tobacco budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=52344;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22412134; PubMed=12524345;
RA Knipple D.C., Rosenfield C.L., Nielsen R., You K.M., Jeong S.E.;
RT "Evolution of the integral membrane desaturase gene family in moths
RT and flies";
RL Genetics 162:1737-1752(2002).
DR EMBL; AF482910; AAM28485.1; -; mRNA.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006491; F:oxidoreductase activity; IEA.
DR GO; GO:0004768; F:stearoyl-CoA 9-desaturase activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001522; Desaturase.
DR InterPro; IPR005804; Fa_desat.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRINTS; PR00075; FACDDSATRASE.
DR PRINTS; PR00024; HOMBOBOX.
KW Fatty acid biosynthesis; Iron; Lipid synthesis; Oxidoreductase;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 183
SQ SEQUENCE 183 AA; 21196 MW; 728DA94FAFCD14FA CRC64;

Query Match 87.5%; Score 35; DB 2; Length 183;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLPQLILL 9
Db 14 LLPQLILL 21
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Job time : 98.3333 secs
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPLQLILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/prodata/1/iaa/backfileseq.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 40 | 100.0 | 9 | 2 | US-09-502-600-35 |
| 2 | 40 | 100.0 | 9 | 2 | US-09-918-243-35 |
| 3 | 40 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 4 | 40 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 5 | 40 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 6 | 40 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 7 | 40 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 8 | 40 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 9 | 40 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 10 | 40 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 11 | 36 | 90.0 | 9 | 2 | US-09-502-600-33 |
| 12 | 36 | 90.0 | 9 | 2 | US-09-918-243-33 |
| 13 | 34 | 85.0 | 73 | 2 | US-09-205-258-1083 |
| 14 | 34 | 85.0 | 73 | 2 | US-10-004-860-1083 |
| 15 | 34 | 85.0 | 302 | 2 | US-09-393-634-37 |
| 16 | 34 | 85.0 | 424 | 2 | US-09-205-258-1079 |
| 17 | 34 | 85.0 | 424 | 2 | US-10-004-860-1079 |
| 18 | 34 | 85.0 | 569 | 2 | US-09-252-991A-22870 |
| 19 | 34 | 85.0 | 812 | 2 | US-09-489-039A-12075 |
| 20 | 33 | 82.5 | 180 | 2 | US-09-270-767-42872 |
| 21 | 33 | 82.5 | 190 | 1 | US-08-339-152A-19 |
| 22 | 33 | 82.5 | 130 | 1 | US-08-007-999B-6 |
| 23 | 33 | 82.5 | 190 | 1 | US-08-689-276A-6 |
| 24 | 33 | 82.5 | 201 | 2 | US-09-919-039-311 |
| 25 | 33 | 82.5 | 201 | 2 | US-09-391-181-99 |
| 26 | 33 | 82.5 | 201 | 2 | US-09-929-769-5 |
| 27 | 33 | 82.5 | 201 | 2 | US-09-990-444-99 |

28 33 82.5 201 2 US-09-997-333-99 Sequence 99, Appl
29 33 82.5 201 2 US-09-992-598-99 Sequence 99, Appl
30 33 82.5 232 1 US-08-956-047-36 Sequence 36, Appl
31 33 82.5 634 1 US-08-339-152A-17 Sequence 17, Appl
32 33 82.5 653 1 US-08-339-152A-16 Sequence 16, Appl
33 33 82.5 653 1 US-08-007-999B-3 Sequence 3, Appl
34 33 82.5 653 1 US-08-689-276A-3 Sequence 3, Appl
35 33 82.5 2787 2 US-09-245-041-15 Sequence 15, Appl
36 33 82.5 2787 2 US-09-358-055B-15 Sequence 15, Appl
37 33 82.5 2787 2 US-09-893-238-15 Sequence 36, Appl
38 32 80.0 9 2 US-09-502-600-36 Sequence 36, Appl
39 32 80.0 9 2 US-09-918-243-36 Sequence 28, Appl
40 32 80.0 12 2 US-09-502-600-28 Sequence 28, Appl
41 32 80.0 12 2 US-09-918-243-28 Sequence 28, Appl
42 32 80.0 91 2 US-09-605-703B-1574 Sequence 1574, Ap
43 32 80.0 135 2 US-09-270-767-37619 Sequence 37619, A
44 32 80.0 135 2 US-09-270-767-52836 Sequence 52836, A
45 32 80.0 142 2 US-09-248-796A-21399 Sequence 21399, A

ALIGNMENTS

RESULT 1
US-09-502-600-35
; Sequence 35, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
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Db 1 LLPLQLILL 9

RESULT 2
US-09-918-243-35
; Sequence 35, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35

Query Match      100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 1 LLPLQILLL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sturner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 6

US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 7

US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 8

US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
;/ STREET: 3174 Porter Drive
;/ CITY: Palo Alto
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 94304
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: DOS
;/ SOFTWARE: FastSeq for Windows Version 2.0
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/764,762
;/ FILING DATE: 16-Jan-2001
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 09/210,084
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Billings, Lucy J.
;/ REGISTRATION NUMBER: 36,749
;/ REFERENCE/DOCKET NUMBER: PF-0252 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-855-0555
;/ TELEFAX: 415-845-4166
;/ INFORMATION FOR SEQ ID NO: 3:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 253 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ IMMEDIATE SOURCE:
;/ LIBRARY: GenBank
;/ CLONE: 532504
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
Db 6 LLPLQIILL 14

RESULT 9
PCT-US96-04294-2
;/ Sequence 2, Application PC/TUS9604294
;/ GENERAL INFORMATION:
;/ APPLICANT: Dixon, Eric P.
;/ APPLICANT: Johnstone, Edward M.
;/ APPLICANT: Little, Sheila P.
;/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
;/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
;/ NUMBER OF SEQUENCES: 3
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Eli Lilly and Company
;/ STREET: Lilly Corporate Center
;/ CITY: Indianapolis
;/ STATE: Indiana
;/ COUNTRY: United States of America
;/ ZIP: 46285
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US96/04294
;/ FILING DATE:
;/ CLASSIFICATION:

;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/416,257
;/ FILING DATE: 04-APR-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Blalock, Donna K.
;/ REGISTRATION NUMBER: 38,082
;/ REFERENCE/DOCKET NUMBER: X9239
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 317-277-1090
;/ TELEFAX: 317-276-3861
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 253 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
PCT-US96-04294-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
Db 6 LLPLQIILL 14

RESULT 10
US-09-949-016-7716
;/ Sequence 7716, Application US/09949016
;/ Patent No. 6812339
;/ GENERAL INFORMATION:
;/ APPLICANT: VENTER, J. Craig et al.
;/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;/ FILE REFERENCE: CL001307
;/ CURRENT APPLICATION NUMBER: US/09/949,016
;/ CURRENT FILING DATE: 2000-04-14
;/ PRIOR APPLICATION NUMBER: 60/241,755
;/ PRIOR FILING DATE: 2000-10-20
;/ PRIOR APPLICATION NUMBER: 60/237,768
;/ PRIOR FILING DATE: 2000-10-03
;/ PRIOR APPLICATION NUMBER: 60/231,498
;/ PRIOR FILING DATE: 2000-09-08
;/ NUMBER OF SEQ ID NOS: 207012
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 7716
;/ LENGTH: 265
;/ TYPE: PRT
;/ ORGANISM: Human
US-09-949-016-7716

Query Match 100.0%; Score 40; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
Db 18 LLPLQIILL 26

RESULT 11
US-09-502-600-33
;/ Sequence 33, Application US/09502600A
;/ Patent No. 6294344
;/ GENERAL INFORMATION:
;/ APPLICANT: O'Brien, Timothy J.
;/ TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
;/ TITLE OF INVENTION: Ovarian Cancer
;/ FILE REFERENCE: D6223CIP-C
;/ CURRENT FILING DATE: 2000-02-11
;/ CURRENT APPLICATION NUMBER: US/09/502,600A

; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33

Query Match 90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 8
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Db 2 LLPLQILL 9

RESULT 12
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match 90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 8
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Db 2 LLPLQILL 9

RESULT 13
US-09-205-258-1083
; Sequence 1083, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER APPLICATION NUMBER: 60/048,884
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; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
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; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1083

; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1083

Query Match 85.0%; Score 34; DB 2; Length 73;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLLLL 9
|||:|
DB 25 LPLQLLLL 32

RESULT 14
US-10-004-860-1083
; Sequence 1083, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1083
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-1083

Query Match 85.0%; Score 34; DB 2; Length 73;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLLLL 9
|||:|
DB 25 LPLQLLLL 32

RESULT 15
US-09-393-634-37
; Sequence 37, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 302
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR02
; NAME/KEY: MOD_RES
; LOCATION: (143)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-37

Query Match 85.0%; Score 34; DB 2; Length 302;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLLLL 9
|:|:|
DB 42 LPLQLLLL 50

Search completed: March 11, 2006, 01:24:26
Job time : 22.2222 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPLQLLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 40 | 100.0 | 9 | 3 | US-09-918-243-35 |
| 2 | 40 | 100.0 | 9 | 3 | US-09-905-083-35 |
| 3 | 40 | 100.0 | 9 | 4 | US-10-372-521-35 |
| 4 | 40 | 100.0 | 9 | 5 | US-10-831-075-35 |
| 5 | 40 | 100.0 | 136 | 5 | US-10-450-763-53737 |
| 6 | 40 | 100.0 | 198 | 4 | US-10-262-511-96 |
| 7 | 40 | 100.0 | 250 | 4 | US-10-262-511-92 |
| 8 | 40 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 9 | 40 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 10 | 40 | 100.0 | 253 | 4 | US-10-071-214-2 |
| 11 | 40 | 100.0 | 253 | 4 | US-10-071-214-48 |
| 12 | 40 | 100.0 | 253 | 4 | US-10-264-283-90 |
| 13 | 40 | 100.0 | 253 | 4 | US-10-395-027-498 |
| 14 | 40 | 100.0 | 253 | 4 | US-10-173-999-48 |
| 15 | 40 | 100.0 | 253 | 4 | US-10-408-765A-639 |
| 16 | 40 | 100.0 | 253 | 5 | US-10-643-795A-95 |
| 17 | 40 | 100.0 | 253 | 5 | US-10-948-518-95 |
| 18 | 40 | 100.0 | 253 | 5 | US-10-868-490A-1 |
| 19 | 40 | 100.0 | 257 | 4 | US-10-344-394-38 |
| 20 | 38 | 95.0 | 229 | 4 | US-10-425-115-227327 |
| 21 | 36 | 90.0 | 9 | 3 | US-09-918-243-33 |
| 22 | 36 | 90.0 | 9 | 3 | US-09-905-083-33 |
| 23 | 36 | 90.0 | 9 | 4 | US-10-372-521-33 |
| 24 | 36 | 90.0 | 9 | 5 | US-10-831-075-33 |
| 25 | 36 | 90.0 | 70 | 4 | US-10-424-599-207950 |
| 26 | 36 | 90.0 | 637 | 5 | US-10-732-923-928 |
| 27 | 36 | 90.0 | 845 | 4 | US-10-282-122A-51875 |

```

28 36 90.0 868 4 US-10-369-493-10255 Sequence 10255, A
29 35 87.5 23 3 US-09-864-761-46097 Sequence 46097, A
30 35 87.5 58 4 US-10-424-599-234176 Sequence 234176,
31 35 87.5 215 4 US-10-425-115-284316 Sequence 284316,
32 35 87.5 305 4 US-10-335-977-6098 Sequence 6098, Ap
33 35 87.5 306 4 US-10-335-977-6097 Sequence 6097, Ap
34 35 87.5 329 4 US-10-335-977-6099 Sequence 6099, Ap
35 35 87.5 477 4 US-10-335-977-6100 Sequence 6100, Ap
36 35 87.5 480 3 US-09-895-913A-92 Sequence 92, Appl
37 35 87.5 477 4 US-10-335-977-6101 Sequence 6101, Ap
38 35 87.5 637 4 US-10-425-114-70206 Sequence 70206, A
39 35 87.5 637 4 US-10-425-115-294490 Sequence 294490,
40 35 87.5 1498 4 US-10-437-963-121544 Sequence 121544,
41 34 85.0 61 4 US-10-425-115-218429 Sequence 218429,
42 34 85.0 70 4 US-10-097-065-220 Sequence 220, App
43 34 85.0 70 4 US-10-372-876-220 Sequence 220, App
44 34 85.0 73 3 US-09-933-767-1083 Sequence 1083, Ap
45 34 85.0 73 4 US-10-004-860-1083 Sequence 1083, Ap

```

ALIGNMENTS

```

RESULT 1
US-09-918-243-35
; Sequence 35, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35

```

```

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LLPLQLLLL 9
    |||||
Db 1 LLPLQLLLL 9

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```

RESULT 2
US-09-905-083-35
; Sequence 35, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-905-083-35

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPQLILL 9
|||
Db 1 LLPQLILL 9

RESULT 3
US-10-372-521-35
; Sequence 35, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-10-372-521-35

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPQLILL 9
|||
Db 1 LLPQLILL 9

RESULT 4
US-10-831-075-35
; Sequence 35, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-10-831-075-35

Query Match 100.0%; Score 40; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPQLILL 9
|||
Db 1 LLPQLILL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match 100.0%; Score 40; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPQLILL 9
|||
Db 12 LLPQLILL 20

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.

; APPLICANT: Zhong, Mei
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Agee, Michelle L.
 ; APPLICANT: Berghs, Constance
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-462C
 ; CURRENT APPLICATION NUMBER: US/10/262,511
 ; PRIOR FILING DATE: 2003-05-28
 ; PRIOR APPLICATION NUMBER: 60/326,483
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: 60/373,815
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,917
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/381,642
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/328,029
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: 60/381,038
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/328,056
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/373,260
 ; PRIOR FILING DATE: 2002-04-17
 ; PRIOR APPLICATION NUMBER: 60/373,826
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,435
 ; PRIOR FILING DATE: 2001-10-05
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 439
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 96
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-262-511-96

Query Match 100.0%; Score 40; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
 Db 6 LLPLQILL 14

RESULT 7
 US-10-262-511-92
 ; Sequence 92, Application US/10262511
 ; Publication No. US20040038223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Feyman, John A.
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Li, Li
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Ort, Tatiana

; APPLICANT: Gorman, Linda
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Agee, Michelle L.
 ; APPLICANT: Berghs, Constance
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-462C
 ; CURRENT APPLICATION NUMBER: US/10/262,511
 ; CURRENT FILING DATE: 2003-05-28
 ; PRIOR APPLICATION NUMBER: 60/326,483
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: 60/373,815
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,917
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/381,642
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/328,029
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: 60/381,038
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/328,056
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/373,260
 ; PRIOR FILING DATE: 2002-04-17
 ; PRIOR APPLICATION NUMBER: 60/373,826
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,435
 ; PRIOR FILING DATE: 2001-10-05
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 439
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 92
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
 Db 3 LLPLQILL 11

RESULT 8
 US-09-888-615-98
 ; Sequence 98, Application US/09888615
 ; Patent No. US20020064856A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOWMAN, GREGORY
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: CAENEPEL, SEAN
 ; APPLICANT: CHARYDCZAK, GLEN
 ; APPLICANT: MANNING, GERARD
 ; APPLICANT: SUDARSANAM, SUCHA
 ; TITLE OF INVENTION: NOVEL PROTEASES
 ; FILE REFERENCE: 038602/1214
 ; CURRENT APPLICATION NUMBER: US/09/888,615
 ; CURRENT FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 9

US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 10

US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart

; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 11

US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart

; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 12

US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US2003014494A1

GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 13
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 14
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; FILE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 15
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US2004010187A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14
|||

Search completed: March 11, 2006, 01:37:23
Job time : 69.4444 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPQLLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 40 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 2 | 40 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 3 | 40 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 4 | 40 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 5 | 33 | 82.5 | 146 | 7 | US-11-000-463-881 |
| 6 | 33 | 82.5 | 181 | 7 | US-11-000-463-409 |
| 7 | 33 | 82.5 | 213 | 7 | US-11-087-099-8768 |
| 8 | 32 | 80.0 | 71 | 7 | US-11-096-568A-27354 |
| 9 | 32 | 80.0 | 71 | 7 | US-11-096-568A-27391 |
| 10 | 32 | 80.0 | 85 | 7 | US-11-096-568A-27353 |
| 11 | 32 | 80.0 | 85 | 7 | US-11-096-568A-27390 |
| 12 | 32 | 80.0 | 1302 | 6 | US-10-395-561-1024 |
| 13 | 31 | 77.5 | 93 | 7 | US-11-230-180-12 |
| 14 | 31 | 77.5 | 140 | 6 | US-10-821-234-1347 |
| 15 | 31 | 77.5 | 213 | 7 | US-11-203-251A-93 |
| 16 | 31 | 77.5 | 278 | 6 | US-10-131-826A-136 |
| 17 | 31 | 77.5 | 278 | 6 | US-10-973-115B-136 |
| 18 | 31 | 77.5 | 328 | 6 | US-10-501-035-268 |
| 19 | 31 | 77.5 | 328 | 7 | US-11-169-041-227 |
| 20 | 31 | 77.5 | 328 | 7 | US-11-072-175-232 |
| 21 | 31 | 77.5 | 461 | 6 | US-10-878-556A-162 |
| 22 | 31 | 77.5 | 465 | 6 | US-10-793-626-1676 |
| 23 | 31 | 77.5 | 469 | 6 | US-10-821-234-1151 |
| 24 | 31 | 77.5 | 480 | 6 | US-10-821-234-1465 |
| 25 | 31 | 77.5 | 498 | 7 | US-11-051-720-1355 |

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|----|----|------|-----|---|----------------------|-------------------|
| 26 | 31 | 77.5 | 499 | 6 | US-10-508-263-94 | Sequence 94, Appl |
| 27 | 31 | 77.5 | 505 | 7 | US-11-051-720-1357 | Sequence 1357, Ap |
| 28 | 31 | 77.5 | 519 | 7 | US-11-051-720-1350 | Sequence 1350, Ap |
| 29 | 31 | 77.5 | 541 | 7 | US-11-051-720-1351 | Sequence 1351, Ap |
| 30 | 31 | 77.5 | 541 | 7 | US-11-096-568A-20889 | Sequence 20889, A |
| 31 | 31 | 77.5 | 544 | 7 | US-11-051-720-1352 | Sequence 1352, Ap |
| 32 | 31 | 77.5 | 588 | 7 | US-11-051-720-1356 | Sequence 1356, Ap |
| 33 | 31 | 77.5 | 597 | 7 | US-11-051-720-1354 | Sequence 1354, Ap |
| 34 | 31 | 77.5 | 619 | 7 | US-11-051-720-1353 | Sequence 1353, Ap |
| 35 | 31 | 77.5 | 650 | 7 | US-11-051-720-1439 | Sequence 1439, Ap |
| 36 | 30 | 75.0 | 256 | 7 | US-11-072-512-3255 | Sequence 3255, Ap |
| 37 | 30 | 75.0 | 434 | 7 | US-11-087-099-2216 | Sequence 2216, Ap |
| 38 | 30 | 75.0 | 478 | 7 | US-11-092-353-4 | Sequence 4, Appli |
| 39 | 30 | 75.0 | 544 | 7 | US-11-245-400-7 | Sequence 7, Appli |
| 40 | 30 | 75.0 | 558 | 7 | US-11-096-568A-26217 | Sequence 26217, A |
| 41 | 29 | 72.5 | 125 | 7 | US-11-096-568A-23862 | Sequence 23862, A |
| 42 | 29 | 72.5 | 184 | 7 | US-11-096-568A-5642 | Sequence 5642, Ap |
| 43 | 29 | 72.5 | 239 | 7 | US-11-096-568A-5641 | Sequence 5641, Ap |
| 44 | 29 | 72.5 | 264 | 7 | US-11-096-568A-5640 | Sequence 5640, Ap |
| 45 | 29 | 72.5 | 349 | 7 | US-11-096-568A-14701 | Sequence 14701, A |

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

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| Query Match | | 100.0% | Score 40; | DB 6; | Length 253; |
| Best Local Similarity | | 100.0% | Pred. No. 1.7; | | |
| Matches | | 9; | Conservative | 0; | Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 | LLPLQLLLL | 9 | | |
| Db | 6 | LLPLQLLLL | 14 | | |

RESULT 2
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; PRIOR FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 5
US-11-000-463-881
; Sequence 881, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-881

Query Match      82.5%; Score 33; DB 7; Length 146;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 7 LLPLHLLL 15

RESULT 6
US-11-000-463-409
; Sequence 409, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
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FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
PRIOR FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 409
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-409

Query Match 82.5%; Score 33; DB 7; Length 181;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
||| :|||
Db 7 LLPLHLLLL 15

RESULT 7

US-11-087-099-8768
Sequence 8768, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 8768
LENGTH: 213
TYPE: PRT
ORGANISM: Zea mays
US-11-087-099-8768

Query Match 82.5%; Score 33; DB 7; Length 213;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
||| :|||
Db 39 LLPLSLLLL 47

RESULT 8

US-11-096-568A-27354
Sequence 27354, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27354

LENGTH: 71
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(71)
OTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354

Query Match 80.0%; Score 32; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIL 7
||| :|||
Db 2 LLPLQIL 8

RESULT 9

US-11-096-568A-27391
Sequence 27391, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27391
LENGTH: 71
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(71)
OTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391

Query Match 80.0%; Score 32; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIL 7
||| :|||
Db 2 LLPLQIL 8

RESULT 10

US-11-096-568A-27353
Sequence 27353, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27353
LENGTH: 85
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(85)
OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353

Query Match 80.0%; Score 32; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIL 7
Db 16 LLPLQIL 22

RESULT 11

US-11-096-568A-27390
; Sequence 27390, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27390
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)-(85)
; OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390

Query Match 80.0%; Score 32; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIL 7
Db 16 LLPLQIL 22

RESULT 12

US-10-995-561-1024
; Sequence 1024, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1024
; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1024

Query Match 80.0%; Score 32; DB 6; Length 1302;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 13 LLPLPLLL 21

RESULT 13

US-11-230-180-12
; Sequence 12, Application US/11230180
; Publication No. US20060035263A1
; GENERAL INFORMATION:
; APPLICANT: Woolf, Clifford J.

; APPLICANT: Samad, Tarek A.
; TITLE OF INVENTION: DRGL1-RESPONSIVE (DRAGON) GENE FAMILY
; FILE REFERENCE: 00786/419002
; CURRENT APPLICATION NUMBER: US/11/230,180
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/10/419,296
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,519
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-230-180-12

Query Match 77.5%; Score 31; DB 7; Length 93;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 9 LLPLLLLL 17

RESULT 14

US-10-821-234-1347
; Sequence 1347, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PE_SEQ_genes Version 1.0
; SEQ ID NO 1347
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1347

Query Match 77.5%; Score 31; DB 6; Length 140;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 88 LLPPQLLL 96

RESULT 15

US-11-203-251A-93
; Sequence 93, Application US/11203251A
; Publication No. US20060039904A1
; GENERAL INFORMATION:
; APPLICANT: MedImmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR FC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; FILE REFERENCE: AE702US
; CURRENT APPLICATION NUMBER: US/11/203,251A
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601,634
; PRIOR FILING DATE: 2004-08-16

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; PRIOR APPLICATION NUMBER: 60/608,852
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-203-251A-93
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Query Match      77.5%; Score 31; DB 7; Length 213;
Best Local Similarity 77.8%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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      ||| :|||
Db      8 LLPLLLLLL 16
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Search completed: March 11, 2006, 01:38:41
Job time : 8 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 40 | 100.0 | 9 | 4 AAE08241 | Aae08241 Human str |
| 2 | 40 | 100.0 | 9 | 8 ADR68797 | Adr68797 Human str |
| 3 | 40 | 100.0 | 136 | 4 ABG23378 | Abg23378 Novel hum |
| 4 | 40 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 5 | 40 | 100.0 | 198 | 8 ADN62900 | Adn62900 Human NOV |
| 6 | 40 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 7 | 40 | 100.0 | 250 | 8 ADN62896 | Adn62896 Human NOV |
| 8 | 40 | 100.0 | 253 | 2 AAR67888 | Aar67888 Human str |
| 9 | 40 | 100.0 | 253 | 2 AAW05383 | Aaw05383 Human amy |
| 10 | 40 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 11 | 40 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 12 | 40 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 13 | 40 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 14 | 40 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 15 | 40 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |
| 16 | 40 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 17 | 40 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 18 | 40 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/an |
| 19 | 40 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 20 | 40 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antiporin |
| 21 | 40 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 22 | 40 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 23 | 40 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 24 | 40 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |

| | | | | | |
|----|----|------|-----|------------|--------------------|
| 25 | 36 | 90.0 | 9 | 4 AAE08238 | Aae08238 Human str |
| 26 | 36 | 90.0 | 9 | 8 ADR68794 | Adr68794 Human str |
| 27 | 35 | 87.5 | 138 | 8 ADX90484 | Adx90484 Plant ful |
| 28 | 35 | 87.5 | 868 | 8 ADS21222 | Ads21222 Bacterial |
| 29 | 34 | 85.0 | 61 | 4 AAO12472 | Aao12472 Human pol |
| 30 | 34 | 85.0 | 812 | 7 ABO65558 | Abo65558 Klebsiell |
| 31 | 33 | 82.5 | 394 | 6 ABU17803 | Abu17803 Protein e |
| 32 | 33 | 82.5 | 397 | 7 ADJ71036 | Adj71036 Human hea |
| 33 | 33 | 82.5 | 804 | 6 ABP70828 | Abp70828 Murine C1 |
| 34 | 32 | 80.0 | 9 | 4 AAE08240 | Aae08240 Human str |
| 35 | 32 | 80.0 | 9 | 4 AAE08320 | Aae08320 Human str |
| 36 | 32 | 80.0 | 9 | 8 ADR68877 | Adr68877 Human str |
| 37 | 32 | 80.0 | 9 | 8 ADR68796 | Adr68796 Human str |
| 38 | 32 | 80.0 | 71 | 4 AAM89706 | Aam89706 Human imm |
| 39 | 32 | 80.0 | 73 | 4 ABG19347 | Abg19347 Novel hum |
| 40 | 32 | 80.0 | 78 | 8 ADL81901 | Adl81901 P. aerugi |
| 41 | 32 | 80.0 | 139 | 7 ADB65713 | Adb65713 Human pro |
| 42 | 32 | 80.0 | 196 | 7 ADJ92327 | Adj92327 Mouse hai |
| 43 | 32 | 80.0 | 267 | 2 AAW22303 | Aaw22303 Rat CRTI. |
| 44 | 32 | 80.0 | 267 | 8 ADL27274 | Adl27274 Amino aci |
| 45 | 32 | 80.0 | 282 | 7 ADD30604 | Add30604 Plant yie |

ALIGNMENTS

RESULT 1

| | | |
|----------|----|--|
| AAE08241 | ID | AAE08241 standard; peptide; 9 AA. |
| XX | AC | AAE08241; |
| XX | DT | 01-NOV-2001 (first entry) |
| XX | DE | Human stratum corneum chymotrypsin enzyme peptide #6 (residues 4-12). |
| XX | KW | Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; |
| KW | KW | cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; |
| KW | KW | antisense therapy; malignant hyperplasia. |
| XX | OS | Homo sapiens. |
| XX | PN | WO200159158-A1. |
| XX | PD | 16-AUG-2001. |
| XX | PF | 07-FEB-2001; 2001WO-US003977. |
| XX | PR | 11-FEB-2000; 2000US-00502600. |
| XX | XX | (UYAR-) UNIV ARKANSAS. |
| XX | PI | O'brien TJ; |
| XX | DR | WPI; 2001-514676/56. |
| XX | PT | Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme. |
| XX | PS | Claim 25; Page 103; 127pp; English. |
| XX | CC | The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide |
| XX | SQ | Sequence 9 AA; |

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 2
ADR68797
ID ADR68797 standard; peptide; 9 AA.
XX
AC ADR68797;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:36.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
XX WPI; 2004-653294/63.
DR
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX
PS Claim 5; SEQ ID NO 36; 117pp; English.
XX
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS87565.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 136 AA;

Query Match 100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.9; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 10 SLLPLQL 18

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX

09-OCT-2001; 2001US-0328044P.
 09-OCT-2001; 2001US-0328056P.
 12-OCT-2001; 2001US-0328849P.
 15-OCT-2001; 2001US-0329414P.
 17-OCT-2001; 2001US-0330142P.
 18-OCT-2001; 2001US-0330309P.
 22-OCT-2001; 2001US-0341058P.
 24-OCT-2001; 2001US-0339266P.
 29-OCT-2001; 2001US-0343629P.
 29-OCT-2001; 2001US-0349375P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
 16-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383656P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 (SMIT/) SMITHSON G.
 (MILL/) MILLET I.
 (PEYM/) PEYMAN J A.
 (KEKU/) KEKUDA R.
 (JUJ/) JU J.
 (LILL/) LI L.
 (GUOX/) GUO X.
 (PATT/) PATTURAJAN M.
 (SPYT/) SPYTEK K A.
 (EDIN/) EDINGER S R.
 (ELLE/) ELLERMAN K.
 (MALY/) MALYANKAR U M.
 (ORTT/) ORT T.
 (GORM/) GORMAN L.
 (ZERR/) ZERHUSEN B D.
 (ANDE/) ANDERSON D W.
 (ZHON/) ZHONG M.
 (CATT/) CATTERTON E.
 (JIWW/) JI W.
 (MILL/) MILLER C E.
 (RAST/) RASTELLI L.
 (STON/) STONE D J.
 (PENA/) PENA C E A.
 (SHEN/) SHENOY S G.
 (SHIM/) SHIMKETS R A.
 (ROTH/) ROTHENBERG M E.
 (LEAC/) LEACH M D.
 (AGEE/) AGEE M L.
 (BERG/) BERGHS C.
 (DIPI/) DIPPO V A.
 (EISE/) EISEN A.
 (GANG/) GANGOLLI E A.
 (RIEG/) RIEGER D K.
 (SPAD/) SPADERNA S K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI: 2004-213931/20.
 N-PSDB; ADN62899.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 40; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db 4 SLLPLQL 12
 RESULT 6
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX
 AC ADA05732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18a protein SEQ ID NO:92.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328949P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 23-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Smithson G, Millet I, Feyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Or T, Gorman L, Zehusien BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergins C, Dippio VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2003-381626/36.
 DR N-PSDB; ADA05731.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; Page 169-170; 586pp; English.
 XX
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cyrostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antileptemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 40; DB 6; Length 250;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLLPLQIL 9
 Db 1 SLLPLQIL 9
 RESULT 7
 ADN62896
 ID ADN62896 standard; protein; 250 AA.
 XX
 AC ADN62896;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18a.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 01-OCT-2002; 2002US-00262511.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.

(PEYM/) PEYMAN J A.
 (KEKU/) KEKUDA R.
 (JUJU/) JU J.
 (LILL/) LI L.
 (GUOX/) GUO X.
 (PATT/) PATTURAJAN M.
 (SPYT/) SPYTEK K A.
 (EDIN/) EDINGER S R.
 (ELLE/) ELLERMAN K.
 (MALY/) MALYANKAR U M.
 (ORTT/) ORT T.
 (GORM/) GORMAN L.
 (ZERH/) ZERHUSEN B D.
 (ANDE/) ANDERSON D W.
 (ZHON/) ZHONG M.
 (CATT/) CATTERTON E.
 (JIWW/) JI W.
 (MILL/) MILLER C E.
 (RAST/) RASTELLI L.
 (STON/) STONE D J.
 (PENA/) PENNA C E A.
 (SHEN/) SHENOY S G.
 (SHIM/) SHIMKETS R A.
 (ROTH/) ROTHENBERG M E.
 (LEAC/) LEACH M D.
 (AGEE/) AGEE M L.
 (BERG/) BERGHS C.
 (DIPI/) DIPIPPO V A.
 (EISE/) EISEN A.
 (GANG/) GANGOLLI E A.
 (RIEG/) RIEGER D K.
 (SPAD/) SPADERNA S K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI; 2004-213931/20.
 N-PSDB; ADN62895.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 Claim 1; SEQ ID NO 92; 395pp; English.
 The invention relates to isolated NOVX polypeptides and polynucleotides.
 NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 treat a medical condition in human related to the aberrant expression and
 activity of NOVX polypeptides. For example, NOVX polypeptides and
 polynucleotides may be used to treat disorders associated with decreased
 expression or activity of NOVX by supplementing the patient our
 production or to rectify mutations. Conversely, antisense NA molecules
 may be administered to down regulate expression of NOVX polypeptides by
 binding with the cells own genes and preventing their expression. NOVX
 polynucleotides and complementary sequences may also be used as DNA
 probes in diagnostic assays to detect and quantitate the presence of
 similar sequences in samples, and so which patients may be in need of
 restorative therapy. NOVX polypeptides may also be used as antigens in
 the production of antibodies and in assays to identify modulators
 (agonists and antagonists) of the expression and activity of NOVX. The
 anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 used to modulate NOVX polynucleotide expression and activity of NOVX
 polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 diagnostic agents for detecting the presence of NOVX in samples. NOVX
 polypeptides and polynucleotides may be used in this way to prevent,
 diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 disorders, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,
 haematopoietic disorders, and the various dyslipidaemias, metabolic
 disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX

SQ Sequence 250 AA;

Query Match 100.0%; Score 40; DB 8; Length 250;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
 |||||
 Db 1 SLLPLQL 9

RESULT 8

AAR67888
 ID AAR67888 standard; protein; 253 AA.

XX

AC AAR67888;

XX 25-MAR-2003 (revised)

DT 09-AUG-1995 (first entry)

XX

DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).

XX

KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;

KW callosities; keratosis pilaris; ichthyoses; eczema.

XX

OS Homo sapiens.

XX

PN WO9500651-A1.

XX

PD 05-JAN-1995.

XX

PF 20-JUN-1994; 94WO-IB000166.

XX

PR 18-JUN-1993; 93DK-00000725.

XX

PA (SYMB-) SYMBICOM AB.

XX

PI Egelrud T, Hansson L;

XX

DR WPI; 1995-052088/07.

XX

DR N-PSDB; AAQ81203.

XX

PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
 PT related vectors, transformed cells and polypeptides, useful for treating
 PT skin disorders, e.g. acne or psoriasis, and for identification of
 PT specific inhibitors.
 XX

PS Disclosure; Page 97; 137pp; English.

XX

CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
 CC and skin care products, especially to treat and prevent acne, xeroderma,
 CC or other hyperkeratotic conditions (e.g. callosities or keratosis
 CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
 CC recombinantly following mammal, insect, plant, or microorganism
 CC transformation with plasmid pBS07. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX

SQ Sequence 253 AA;

Query Match 100.0%; Score 40; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
 |||||
 Db 4 SLLPLQL 12

RESULT 9

```

AAW05383
ID AAW05383 standard; protein; 253 AA.
XX
XX AAW05383;
XX AC
XX 31-DEC-1996 (first entry)
XX DT
XX DE Human amyloid precursor protein protease.
XX
XX Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
XX KW therapy.
XX KW
XX OS Homo sapiens.
XX
XX WO9631122-A1.
XX PN
XX
XX 10-OCT-1996.
XX PD
XX 02-APR-1996; 96WO-US004294.
XX PF
XX 04-APR-1995; 95US-00416257.
XX PR
XX (ELIL ) LILLY & CO ELI.
XX PA
XX Dixon EP, Johnstone EM, Little SP;
XX PI
XX WPI; 1996-464694/46.
XX DR
XX N-PSDB; AAT39783.
XX
XX New isolated human amyloid precursor protein protease - used to develop
XX PT prods. for the treatment or diagnosis of associated conditions, esp.
XX PT Alzheimer's disease.
XX
XX Claim 1; Page 44-45; 55pp; English.
XX PS
XX
XX Human amyloid precursor protein protease (AAW05383) is involved in the
XX CC processing or clearance of amyloid precursor protein to form beta-amyloid
XX CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
XX CC obt'd. from a human lung library. Recombinant protease can be produced in
XX CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
XX CC (partic. AV-120 host cells. It is used to develop products for the design
XX CC and testing of cpds. useful for treating or preventing conditions
XX CC associated with beta-amyloid peptide, esp. Alzheimer's disease
XX
XX Sequence 253 AA;
SQ
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
Db 4 SLLPLQL 12
|||||
|
RESULT 10
ID ABB84421
XX ABB84421 standard; peptide; 253 AA.
XX
XX ABB84421;
XX AC
XX
XX 08-NOV-2002 (first entry)
XX DT
XX Human SCCE protein N-terminal fragment SEQ ID 48.
XX DE
XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
XX KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
XX KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
XX KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
XX Homo sapiens.
XX OS
XX WO200262135-A2.
XX PN

15-AUG-2002.
08-FEB-2002; 2002WO-IB001300.
09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
(EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
XX Egelrud T, Hansson L;
XX
XX WPI; 2002-643380/69.
XX
Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
XX Example 6; Page 37; 74pp; English.
XX
This invention describes a novel non-human transgenic mammal or mammalian
XX embryo having integrated within its genome, a heterologous nucleotide
XX sequence comprising at least a significant part of a nucleotide sequence
XX coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
XX operably linked to a promoter that drives expression of heterologous scce
XX or its variant in skin. The product of the invention is useful as a model
XX for the study of disease with the aim of improving treatment, to relieve
XX or ameliorate a pathogenic condition, for development or testing of a
XX cosmetic or a pharmaceutical formulation, and for the development of a
XX diagnostic method. It can also be used as a model for a skin disease or
XX skin cancer. The invention is also useful for screening or identifying a
XX compound or composition effective for the prevention or treatment of an
XX abnormal or unwanted phenotype, and for screening or identifying a
XX compound or composition effective for the prevention or treatment of
XX inflammatory skin diseases selected from diseases consisting of epidermal
XX hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
XX pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
XX with epidermal hyperkeratosis. The mammal of the invention is also useful
XX as a model for further studies of itch mechanisms and the testing of
XX potential compounds and compositions for relieve of various skin diseases
XX where itch is a component. This sequence represents the N-terminal
XX fragment of the human stratum corneum chymotryptic enzyme, SCCE
XX synonymous with human kallikrein 7 (KLK7), used in the development of the
XX transgenic mammals described in the invention
XX
XX Sequence 253 AA;
SQ
Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
Db 4 SLLPLQL 12
|||||
|
RESULT 11
ID ABB84406
XX ABB84406 standard; protein; 253 AA.
XX
XX ABB84406;
XX AC
XX
XX 08-NOV-2002 (first entry)
XX DT
XX Human SCCE protein.
XX DE
XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
XX KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
XX KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
XX KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
XX Homo sapiens.
XX OS

```

XX WO200262135-A2.
PN 15-AUG-2002.
XX 08-FEB-2002; 2002WO-IB001300.
XX PF 09-FEB-2001; 2001CA-02332655.
XX PR 09-FEB-2001; 2001DK-00000218.
XX (EGL/) EGBLUD T.
PA (HANS/) HANSSON L.
XX Egelrud T, Hansson L;
PI WPI; 2002-643380/69.
DR N-PSDB; ABQ76226.
XX Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX Claim 10; Page 58-59; 74pp; English.
XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the human stratum
CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
CC with human kallikrein 7 (KLK7) and is used in the development of the
CC transgenic mammals described in the invention
XX Sequence 253 AA;
SQ Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
Db 4 SLLPLQL 12
RESULT 12
AAU82740
ID AAU82740 standard; protein; 253 AA.
XX AC AAU82740;
XX 23-APR-2002 (first entry)
DT Amino acid sequence of novel human protease #39.
DE Human; protease; cancer; immune-related disorder; cardiovascular disease;
XX neuronal-associated disease; metabolic disorder; inflammatory disorder;
KW nervous system disorder; sexual dysfunction; pain; mood disorder;
XX

KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
XX ocular disease; cytostatic; enzyme.
OS Homo sapiens.
XX WO200200860-A2.
XX 03-JAN-2002.
XX 26-JUN-2001; 2001WO-US020171.
XX 26-JUN-2000; 2000US-0214047P.
XX (SUGE-) SUGEN INC.
XX Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Charyczak G;
XX WPI; 2002-139913/18.
DR N-PSDB; ABK31782.
XX Nucleic acids encoding novel human proteases, useful for useful for
PT treating diseases and disorders such as cancers, immune-related diseases
PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
PT disorders.
XX Claim 6; Fig 2N; 313pp; English.
XX The present invention relates to the isolation of novel human proteases,
CC and the nucleic acids encoding them. The sequences of the invention are
CC useful for treating diseases and disorders such as cancers (e.g. breast,
CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
CC disorders, neurological disorders, hypotension, hypertension, psychotic
CC disease) and dyskinesias. The nucleic acids and polypeptides are also
CC useful for treating viral infections caused by human immunodeficiency
CC virus (HIV), and non-viral infections such as ocular disease (e.g.
CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
CC human proteases of the invention
XX Sequence 253 AA;
SQ Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
Db 4 SLLPLQL 12
RESULT 13
ABU07440
ID ABU07440 standard; protein; 253 AA.
XX AC ABU07440;
XX 28-JAN-2003 (first entry)
DT Protein differentially regulated in prostate cancer #43.
DE Prostate cancer; gene expression; differential regulation;
XX molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX Homo sapiens.
XX

PN WO200281638-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US010824.
 XX
 PR 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 PI Sun Z, Jay G;
 XX
 DR WPI; 2003-058520/05.
 DR N-PSDB; ABX10343.
 XX
 PT Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX
 PS Claim 1; Page 293-294; 416pp; English.
 XX
 CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db 4 SLLPLQL 12
 RESULT 14
 ABU07471
 ID ABU07471 standard; protein; 253 AA.
 XX
 AC ABU07471;

XX 28-JAN-2003 (first entry)
 XX Protein differentially regulated in prostate cancer #74.
 XX Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX
 OS Homo sapiens.
 PN WO200281638-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US010824.
 XX
 PR 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 PI Sun Z, Jay G;
 XX
 DR WPI; 2003-058520/05.
 DR N-PSDB; ABX10375.
 XX
 PT Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX
 PS Claim 1; Page 351; 416pp; English.
 XX
 CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 SLLPLQIL 9
Db      4 SLLPLQIL 12

RESULT 15
ABR58471
ID  ABR58471 standard; protein; 253 AA.
XX
XX  AC  ABR58471;
XX  DT  07-JUL-2003 (first entry)
XX  DE  Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX  KW  Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX  OS  Homo sapiens.
XX  PN  WO2003029468-A1.
XX  PD  10-APR-2003.
XX  PF  02-OCT-2002; 2002WO-US031467.
XX  PR  02-OCT-2001; 2001US-032713SP.
XX  PR  30-MAY-2002; 2002US-0384531P.
XX  PA  (CORI-) CORIXA CORP.
XX  PI  Algate PA, Mannion J;
XX  DR  WPI; 2003-372001/35.
XX  PT  New polynucleotide and polypeptide useful for diagnosing and/or treating
XX  PT  cancer, particularly ovarian cancer, and as a vaccine.
XX  PS  Claim 2; Page 157-158; 169pp; English.
XX  CC  The invention relates to a novel isolated polynucleotide. The
XX  CC  polynucleotides of the invention have cytostatic activity, and may have a
XX  CC  use in gene therapy, and in a vaccine. The composition and methods are
XX  CC  useful in diagnosing and/or treating cancer, particularly ovarian cancer.
XX  CC  The composition may also be used as a vaccine to prevent cancer. The
XX  CC  present sequence is used in the exemplification of the invention
XX  SQ  Sequence 253 AA;

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLPLQIL 9
Db      4 SLLPLQIL 12

Search completed: March 11, 2006, 00:24:16
Job time : 88.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 40 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 38 | 95.0 | 146 | 2 H75201 | hypothetical prote |
| 3 | 33 | 82.5 | 370 | 2 AB3334 | daunorubicin resis |
| 4 | 32 | 80.0 | 218 | 2 T02912 | probable transcrip |
| 5 | 32 | 80.0 | 264 | 2 C97402 | probable acyltrans |
| 6 | 32 | 80.0 | 266 | 2 AC2620 | 1-acyl-sn-glycerol |
| 7 | 32 | 80.0 | 266 | 2 JC7300 | tax-responsive ele |
| 8 | 32 | 80.0 | 267 | 2 JC4857 | hepatocarcinogenes |
| 9 | 32 | 80.0 | 282 | 2 B85327 | probable transcrip |
| 10 | 32 | 80.0 | 494 | 2 C43349 | probable succinogl |
| 11 | 32 | 80.0 | 494 | 2 B95976 | probable transport |
| 12 | 32 | 80.0 | 582 | 2 S40176 | Exor protein - Rhl |
| 13 | 32 | 80.0 | 622 | 2 S61692 | probable membrane |
| 14 | 31 | 77.5 | 196 | 2 G65039 | hypothetical prote |
| 15 | 31 | 77.5 | 303 | 2 C84914 | hypothetical prote |
| 16 | 31 | 77.5 | 354 | 2 T48649 | glycerol-3-phospha |
| 17 | 31 | 77.5 | 372 | 2 A98157 | probable permease |
| 18 | 31 | 77.5 | 372 | 2 AB3130 | ABC transporter, m |
| 19 | 31 | 77.5 | 392 | 2 D83934 | hypothetical prote |
| 20 | 31 | 77.5 | 395 | 2 D69779 | antibiotic resista |
| 21 | 31 | 77.5 | 398 | 2 C91063 | hypothetical prote |
| 22 | 31 | 77.5 | 401 | 2 B90120 | SNF1-related prote |
| 23 | 31 | 77.5 | 413 | 2 AC0834 | probable membrane |
| 24 | 31 | 77.5 | 470 | 2 A90083 | hypothetical prote |
| 25 | 31 | 77.5 | 475 | 1 A69149 | O-antigen transpor |
| 26 | 31 | 77.5 | 754 | 2 AE0614 | probable competenc |
| 27 | 31 | 77.5 | 783 | 2 A46136 | myosin-heavy-chain |
| 28 | 31 | 77.5 | 913 | 2 AC2445 | hypothetical prote |
| 29 | 30 | 75.0 | 155 | 2 I45913 | interleukin-2 prec |

| | | | | |
|----|------|-----|----------|--------------------|
| 30 | 75.0 | 155 | 2 S38662 | interleukin-2 - go |
| 31 | 75.0 | 155 | 2 S11488 | interleukin-2 prec |
| 32 | 75.0 | 168 | 2 E96979 | probable membrane |
| 33 | 75.0 | 189 | 2 T43766 | hypothetical prote |
| 34 | 75.0 | 190 | 2 T39622 | probable phosphate |
| 35 | 75.0 | 208 | 2 T17092 | NADH2 dehydrogenas |
| 36 | 75.0 | 214 | 1 G69798 | hypothetical prote |
| 37 | 75.0 | 223 | 2 F83598 | cell division prot |
| 38 | 75.0 | 277 | 2 H84314 | cytochrome a3 con |
| 39 | 75.0 | 289 | 2 T43663 | probable high affi |
| 40 | 75.0 | 333 | 1 HLHUCB | T-cell surface gly |
| 41 | 75.0 | 349 | 2 E82656 | conserved hypothet |
| 42 | 75.0 | 369 | 2 S35603 | surfactant protein |
| 43 | 75.0 | 371 | 1 JN0450 | conglutinin precu |
| 44 | 75.0 | 371 | 2 I45878 | conglutinin - bovi |
| 45 | 75.0 | 375 | 2 S47704 | hypothetical 41.1K |

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A53968
R:Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A:Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A:Reference number: A53968; MUID:94308225; PMID:8034709
A:Accession: A53968
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <HAN>
A:Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:GS21214; PIDN:?
C:Genetics:
A:Gene: GDB:PRSS6; SCCE
A:Cross-references: GDB:377730
A:Map position: 7q35-7q35
C:Superfamily: trypsin; trypsin homology
F:30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 SLLPLQL 9
|||
DB 4 SLLPLQL 12
|||

RESULT 2

H75201
hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75201
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: H75201
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <KAM>
A:Cross-references: UNIPROT:Q9V2D5; UNIPARC:UPI0000063243; GB:AJ248283; GB:AL096836; NID:
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0088
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

Query Match 95.0%; Score 38; DB 2; Length 146;
 Best Local Similarity 88.9%; Pred. No. 2.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQL 9
 :|||||:
 Db 66 SLLPLQL 74

RESULT 3
 AB3334
 daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain 1
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AB3334
 R:DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujeer, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goldtman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AB3334
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <KUR>
 A:Cross-references: UNIPROT:Q8YHY9; UNIPARC:UPI0000057D7A; GB:AE008917;
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0656
 A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 370;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
 :|||||:
 Db 293 ILLPLQVL 300

RESULT 4
 T02912
 probable transcription factor MYB41 [similarity] - Arabidopsis thaliana (fragment)
 N:Alternate names: protein T1J38.220
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Oct-2004
 C:Accession: T02912; T51654
 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuel
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z14766
 A:Accession: T02912
 A:Molecule type: DNA
 A:Residues: 1-218 <BEV>
 A:Cross-references: UNIPROT:Q9ZTE3; UNIPARC:UPI00000A46AC; EMBL:AL035524
 A:Experimental source: cultivar Columbia; BAC clone T13J8
 R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
 Paz-Ares, J.; Weisshaar, B.
 Plant J. 16, 263-276, 1998
 A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
 A:Reference number: Z14349; MUID:9839469; PMID:9839469
 A:Accession: T51654
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-218 <KRA>
 A:Cross-references: UNIPARC:UPI00000A46AC; EMBL:AF062882; PIDN:AAC83604.1
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: MYB41
 A:Map position: 4
 A:Note: T13J8.220
 A:Note: intron positions not resolved
 C:Keywords: transcription factor
 F:1-48/Domain: myb DNA-binding repeat homology (fragment) <MYB>

Query Match 80.0%; Score 32; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
 :|||||:
 Db 104 SLLPLQ 110

RESULT 5
 C97402
 probable acyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58,
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
 C:Accession: C97402
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C97402
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <KUR>
 A:Cross-references: UNIPROT:Q8UIE2; UNIPARC:UPI00000D17A6; GB:AE007869; PIDN:AAK86172.1;
 C:Genetics:
 A:Gene: AGR_C 621
 A:Map position: circular chromosome
 C:Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase

Query Match 80.0%; Score 32; DB 2; Length 264;
 Best Local Similarity 75.0%; Pred. No. 67;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
 :|||||:
 Db 19 ILLPLQLL 26

RESULT 6
 AC2620
 1-acyl-sn-glycerol-3-phosphate acyltransferase pIsC [imported] - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
 C:Accession: AC2620
 R:Wood, D.W.; Scubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AC2620
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <KUR>
 A:Cross-references: UNIPROT:Q8UIE2; UNIPARC:UPI00000D17A6; GB:AE008688; PIDN:AAL41377.1;
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: pIsC
 A:Map position: circular chromosome
 C:Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase

Query Match 80.0%; Score 32; DB 2; Length 264;
 Best Local Similarity 75.0%; Pred. No. 67;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
 :|||||:
 Db 19 ILLPLQLL 26

RESULT 7
JC7300
tax-responsive element-binding protein 5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JC7300
R:Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
DNA Res. 7, 187-193, 2000
A:Title: Isolation and characterization of the gene encoding mouse tax-responsive element
A:Reference number: JC7300
A:Accession: JC7300
A:Molecule type: mRNA
A:Residues: 1-266 <MAS>
A:Cross-references: UNIPROT:Q9ES53; UNIPARC:UPI00000E73B0; DDBJ:AB036745
C:Genetics:
A:Gene: trebs
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor

Query Match 80.0%; Score 32; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLPLQL 9
|||
Db 187 LLPLQL 193

RESULT 8
JC4857
hepatocarcinogenesis-related transcription factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4857
R:Kishimoto, T.; Kikura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
Biochem. Biophys. Res. Commun. 224, 746-751, 1996
A:Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREB
A:Reference number: JC4857
A:Accession: JC4857
A:Molecule type: mRNA
A:Residues: 1-267 <KIS>
A:Cross-references: UNIPROT:Q9R1S4; UNIPARC:UPI00000E80AD
C:Comment: This is a basic-leucine zipper type transcription factor involved in hepatocarcinogenesis
C:Genetics:
A:Gene: htf
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor
F:58-98/Domain: fos/jun DNA-binding domain homology <FJD>
F:89-126/Region: leucine zipper motif

Query Match 80.0%; Score 32; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLPLQL 9
|||
Db 188 LLPLQL 194

RESULT 9
B85327
probable transcription factor MYB41 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C:Accession: B85327
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: B85327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>

A:Cross-references: UNIPROT:Q9M0J5; UNIPARC:UPI00000BD4E; GB:NC_001268; NID:G7269665; P
C:Genetics:
A:Gene: AT4g28110
A:Map position: 4
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 80.0%; Score 32; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
|||
Db 168 SLLPLQ 174

RESULT 10
C49349
probable succinoglycan transport protein ExoT - Rhizobium meliloti
C:Species: Rhizobium meliloti
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: C49349
R:Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J. Bacteriol. 175, 7045-7055, 1993
A:Title: Genes needed for the modification, polymerization, export, and processing of suc
A:Reference number: A49349; MUID:94042870; PMID:8226646
A:Accession: C49349
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <GLU>
A:Cross-references: UNIPROT:P33699; UNIPARC:UPI000012A381; GB:L20758; NID:G393240; PIDN:
C:Superfamily: hypothetical protein b2046
C:Keywords: transmembrane protein

Query Match 80.0%; Score 32; DB 2; Length 494;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 8
|||
Db 122 SLLPLQ 129

RESULT 11
B95976
probable transport protein, similar to Wzx exoT [imported] - Sinorhizobium meliloti (str
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95976
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: B95976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <KUR>
A:Cross-references: UNIPROT:P33699; UNIPARC:UPI000012A381; GB:AL591985; PIDN:CAC49474.1;
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: exoT; SMD20950
A:Genome: plasmid
C:Superfamily: hypothetical protein b2046

Query Match 80.0%; Score 32; DB 2; Length 494;

Best Local Similarity 75.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2;

QY 1 SLLPLQI 8
|||:|:
Db 122 SLLPLQL 129

RESULT 12

S40176

Exot protein - Rhizobium meliloti

C:Species: Rhizobium meliloti

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000

C:Accession: S40176

R:Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.

submitted to the EMBL Data Library, April 1993

A:Description: Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, exoT and exoI
seq.

A:Reference number: S40173

A:Accession: S40176

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-582 <BEC>

A:Cross-references: UNIPARC:UPI00001787P9; EMBL:Z22646

C:Superfamily: hypothetical protein b2046

Query Match 80.0%; Score 32; DB 2; Length 582;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQI 8
|||:|:
Db 122 SLLPLQL 129

RESULT 13

S61692

probable membrane protein YOR137c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein O3329; hypothetical protein YOR3329c

C:Species: Saccharomyces cerevisiae

C>Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C:Accession: S61692; S67022

R:Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia

submitted to the EMBL Data Library, December 1995

A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome

A:Reference number: S61643

A:Accession: S61692

A:Molecule type: DNA

A:Residues: 1-622 <BEN>

A:Cross-references: UNIPROT:Q12212; UNIPARC:UPI000006BB6F; EMBL:X94335; NID:gl262139; PI

R:Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge, W.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66965

A:Accession: S67022

A:Molecule type: DNA

A:Residues: 1-622 <VOS>

A:Cross-references: UNIPARC:UPI000006BB6F; EMBL:Z75045; NID:gl420348; PID:e252028; PID:9

A:Experimental source: strain S288C

C:Genetics:

A:Cross-references: SGD:S0005663

A:Map position: 15R

C:Keywords: transmembrane protein

F;11-27/Domain: transmembrane #status predicted <TMM>

Query Match 80.0%; Score 32; DB 2; Length 622;

Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLLPLQI 9
|||:|:
Db 141 SALIPLQL 149

RESULT 14

G65039

hypothetical protein b2612 - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: G65039

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G65039

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-196 <BLAT>

A:Cross-references: UNIPARC:UPI000016ED74; GB:AE000347; GB:U00096; NID:g2367142; PIDN:AA

A:Experimental source: strain K-12, substrain MG1655

Query Match 77.5%; Score 31; DB 2; Length 196;

Best Local Similarity 87.5%; Pred. No. 78;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
|||:|:
Db 123 LLAPLQIL 130

RESULT 15

C84914

hypothetical protein At2g47360 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84914

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84914

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303 <STO>

A:Cross-references: UNIPROT:O22910; UNIPARC:UPI00000A2116; GB:AE002093; NID:g2275214; PI

C:Genetics:

A:Gene: At2g47360

A:Map position: 2

Query Match 77.5%; Score 31; DB 2; Length 303;

Best Local Similarity 77.8%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
|||:|:
Db 29 SLLPLSFL 37

Search completed: March 11, 2006, 00:40:51

Job time : 15.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--------------|
| 1 | 40 | 100.0 | 66 | 2 | Q6DTY1_HUMAN |
| 2 | 40 | 100.0 | 253 | 1 | KLK7_HUMAN |
| 3 | 38 | 95.0 | 146 | 2 | Q9V2D5_PYRAB |
| 4 | 37 | 92.5 | 208 | 2 | O21527_CLEGA |
| 5 | 36 | 90.0 | 4183 | 2 | Q4Q1C5_LEIWA |
| 6 | 35 | 87.5 | 545 | 2 | Q5N0S0_SYNPF |
| 7 | 34 | 85.0 | 73 | 2 | Q8VCA9_MOUSE |
| 8 | 34 | 85.0 | 104 | 2 | Q8R5D6_MOUSE |
| 9 | 34 | 85.0 | 138 | 2 | Q6PKE2_MOUSE |
| 10 | 34 | 85.0 | 201 | 1 | FKB11_MOUSE |
| 11 | 34 | 85.0 | 246 | 2 | O585W6_9TRYP |
| 12 | 34 | 85.0 | 361 | 1 | INHA_TRIVU |
| 13 | 34 | 85.0 | 373 | 2 | Q4R9Q7_GEOSL |
| 14 | 34 | 85.0 | 745 | 2 | Q4RXR8_TETNG |
| 15 | 33 | 82.5 | 148 | 2 | Q6N500_RHOPA |
| 16 | 33 | 82.5 | 302 | 2 | Q6GNT6_XENLA |
| 17 | 33 | 82.5 | 370 | 2 | Q8FYX1_BRUSU |
| 18 | 33 | 82.5 | 370 | 2 | Q8YHY9_BRUME |
| 19 | 33 | 82.5 | 374 | 2 | Q57CF5_BRUAB |
| 20 | 33 | 82.5 | 379 | 2 | Q7U5J6_SYNPF |
| 21 | 33 | 82.5 | 381 | 2 | Q7V4U4_PRONM |
| 22 | 33 | 82.5 | 392 | 2 | Q732B9_BACCI |
| 23 | 33 | 82.5 | 392 | 2 | Q819M8_BACCR |
| 24 | 33 | 82.5 | 393 | 2 | Q6HL6_EACHK |
| 25 | 33 | 82.5 | 393 | 2 | Q5NY82_AZOSE |
| 26 | 33 | 82.5 | 393 | 2 | Q635X8_BACCC |
| 27 | 33 | 82.5 | 394 | 2 | Q6HU78_BACAN |
| 28 | 33 | 82.5 | 494 | 2 | Q4LIC3_9BURK |
| 29 | 33 | 82.5 | 1017 | 1 | EMILL_MOUSE |
| 30 | 32 | 80.0 | 68 | 2 | Q6KG65_9CAUD |
| 31 | 32 | 80.0 | 72 | 2 | Q8VBB6_WSSV |

32 32 80.0 78 2 Q7WXY8_PSEAE
33 32 80.0 102 2 Q8BRV0_MOUSE
34 32 80.0 161 2 Q4KJH4_PSEFS
35 32 80.0 171 2 Q7U5R4_SYNPF
36 32 80.0 196 2 Q9D226_MOUSE
37 32 80.0 205 2 Q65323_ORYSA
38 32 80.0 218 2 Q9ZTE3_ARATH
39 32 80.0 226 2 Q5AXD4_EMENI
40 32 80.0 230 2 Q876R3_EMENI
41 32 80.0 258 2 Q4HS88_CAMUP
42 32 80.0 264 2 Q8UIE2_AGR75
43 32 80.0 267 1 XBP1_MOUSE
44 32 80.0 267 1 XBP1_RAT
45 32 80.0 282 2 Q9M0J5_ARATH

ALIGNMENTS

RESULT 1

Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646152; AAT66047.1; -; mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
|||
DB 4 SLLPLQL 12
|||

RESULT 2

KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

| | | | | | |
|----|-----|--|----|----------|--|
| RN | [2] | NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION. | CC | -! | SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and |
| RP | | TISSUE=Keratinocyte; DOI=10.1016/S0378-1119(00)00280-8; | CC | | also observed at the apical membrane and in cytoplasm at the |
| RC | | PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8; | CC | | invasive front. |
| RX | | Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., | CC | -! | ALTERNATIVE PRODUCTS: |
| RA | | Diamandis E.P.; | CC | | Event=Alternative splicing; Named isoforms=2; |
| RA | | "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic | CC | | Name=1; Synonyms=Long; |
| RT | | enzyme is a new member of the human kallikrein gene family - genomic | CC | | isoId=P49862-1; Sequences=Displayed; |
| RT | | characterization, mapping, tissue expression and hormonal | CC | | Name=2; Synonyms=Short; |
| RT | | regulation."; | CC | | isoId=P49862-2; Sequences=VSP_013581; |
| RL | | Gene 254:119-128(2000). | CC | -! | TISSUE SPECIFICITY: Abundantly expressed in the skin and is |
| RN | [3] | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. | CC | | expressed by keratinocytes in the epidermis. Also expressed in the |
| RP | | PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; | CC | | brain, mammary gland, cerebellum, spinal cord and kidney. Lower |
| RX | | Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McQuaig J., | CC | | levels in salivary glands, uterus, thymus, thyroid, placenta, |
| RA | | Moss P., Paepfer B., Wang K.; | CC | | trachea and testis. Up-regulated in ovarian carcinoma, especially |
| RT | | "Sequencing and expression analysis of the serine protease gene | CC | | late-stage serous carcinoma, compared with normal ovaries and |
| RT | | cluster located in chromosome 19q13 region."; | CC | | benign adenomas (at the protein level). |
| RL | | Gene 257:119-130(2000). | CC | -! | INDUCTION: By estrogens and glucocorticoids in a breast carcinoma |
| RN | [4] | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. | CC | | cell line. |
| RP | | Hansson L., Baekkan A., Ny A., Edlund M., Edholm E., Tornell J., | CC | -! | SIMILARITY: Belongs to the peptidase S1 family. Kallikrein |
| RA | | Wallbrandt P., Egelrud T.; | CC | | subfamily. |
| RA | | "Epidermal overexpression of stratum corneum chymotryptic enzyme in | CC | -! | SIMILARITY: Contains 1 peptidase S1 domain. |
| RT | | RT mice; a model for chronic itchy dermatitis."; | CC | | This Swiss-Prot entry is copyright. It is produced through a collaboration |
| RL | | Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases. | CC | | between the Swiss Institute of Bioinformatics and the EMBL outstation - |
| RN | [5] | NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, | CC | | the European Bioinformatics Institute. There are no restrictions on its |
| RP | | AND TISSUE SPECIFICITY. | CC | | use as long as its content is in no way modified and this statement is not |
| RC | | TISSUE=Ovarian carcinoma; | CC | | removed. |
| RX | | MEDLINE=22623266; PubMed=12738725; | CC | | EMBL; L33404; AAC37551.1; -; mRNA. |
| RA | | Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.; | DR | | EMBL; AF166330; AAD49718.1; -; Genomic_DNA. |
| RT | | "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer | DR | | EMBL; AF243527; AAG33360.1; -; Genomic_DNA. |
| RT | | produces novel variants with potential as cancer biomarkers."; | DR | | EMBL; AF332583; AAK69624.1; -; Genomic_DNA. |
| RL | | Clin. Cancer Res. 9:1710-1720(2003). | DR | | EMBL; AF411214; AAN03662.1; -; mRNA. |
| RN | [6] | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1). | DR | | EMBL; AF411215; AAN03663.1; -; mRNA. |
| RP | | TISSUE=Skin; | DR | | EMBL; BC032005; AAH32005.1; -; mRNA. |
| RC | | MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899; | DR | | PIR; A53968; A53968. |
| RA | | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | DR | | HSP; P00760; IEZK. |
| RA | | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | DR | | MEROPS; S01.300; -. |
| RA | | Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.P., Bhat N.K., | DR | | Ensembl; ENSG00000169035; Homo sapiens. |
| RA | | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | DR | | HGNC; HGNC:6368; KLK7. |
| RA | | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | DR | | H-InvDB; HIX0015373; -. |
| RA | | Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., | DR | | MIM; 604438; -. |
| RA | | Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C., | DR | | GO; GO:0008236; F:serine-type peptidase activity; TAS. |
| RA | | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., | DR | | GO; GO:0008544; P:epidermis development; TAS. |
| RA | | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | DR | | InterPro; IPR001254; Peptidase_S1_S6. |
| RA | | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | DR | | InterPro; IPR001314; Peptidase_S1A. |
| RA | | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | DR | | Pfam; PF00089; Trypsin; 1. |
| RA | | Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., | DR | | PRINTS; PR00722; CHYMOTRYPSIN. |
| RA | | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | DR | | SMART; SM00020; Tryp_SPC; 1. |
| RA | | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | DR | | PROSITE; PS02040; TRYPSIN_DOM; 1. |
| RA | | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | DR | | PROSITE; PS00134; TRYPSIN_HIS; 1. |
| RA | | Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., | DR | | PROSITE; PS00135; TRYPSIN_SER; 1. |
| RA | | Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.; | KW | | Alternative splicing; Direct protein sequencing; Glycoprotein; |
| RT | | "Generation and initial analysis of more than 15,000 full-length human | | | Hydrolase; Protease; Serine protease; Signal; Zymogen. |
| RL | | and mouse cDNA sequences."; | FT | SIGNAL | 1 22 |
| RL | | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | FT | PROPEP | 23 29 |
| RN | [7] | CHARACTERIZATION. | FT | CHAIN | 30 253 |
| RP | | MEDLINE=95314630; PubMed=7794273; | FT | DOMAIN | 30 250 |
| RA | | Skytt A., Stroomqvist M., Egelrud T.; | FT | ACT SITE | 70 70 |
| RT | | "Primary substrate specificity of recombinant human stratum corneum | FT | ACT SITE | 112 112 |
| RL | | chymotryptic enzyme."; | FT | ACT SITE | 205 205 |
| CC | -! | FUNCTION: May catalyze the degradation of intercellular cohesive | FT | CAREOHVD | 246 246 |
| CC | | structures in the cornified layer of the skin in the continuous | FT | DISULFID | 36 137 |
| CC | | shedding of cells from the skin surface. Specific for amino acid | FT | DISULFID | 55 71 |
| CC | | residues with aromatic side chains in the P1 position. SCCE | FT | DISULFID | 144 211 |
| CC | | cleaves insulin B chain at 6-Leu- -Cys-7, 16-Tyr- -Leu-17, 25- | FT | DISULFID | 176 190 |
| CC | | phe- -Tyr-26, and 26-Tyr- -Thr-27. Could play a role in the | FT | DISULFID | 201 226 |
| CC | | activation of precursors to inflammatory cytokines. | FT | VARSPIC | ? 239 |
| CC | | | FT | | Missing (in isoform 2). |
| | | | FT | | /FTId=VSP_013581. |
| | | | FT | | C -> W (in Ref. 6; AAH32005). |
| | | | FT | CONFLICT | 226 226 |
| | | | FT | SEQUENCE | 253 AA; 27525 MW; 2D68B6B15A76A68 CRC64; |

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Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 3
Q9V2D5 PYRAB
ID Q9V2D5 PYRAB PRELIMINARY; PRT; 146 AA.
AC Q9V2D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PYRAB01390; ORFNames=PAB0088;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
DR EMBL; AJ248283; CAB49063.1; -; Genomic_DNA.
DR PIR; H75201; H75201.
DR InterPro; IPR008537; DUF819.
DR Pfam; PF05684; DUF819; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;

Query Match      95.0%; Score 38; DB 2; Length 146;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 66 SLLPLQL 74

RESULT 4
O21527 CLEGA
ID O21527 CLEGA PRELIMINARY; PRT; 208 AA.
AC O21527;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Clethrionomys gapperi (Southern red-backed vole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Arvicolinae; Clethrionomys.
OX NCBI_TaxID=56223;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98152303; PubMed=9491603;
RA Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
RT "Molecular systematics and paleobiogeography of the South American
sigmodontine rodents.";
RL Mol. Biol. Evol. 15:35-49(1998).
DR EMBL; U83808; AAB87188.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.

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DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0018491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; P:ATP synthase coupled electron transport; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR003918; NADHub_oxred4.
DR InterPro; IPR000260; Oxidored_q5_N.
DR Pfam; PF01059; Oxidored_q5_N; 1.
DR PRINTS; PR01437; NUOXDRDTASE4.
KW Mitochondrion.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;

Query Match      92.5%; Score 37; DB 2; Length 208;
Best Local Similarity 88.9%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 97 SLLPLQL 105

RESULT 5
Q4Q1C5 LEIMA
ID Q4Q1C5 LEIMA PRELIMINARY; PRT; 4183 AA.
AC Q4Q1C5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF36.2940;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neill S.,
Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005272; CAJ09256.1; -; Genomic_DNA.
DR InterPro; IPR001547; Glyco_hydro_5.
DR InterPro; IPR000403; P13/4_kinase_cat.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR SMART; SM00146; P13Kc; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
KW Hypothetical protein; Nucleotide-binding.
SQ SEQUENCE 4183 AA; 452241 MW; 3F6FB63A80F3EB02 CRC64;

Query Match      90.0%; Score 36; DB 2; Length 4183;
Best Local Similarity 77.8%; Pred. No. 11e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 2801 SLLPLQL 2809

RESULT 6
Q5N0S0 SYN6P
ID Q5N0S0 SYN6P PRELIMINARY; PRT; 545 AA.
AC Q5N0S0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Probable Na+/H+-exchanging protein.
GN OrderedLocNames=syc1910.c;
OS Synchococcus sp. (strain_PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=269084;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCC6301;
RA Sugita M.;
RT "Complete genome structure of the unicellular cyanobacterium Anacystis
RL nidulans 6301 (Synecococcus sp. PCC6301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008231; BAD80100.1; -; Genomic DNA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR006153; Na_H_porter.
DR InterPro; IPR006015; Usp.
DR InterPro; IPR006016; UspA.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR Pfam; PF00582; Usp; 1.
DR PRINTS; PR01438; UNVRSLSTRESS.
KW Complete proteome.
SQ SEQUENCE 545 AA; 58143 MW; 2DB84E920CD7DEDC CRC64;

Query Match 87.5%; Score 35; DB 2; Length 545;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
DB 193 LLLPLQVL 200

RESULT 7
O8VCA9 MOUSE
ID Q8VCA9_MOUSE PRELIMINARY; PRT; 73 AA.
AC Q8VCA9;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fkbp11 protein.
DE Name=Fkbp11;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshuyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
DR Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
DR Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
DR InterPro; IPR001179; Fkbp_PPase.
DR Pfam; PF00254; Fkbp_C; 1.
DR PROSITE; PS50059; Fkbp_PPase; 1.
DR SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 104;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
DB 6 LLLPLQLL 13

RESULT 8
Q8R5D6 MOUSE
ID Q8R5D6_MOUSE PRELIMINARY; PRT; 104 AA.
AC Q8R5D6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fkbp11 protein.
DE Name=Fkbp11;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshuyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
DR Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
DR Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
DR InterPro; IPR001179; Fkbp_PPase.
DR Pfam; PF00254; Fkbp_C; 1.
DR PROSITE; PS50059; Fkbp_PPase; 1.
DR SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 104;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
DB 6 LLLPLQLL 13
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RESULT 9
Q6PK22 MOUSE PRELIMINARY; PRT; 138 AA.
AC Q6PK22
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RA Strausberg R.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002311; AAH02311.1; -; mRNA.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0014021; C:integral to membrane; TAS.
DR InterPro; IPR001195; Fkbp_PPIase.
DR Pfam; PF00254; Fkbp_C; 1.
DR PROSITE; PS50059; Fkbp_PPIase; 1.
SQ SEQUENCE 138 AA; 15105 MW; C130B8B0EFD59D CRC64;

Query Match 85.0%; Score 34; DB 2; Length 138;
Best Local Similarity 87.5%; Pred. NO. 96;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 6 LLLPLQLL 13
|||||:|

RESULT 10
FKB11_MOUSE
ID FKB11_MOUSE STANDARD; PRT; 201 AA.
AC Q9D1M7; Q9CRE4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

```

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DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
DE trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
DE (FKBP-19).
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimson S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierka R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte A., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verdaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RT Nature 420:563-573(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: PPIases accelerate the folding of proteins during
CC protein synthesis.
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC -!- SIMILARITY: Contains 1 PPIase FKBP-type domain.

```

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
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use as long as its content is in no way modified and this statement is not
removed.

EMBL; AK003331; BAB22719.1; -; mRNA.
EMBL; AK003332; BAB31559.1; -; mRNA.
EMBL; BC037596; AAH37596.1; -; mRNA.
HSSP; P20071; LTCO.
Ensembl; ENSMUSG00000003355; Mus musculus.
MGI; MGI:1913370; Fkbp11.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP_C; 1.
PROSITE; PS0059; FKBP_PPIASE; 1.
Isomerase; Rotamase; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 201 FK506 binding protein 11.
FT DOMAIN 57 144 PPIase FKBP-type.
FT CONFLICT 53 53 S -> F (in Ref. 1; BAB31559).
FT CONFLICT 198 198 S -> R (in Ref. 1; BAB31559).
SQ SEQUENCE 201 AA; 22137 MW; 94D955C57264BD82 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 201;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
DB 6 LLLPLQLL 13

RESULT 11

Q585W6_9TRYP PRELIMINARY; PRT; 246 AA.
AC Q585W6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFName=Trp927.6.3680;
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RC STRAIN=GUTat10.1;
RA Shedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Haas B., Blandin G., El-Sayed N.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009259; AAX80785.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 27875 MW; 706DD83BA6B46AB CRC64;

Query Match 85.0%; Score 34; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
DB 163 LMLPLQIL 170

RESULT 12

INHA TRIVU
ID INHA TRIVU STANDARD; PRT; 361 AA.
AC Q77755;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Inhibin alpha chain precursor.
GN Name=INHA;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
RA Vamontfort D., Fidler A.B., Heath D.A., Lawrence S.B., Tisdall D.J.,
RA Greenwood P.J., McNatty K.;
RT "cDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
vulpecula)";
RL J. Mol. Endocrinol. 21:141-152(1998).
CC -!- FUNCTION: Inhibins and activins inhibit and activate,
respectively, the secretion of follitropin by the pituitary gland.
Inhibins/activins are involved in regulating a number of diverse
functions such as hypothalamic and pituitary hormone secretion,
gonadal hormone secretion, germ cell development and maturation,
erythroid differentiation, insulin secretion, nerve cell survival,
embryonic axial development or bone growth, depending on their
subunit composition. Inhibins appear to oppose the functions of
activins.
CC -!- SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A
is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
beta-B.
CC -!- PTM: Proteolytic processing yields a number of bioactive forms,
consisting either solely of the mature alpha chain, of the most N-
terminal propeptide linked through a disulfide bond to the mature
alpha chain, or of the entire proprotein.
CC -!- SIMILARITY: Belongs to the TGF-beta family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; AF033340; AAC63945.1; -; mRNA.
GO; GO:0005576; C:extracellular region; ISS.
GO; GO:0017106; F:activin inhibitor activity; ISS.
GO; GO:0005125; F:cytokine activity; ISS.
GO; GO:0008083; F:growth factor activity; ISS.
GO; GO:0005179; F:hormone activity; ISS.
GO; GO:0005515; F:protein binding; ISS.
GO; GO:0007050; P:cell cycle arrest; ISS.
GO; GO:0030154; P:cell differentiation; ISS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
GO; GO:0007267; P:cell-cell signaling; ISS.
GO; GO:0030218; P:erythrocyte differentiation; ISS.
GO; GO:0042541; P:hemoglobin biosynthesis; ISS.
GO; GO:0006917; P:induction of apoptosis; ISS.
GO; GO:0045578; P:negative regulation of B cell differentiation; ISS.
GO; GO:0045786; P:negative regulation of cell cycle; ISS.
GO; GO:0046882; P:negative regulation of follicle-stimulating. .; ISS.
GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; ISS.
GO; GO:0045650; P:negative regulation of macrophage different. .; ISS.
GO; GO:0042326; P:negative regulation of phosphorylation; ISS.
GO; GO:0007399; P:neurogenesis; ISS.

DR GO: 0001541; P: ovarian follicle development; ISS.
 DR GO: 0046881; P: positive regulation of follicle-stimulating. . . ; ISS.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR Pfam; PF0001839; TGFb.
 DR PRINTS; PR00669; INHIBINA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein; Growth factor; Hormone; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 64
 FT PROPEP 65 230
 FT CHAIN 231 361
 FT SITE 64 65
 FT SITE 230 231
 FT CARBOHYD 48 48
 FT CARBOHYD 144 144
 FT CARBOHYD 266 266
 FT DISULFID 260 323
 FT DISULFID 289 358
 FT DISULFID 293 360
 FT DISULFID 322 322
 SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDAA87D CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 361;
 Best Local Similarity 87.5%; Pred. No. 2.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLLPLQL 9
 DB 4 LLLPLQL 11
 RESULT 13
 Q749Q7_GEOSL
 ID Q749Q7_GEOSL PRELIMINARY; PRT; 373 AA.
 AC Q749Q7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocustNames=GSU2685;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.B., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan J.F., Haft D.H., Selengut J.,
 RA Daviden J.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.P., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments";
 RL Science 302:1967-1969 (2003).
 DR EMBL; AE017180; AAR36057.1; -; Genomic_DNA.
 DR TIGR; GSU2685;
 DR GO: 0016020; C-membrane; IEA.
 DR GO: 0005524; F-ATP binding; IEA.
 DR GO: 0042626; F-ATPase activity, coupled to transmembrane m. . . ; IEA.
 DR GO: 0006810; P-transport; IEA.
 DR InterPro; IPR000412; ABC 2.
 DR Pfam; PF01061; ABC2 membrane; 1.
 DR PROSITE; PSS1012; ABC_TM2; 1.
 KW Complete proteome.
 SQ SEQUENCE 373 AA; 40412 MW; 94B9D6AFF570D4A2 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 373;
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLLPLQL 9
 DB 293 LLLPLQL 300
 RESULT 14
 Q4RKR8_TETNG
 ID Q4RKR8_TETNG PRELIMINARY; PRT; 745 AA.
 AC Q4RKR8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 5 SCAP15026, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00032814001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Laratier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; CAAE01015026; CAG11014.1; -; Genomic_DNA.
 FT NON_TER 1 1
 SQ SEQUENCE 745 AA; 83291 MW; 697BD870E8019DF1 CRC64;
 Query Match 85.0%; Score 34; DB 2; Length 745;
 Best Local Similarity 77.8%; Pred. No. 5.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 DB 692 SLLPLQL 700
 RESULT 15
 Q6N500_RHOA
 ID Q6N500_RHOA PRELIMINARY; PRT; 148 AA.
 AC Q6N500;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein precursor.
 GN OrderedLocustNames=RPA3183;
 OS Rhodospseudomonas palustris.

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OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Peres C.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; EX572603; CAE28624.1; -; Genomic_DNA.
DR InterPro; IPR000975; Interleukin_1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 148 AA; 16860 MW; 9501B7C6C2808F45 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. NO. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
DB 7 SLLPLMLL 15

Search completed: March 11, 2006, 00:38:50
Job time : 97.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 40 | 100.0 | 9 | 2 | US-09-502-600-36 |
| 2 | 40 | 100.0 | 9 | 2 | US-09-918-243-36 |
| 3 | 40 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 4 | 40 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 5 | 40 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 6 | 40 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 7 | 40 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 8 | 40 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 9 | 40 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 10 | 40 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 11 | 36 | 90.0 | 9 | 2 | US-09-502-600-33 |
| 12 | 36 | 90.0 | 9 | 2 | US-09-918-243-33 |
| 13 | 34 | 85.0 | 812 | 2 | US-09-489-039A-12075 |
| 14 | 32 | 80.0 | 9 | 2 | US-09-502-600-35 |
| 15 | 32 | 80.0 | 9 | 2 | US-09-502-600-116 |
| 16 | 32 | 80.0 | 9 | 2 | US-09-918-243-35 |
| 17 | 32 | 80.0 | 9 | 2 | US-09-918-243-116 |
| 18 | 32 | 80.0 | 139 | 2 | US-10-104-047-3867 |
| 19 | 32 | 80.0 | 285 | 2 | US-09-270-767-39889 |
| 20 | 32 | 80.0 | 295 | 2 | US-09-270-767-55106 |
| 21 | 32 | 80.0 | 557 | 2 | US-09-489-039A-10804 |
| 22 | 31 | 77.5 | 181 | 2 | US-09-543-681A-5937 |
| 23 | 31 | 77.5 | 246 | 2 | US-10-012-231A-338 |
| 24 | 31 | 77.5 | 246 | 2 | US-10-015-389A-338 |
| 25 | 31 | 77.5 | 246 | 2 | US-10-006-768A-338 |
| 26 | 31 | 77.5 | 246 | 2 | US-10-015-671A-338 |
| 27 | 31 | 77.5 | 246 | 2 | US-10-015-393A-338 |

28 31 77.5 246 2 US-10-011-833A-338 Sequence 338, App
29 31 77.5 246 2 US-10-006-041A-338 Sequence 338, App
30 31 77.5 246 2 US-10-012-064A-338 Sequence 338, App
31 31 77.5 307 2 US-09-177-249-13 Sequence 13, Appl
32 31 77.5 307 2 US-09-812-283-13 Sequence 13, Appl
33 31 77.5 461 2 US-09-605-703B-436 Sequence 436, App
34 31 77.5 472 2 US-09-543-681A-5049 Sequence 5049, Ap
35 31 77.5 893 2 US-09-605-703B-434 Sequence 434, App
36 31 77.5 1279 2 US-09-170-496B-293 Sequence 58, Appl
37 31 77.5 1279 2 US-09-364-425B-58 Sequence 95, Appl
38 30 75.0 41 2 US-10-317-252B-95 Sequence 5, Appli
39 30 75.0 135 1 US-08-383-621-5 Sequence 5, Appli
40 30 75.0 135 2 US-08-459-906-5 Sequence 5, Appli
41 30 75.0 169 2 US-09-328-352-7861 Sequence 7861, Ap
42 30 75.0 231 2 US-09-252-991A-22663 Sequence 22663, A
43 30 75.0 308 2 US-09-252-991A-27921 Sequence 27921, A
44 30 75.0 333 2 US-09-949-016-6128 Sequence 6128, Ap
45 30 75.0 340 2 US-09-949-016-10615 Sequence 10615, A

ALIGNMENTS

RESULT 1
US-09-502-600-36
; Sequence 36, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-502-600-36

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
|||
Db 1 SLLPLQL 9

RESULT 2
US-09-918-243-36
; Sequence 36, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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/
/
/ FEATURE:
/ NAME/KEY: CHAIN
/ OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36

Query Match      100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; REFERENCE/DOCKET NUMBER: PF-0252 US
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5

/
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/824,874
/ FILING DATE: Filed Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0252 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
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Db 4 SLLPLQL 12

RESULT 6
US-08-930-188-2
; Sequence 2, Application US/08930188
; Patent No. 6093397
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,188
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-188-2

; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
   |||||
Db 4 SLLPLQL 12

RESULT 7
US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
   |||||
Db 4 SLLPLQL 12

RESULT 8
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
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/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 532504
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 9
PCT-US96-04294-2
/ Sequence 2. Application PC/TUS9604294
/ GENERAL INFORMATION:
/ APPLICANT: Dixon, Eric P.
/ APPLICANT: Johnstone, Edward M.
/ APPLICANT: Little, Sheila P.
/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Eli Lilly and Company
/ STREET: Lilly Corporate Center
/ CITY: Indianapolis
/ STATE: Indiana
/ COUNTRY: United States of America
/ ZIP: 46285
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/04294
/ FILING DATE:
/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/416,257
/ FILING DATE: 04-APR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bialock, Donna K.
/ REGISTRATION NUMBER: 38,082
/ REFERENCE/DOCKET NUMBER: X9239
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 317-277-1090
/ TELEFAX: 317-276-3861
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US96-04294-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 10
US-09-949-016-7716
/ Sequence 7716, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7716
/ LENGTH: 265
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-7716

Query Match 100.0%; Score 40; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 16 SLLPLQL 24

RESULT 11
US-09-502-600-33
/ Sequence 33, Application US/09502600A
/ Patent No. 6294344
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
/ TITLE OF INVENTION: Ovarian Cancer
/ FILE REFERENCE: D6223C1F-C
/ CURRENT FILING DATE: 2000-02-11
/ CURRENT APPLICATION NUMBER: US/09/502,600A

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; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
Db 1 LLLPLQIL 8

RESULT 12
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CLIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
Db 1 LLLPLQIL 8

RESULT 13
US-09-489-039A-12075
; Sequence 12075, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12075
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075
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Query Match      85.0%; Score 34; DB 2; Length 812;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
Db 429 LLLPLQIL 436

RESULT 14
US-09-502-600-35
; Sequence 35, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35

Query Match      80.0%; Score 32; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLLPLQIL 9
Db 1 LLLPLQIL 7

RESULT 15
US-09-502-600-116
; Sequence 116, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-502-600-116

Query Match      80.0%; Score 32; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
Db 3 SLLPLQ 9

Search completed: March 11, 2006, 01:24:27
Job time : 22.2222 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------------|--------------------|
| 1 | 40 | 100.0 | 9 | 3 US-09-918-243-36 | Sequence 36, Appl |
| 2 | 40 | 100.0 | 9 | 3 US-09-905-083-36 | Sequence 36, Appl |
| 3 | 40 | 100.0 | 9 | 4 US-10-372-521-36 | Sequence 36, Appl |
| 4 | 40 | 100.0 | 9 | 5 US-10-831-075-36 | Sequence 36, Appl |
| 5 | 40 | 100.0 | 136 | 5 US-10-450-763-53737 | Sequence 53737, A |
| 6 | 40 | 100.0 | 198 | 4 US-10-262-511-96 | Sequence 96, Appl |
| 7 | 40 | 100.0 | 250 | 4 US-10-262-511-92 | Sequence 92, Appl |
| 8 | 40 | 100.0 | 253 | 3 US-09-888-615-98 | Sequence 98, Appl |
| 9 | 40 | 100.0 | 253 | 3 US-09-764-762-3 | Sequence 3, Appl |
| 10 | 40 | 100.0 | 253 | 4 US-10-071-214-2 | Sequence 2, Appl |
| 11 | 40 | 100.0 | 253 | 4 US-10-071-214-48 | Sequence 48, Appl |
| 12 | 40 | 100.0 | 253 | 4 US-10-264-283-90 | Sequence 90, Appl |
| 13 | 40 | 100.0 | 253 | 4 US-10-295-027-498 | Sequence 498, Appl |
| 14 | 40 | 100.0 | 253 | 4 US-10-173-999-48 | Sequence 48, Appl |
| 15 | 40 | 100.0 | 253 | 4 US-10-408-765A-639 | Sequence 639, Appl |
| 16 | 40 | 100.0 | 253 | 5 US-10-643-795A-95 | Sequence 95, Appl |
| 17 | 40 | 100.0 | 253 | 5 US-10-948-518-95 | Sequence 95, Appl |
| 18 | 40 | 100.0 | 253 | 5 US-10-868-490A-1 | Sequence 1, Appl |
| 19 | 40 | 100.0 | 257 | 4 US-10-344-394-38 | Sequence 38, Appl |
| 20 | 36 | 90.0 | 9 | 3 US-09-918-243-33 | Sequence 33, Appl |
| 21 | 36 | 90.0 | 9 | 3 US-09-905-083-33 | Sequence 33, Appl |
| 22 | 36 | 90.0 | 9 | 4 US-10-372-521-33 | Sequence 33, Appl |
| 23 | 36 | 90.0 | 9 | 5 US-10-831-075-33 | Sequence 33, Appl |
| 24 | 35 | 87.5 | 138 | 4 US-10-425-114-53148 | Sequence 53148, A |
| 25 | 35 | 87.5 | 868 | 4 US-10-369-493-10255 | Sequence 10255, A |
| 26 | 34 | 85.0 | 56 | 4 US-10-424-599-164977 | Sequence 164977, A |
| 27 | 34 | 85.0 | 70 | 4 US-10-424-599-207950 | Sequence 207950, A |

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28 34 85.0 379 4 US-10-437-963-111334 Sequence 111334,
29 33 82.5 46 4 US-10-424-599-265948 Sequence 265948,
30 33 82.5 86 4 US-10-424-599-199921 Sequence 199921,
31 33 82.5 137 4 US-10-425-115-264649 Sequence 264649,
32 33 82.5 394 4 US-10-282-122A-45727 Sequence 45727, A
33 33 82.5 397 4 US-10-408-765A-2842 Sequence 2842, Ap
34 33 82.5 804 4 US-10-236-055A-28 Sequence 28, Appl
35 32 80.0 9 3 US-09-918-243-35 Sequence 35, Appl
36 32 80.0 9 3 US-09-918-243-116 Sequence 116, App
37 32 80.0 9 3 US-09-905-083-35 Sequence 35, Appl
38 32 80.0 9 3 US-09-905-083-116 Sequence 116, App
39 32 80.0 9 4 US-10-372-521-35 Sequence 35, Appl
40 32 80.0 9 4 US-10-372-521-116 Sequence 116, App
41 32 80.0 9 5 US-10-831-075-35 Sequence 35, Appl
42 32 80.0 9 5 US-10-831-075-116 Sequence 116, App
43 32 80.0 54 4 US-10-425-115-368614 Sequence 368614,
44 32 80.0 73 5 US-10-450-763-49706 Sequence 49706, A
45 32 80.0 74 4 US-10-424-599-252879 Sequence 252879,

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ALIGNMENTS

RESULT 1

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US-09-918-243-36
; Sequence 36, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36

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Query Match      100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SLLPLQL 9
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Db      1 SLLPLQL 9

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RESULT 2

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US-09-905-083-36
; Sequence 36, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-905-083-36

Query Match      100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 3
US-10-372-521-36
; Sequence 36, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-10-372-521-36

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 4
US-10-831-075-36
; Sequence 36, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-10-831-075-36

Query Match      100.0%; Score 40; DB 5; Length 9;
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; Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

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Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 10 SLLPLQL 18

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
```

APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 96
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 40; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 7
US-10-262-511-92
Sequence 92, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Elleman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana

APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 92
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 8
US-09-888-615-98
Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-615-98

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 9

US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 10

US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 11

US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 12

US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US20030144494A1

GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 13
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 14
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 15
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US2004010187A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
 |||||
Db 4 SLLPLQL 12

Search completed: March 11, 2006, 01:37:24
Job time : 70.444 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-36

Perfect score: 40

Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/2/pubpa/US08_NEW_PUB.pbp.*
- 2: /cgn2_6/prodata/2/pubpa/US06_NEW_PUB.pbp.*
- 3: /cgn2_6/prodata/2/pubpa/US07_NEW_PUB.pbp.*
- 4: /cgn2_6/prodata/2/pubpa/PCT_NEW_PUB.pbp.*
- 5: /cgn2_6/prodata/2/pubpa/US09_NEW_PUB.pbp.*
- 6: /cgn2_6/prodata/2/pubpa/US10_NEW_PUB.pbp.*
- 7: /cgn2_6/prodata/2/pubpa/US11_NEW_PUB.pbp.*
- 8: /cgn2_6/prodata/2/pubpa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 40 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 2 | 40 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 3 | 40 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 4 | 40 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 5 | 34 | 85.0 | 71 | 7 | US-11-096-568A-27354 |
| 6 | 34 | 85.0 | 71 | 7 | US-11-096-568A-27391 |
| 7 | 34 | 85.0 | 85 | 7 | US-11-096-568A-27353 |
| 8 | 34 | 85.0 | 85 | 7 | US-11-096-568A-27390 |
| 9 | 32 | 80.0 | 139 | 7 | US-11-072-512-3867 |
| 10 | 31 | 77.5 | 401 | 7 | US-11-087-099-6642 |
| 11 | 30 | 75.0 | 41 | 7 | US-11-121-612-95 |
| 12 | 30 | 75.0 | 202 | 7 | US-11-098-686-10163 |
| 13 | 30 | 75.0 | 333 | 7 | US-11-181-234-5 |
| 14 | 30 | 75.0 | 333 | 7 | US-11-181-234-7 |
| 15 | 29 | 72.5 | 68 | 7 | US-11-096-568A-6331 |
| 16 | 29 | 72.5 | 79 | 7 | US-11-096-568A-6330 |
| 17 | 29 | 72.5 | 125 | 7 | US-11-096-568A-23862 |
| 18 | 29 | 72.5 | 326 | 7 | US-11-096-568A-20656 |
| 19 | 29 | 72.5 | 336 | 7 | US-11-096-568A-30761 |
| 20 | 29 | 72.5 | 336 | 7 | US-11-096-568A-30760 |
| 21 | 29 | 72.5 | 419 | 7 | US-11-067-884-8 |
| 22 | 29 | 72.5 | 498 | 7 | US-11-096-568A-30759 |
| 23 | 28 | 70.0 | 40 | 7 | US-11-121-612-80 |
| 24 | 28 | 70.0 | 40 | 7 | US-11-121-612-144 |
| 25 | 28 | 70.0 | 40 | 7 | US-11-121-612-176 |

| | | | | | | |
|----|----|------|-----|---|----------------------|--------------------|
| 26 | 28 | 70.0 | 40 | 7 | US-11-121-612-246 | Sequence 246, App |
| 27 | 28 | 70.0 | 40 | 7 | US-11-121-612-247 | Sequence 247, App |
| 28 | 28 | 70.0 | 40 | 7 | US-11-121-612-248 | Sequence 248, App |
| 29 | 28 | 70.0 | 40 | 7 | US-11-121-612-249 | Sequence 249, App |
| 30 | 28 | 70.0 | 40 | 7 | US-11-121-612-320 | Sequence 320, App |
| 31 | 28 | 70.0 | 40 | 7 | US-11-121-612-342 | Sequence 342, App |
| 32 | 28 | 70.0 | 40 | 7 | US-11-121-612-349 | Sequence 349, App |
| 33 | 28 | 70.0 | 41 | 7 | US-11-121-612-100 | Sequence 100, App |
| 34 | 28 | 70.0 | 41 | 7 | US-11-121-612-270 | Sequence 270, App |
| 35 | 28 | 70.0 | 72 | 6 | US-10-895-064-631 | Sequence 631, App |
| 36 | 28 | 70.0 | 72 | 7 | US-11-129-741-631 | Sequence 631, App |
| 37 | 28 | 70.0 | 98 | 6 | US-10-467-657-3826 | Sequence 3826, App |
| 38 | 28 | 70.0 | 102 | 7 | US-11-072-512-2266 | Sequence 2266, App |
| 39 | 28 | 70.0 | 109 | 6 | US-10-821-234-1175 | Sequence 1175, App |
| 40 | 28 | 70.0 | 145 | 7 | US-11-205-225-8 | Sequence 8, Appli |
| 41 | 28 | 70.0 | 299 | 7 | US-11-096-568A-12300 | Sequence 12300, A |
| 42 | 28 | 70.0 | 317 | 7 | US-11-205-225-2 | Sequence 2, Appli |
| 43 | 28 | 70.0 | 334 | 7 | US-11-096-568A-18598 | Sequence 18598, A |
| 44 | 28 | 70.0 | 354 | 7 | US-11-096-568A-18597 | Sequence 18597, A |
| 45 | 28 | 70.0 | 359 | 7 | US-11-089-425A-4 | Sequence 4, Appli |

ALIGNMENTS

RESULT 1

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9

DB 4 SLLPLQL 12

RESULT 2

US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

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/ ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLPLQL 9
Db      4 SLLPLQL 12

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLPLQL 9
Db      4 SLLPLQL 12

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SLLPLQL 9
Db      4 SLLPLQL 12

RESULT 5
US-11-096-568A-27354
; Sequence 27354, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27354
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354

Query Match      85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLLPLQL 9
Db      1 MLLPLQL 8

RESULT 6
US-11-096-568A-27391
; Sequence 27391, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27391
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391

Query Match      85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLLPLQL 9
Db      1 MLLPLQL 8

RESULT 7
US-11-096-568A-27353
; Sequence 27353, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
```

```
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27353
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(85)
; OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353

Query Match
Best Local Similarity 85.0%; Score 34; DB 7; Length 85;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
   :|||||
Db 15 MLLPLQIL 22

RESULT 8
US-11-096-568A-27390
; Sequence 27390, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27390
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(85)
; OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390

Query Match
Best Local Similarity 85.0%; Score 34; DB 7; Length 85;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
   :|||||
Db 15 MLLPLQIL 22

RESULT 9
US-11-072-512-3867
; Sequence 3867, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HTO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
```

```
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3867
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3867

Query Match
Best Local Similarity 80.0%; Score 32; DB 7; Length 139;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
   |||||
Db 33 SLLPLQ 39

RESULT 10
US-11-087-099-6642
; Sequence 6642, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6642
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Guillardia theta
US-11-087-099-6642

Query Match
Best Local Similarity 77.5%; Score 31; DB 7; Length 401;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
   |||||
Db 304 SFLPLQLV 312

RESULT 11
US-11-121-612-95
; Sequence 95, Application US/11121612
; Publication No. US20060025339A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847MD
; CURRENT APPLICATION NUMBER: US/11/121,612
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
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; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/317,252
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide sequence
; NAME/KEY: MOD RES
; LOCATION: (41)..(41)
; OTHER INFORMATION: AMIDATION
US-11-121-612-95
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Query Match          75.0%; Score 30; DB 7; Length 41;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;
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```
QY      1 SLLPLQIL 9
        |||||:|
Db       7 SLDLPQLL 15
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RESULT 12
US-11-098-686-10163
; Sequence 10163, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10163
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10163
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```
Query Match          75.0%; Score 30; DB 7; Length 202;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 LLLPLQIL 9
        |||||:|
Db      146 LLLPLTIL 153
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RESULT 13
US-11-181-234-5
; Sequence 5, Application US/11181234
; Publication No. US20060021075A1
; GENERAL INFORMATION:
; APPLICANT: WANG, CHYUNG-RU
; TITLE OF INVENTION: GROUP 1 CD1 TRANSGENIC MICE AND THEIR
; FILE REFERENCE: 21117.0001U2
; CURRENT APPLICATION NUMBER: US/11/181,234
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: 60/588,192
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; PRIOR FILING DATE: 2004-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-11-181-234-5
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Query Match          75.0%; Score 30; DB 7; Length 333;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 LLLPLQIL 9
        |||||:|
Db       2 LLLPPQLL 9
```

```
RESULT 14
US-11-181-234-7
; Sequence 7, Application US/11181234
; Publication No. US20060021075A1
; GENERAL INFORMATION:
; APPLICANT: WANG, CHYUNG-RU
; TITLE OF INVENTION: GROUP 1 CD1 TRANSGENIC MICE AND THEIR
; FILE REFERENCE: 21117.0001U2
; CURRENT APPLICATION NUMBER: US/11/181,234
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: 60/588,192
; PRIOR FILING DATE: 2004-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-11-181-234-7
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```
Query Match          75.0%; Score 30; DB 7; Length 333;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 LLLPLQIL 9
        |||||:|
Db       2 LLLPPQLL 9
```

```
RESULT 15
US-11-096-568A-6331
; Sequence 6331, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6331
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(68)
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; OTHER INFORMATION: Ceres Seq. ID no. 14314773
US-11-096-568A-6331

Query Match 72.5%; Score 29; DB 7; Length 68;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQ 7
Db 30 NLLPLQ 36

Search completed: March 11, 2006, 01:38:42
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GFLVCRGTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 50 | 100.0 | 9 | 4 AAE08285 | Aae08285 Human str |
| 2 | 50 | 100.0 | 9 | 8 ADR68841 | Adr68841 Human str |
| 3 | 50 | 100.0 | 181 | 6 ADA05738 | Ada05738 Human NOV |
| 4 | 50 | 100.0 | 181 | 8 ADN62902 | Adn62902 Human NOV |
| 5 | 50 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 6 | 50 | 100.0 | 198 | 8 ADN62900 | Adn62900 Human NOV |
| 7 | 50 | 100.0 | 224 | 6 ADA05744 | Ada05744 Human NOV |
| 8 | 50 | 100.0 | 224 | 8 ADN62908 | Adn62908 Human NOV |
| 9 | 50 | 100.0 | 224 | 9 ADV21100 | Adv21100 Human str |
| 10 | 50 | 100.0 | 225 | 4 AAB98502 | Aab98502 Human str |
| 11 | 50 | 100.0 | 247 | 6 ADA05742 | Ada05742 Human NOV |
| 12 | 50 | 100.0 | 247 | 8 ADN62906 | Adn62906 Human NOV |
| 13 | 50 | 100.0 | 250 | 6 ADA05732 | Ada05732 Human NOV |
| 14 | 50 | 100.0 | 250 | 8 ADN62896 | Adn62896 Human NOV |
| 15 | 50 | 100.0 | 252 | 6 ADA05734 | Ada05734 Human NOV |
| 16 | 50 | 100.0 | 252 | 8 ADN62898 | Adn62898 Human NOV |
| 17 | 50 | 100.0 | 253 | 2 AAR67888 | Aar67888 Human str |
| 18 | 50 | 100.0 | 253 | 2 AAW05383 | Aaw05383 Human str |
| 19 | 50 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 20 | 50 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 21 | 50 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 22 | 50 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 23 | 50 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 24 | 50 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |

| | | | | | |
|----|----|-------|-----|------------|--------------------|
| 25 | 50 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 26 | 50 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 27 | 50 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/an |
| 28 | 50 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 29 | 50 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antipsori |
| 30 | 50 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 31 | 50 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 32 | 50 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 33 | 50 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |
| 34 | 47 | 94.0 | 249 | 5 ABB84420 | Abb84420 Porcine S |
| 35 | 45 | 90.0 | 247 | 4 AAU86677 | Aau86677 Novel hum |
| 36 | 45 | 90.0 | 247 | 4 AAU23217 | Aau23217 Novel hum |
| 37 | 45 | 90.0 | 247 | 4 AAU23752 | Aau23752 Novel hum |
| 38 | 45 | 90.0 | 247 | 4 AAU17043 | Aau17043 Human nov |
| 39 | 45 | 90.0 | 247 | 7 ADB60011 | Adb60011 Connectiv |
| 40 | 45 | 90.0 | 250 | 3 AAB21298 | Aab21298 Human KJK |
| 41 | 45 | 90.0 | 250 | 5 ABP64969 | Abp64969 Human pro |
| 42 | 45 | 90.0 | 250 | 6 ABR55400 | Abr55400 Amino aci |
| 43 | 45 | 90.0 | 250 | 8 ADN05516 | Adn05516 Antipsori |
| 44 | 45 | 90.0 | 250 | 9 ADY53877 | Ady53877 Human kal |
| 45 | 45 | 90.0 | 251 | 4 AAU16971 | Aau16971 Human nov |

ALIGNMENTS

RESULT 1
AAE08285
ID AAE08285 standard; peptide; 9 AA.
XX AAE08285;
AC AAE08285;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #50 (residues 207-215).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
FN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
(UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
WPI; 2001-514676/56.
XX
Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
Claim 25; Page 113; 127pp; English.
XX
The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
 Db 1 GPLVCRGTL 9

RESULT 2

ADR68841

ID ADR68841 standard; peptide; 9 AA.

XX ADR68841;

XX DT 02-DEC-2004 (first entry)

XX DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:80.

XX KW serine protease; stratum corneum chymotrytic enzyme; SCCE;

XX KW immune response; ovarian cancer; lung cancer; prostate cancer;

XX KW pancreatic cancer; colon cancer.

XX OS Homo sapiens.

XX PN WO2004075723-A2.

XX PD 10-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US005134.

XX PR 21-FEB-2003; 2003US-00372521.

XX PA (UYAR-) UNIV ARKANSAS.

XX PI O'Brien TJ, Cannon MJ, Santin A;

XX DR WPI; 2004-653294/63.

XX PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
 PT vaccinating an individual against SCCE, and in monitoring and developing
 PT immunotherapies for ovarian and other malignancies.

XX PS Claim 5; SEQ ID NO 80; 117pp; English.

XX CC The invention relates to a novel method for vaccinating an individual
 CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
 CC an individual with a SCCE peptide, which elicits an immune response in
 CC the individual. A peptide of the invention acts as a stratum corneum
 CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
 CC an individual against SCCE, particularly an individual having, suspected
 CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
 CC cancer. The oligonucleotide is useful for treating a neoplastic state in
 CC an individual, such as ovarian, breast, lung, colon, prostate, or
 CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
 CC peptides are also useful in the monitoring and development of
 CC immunotherapies for ovarian and other malignancies. The present sequence
 CC represents a peptide fragment of serine protease SCCE (stratum corneum
 CC chymotrytic enzyme).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
 Db 1 GPLVCRGTL 9

RESULT 3

ADA05738

ADA05738 standard; protein; 181 AA.

XX ADA05738;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV18d protein SEQ ID NO:98.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-032749P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 16-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

XX PA (CURA-) CURAGEN CORP.

XX PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerkusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX DR WPI; 2003-381626/36.

XX DR N-PSDB; ADA05737.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing,

PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX PS Claim 1; Page 171; 586pp; English.

CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 50; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. NO. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 133 GPLVCRGTL 141
|||||

RESULT 4
ADN62902
ID ADN62902 standard; protein; 181 AA.
AC
AC ADN62902;
XX
XX
XX 01-JUL-2004 (first entry)
XX
XX Human NOV18d.
XX
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
OS
OS Homo sapiens.
XX
XX US2004038223-A1.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 01-OCT-2002; 2002US-00262511.
PF
XX
XX 02-OCT-2001; 2001US-0326483P.
PR
XX
XX 05-OCT-2001; 2001US-0327435P.
PR
XX
XX 09-OCT-2001; 2001US-0327917P.
PR
XX
XX 09-OCT-2001; 2001US-0328029P.
PR
XX
XX 09-OCT-2001; 2001US-0328044P.
PR
XX
XX 12-OCT-2001; 2001US-0328056P.
PR
XX
XX 15-OCT-2001; 2001US-0328849P.
PR
XX
XX 17-OCT-2001; 2001US-0329414P.
PR
XX
XX 18-OCT-2001; 2001US-0330142P.
PR
XX
XX 22-OCT-2001; 2001US-0341058P.
PR
XX
XX 24-OCT-2001; 2001US-0339266P.
PR
XX
XX 24-OCT-2001; 2001US-0343629P.
PR
XX
XX 29-OCT-2001; 2001US-0349575P.
PR
XX
XX 01-NOV-2001; 2001US-0346357P.
PR
XX
XX 17-APR-2002; 2002US-0373260P.
PR
XX
XX 19-APR-2002; 2002US-0373815P.
PR
XX
XX 19-APR-2002; 2002US-0373817P.
PR
XX
XX 19-APR-2002; 2002US-0373826P.
PR
XX
XX 19-APR-2002; 2002US-0373884P.
PR
XX
XX 22-APR-2002; 2002US-0374977P.
PR
XX
XX 16-MAY-2002; 2002US-0381037P.
PR
XX
XX 16-MAY-2002; 2002US-0381038P.
PR
XX
XX 16-MAY-2002; 2002US-0381042P.
PR
XX
XX 28-MAY-2002; 2002US-0381642P.
PR
XX
XX 29-MAY-2002; 2002US-0383656P.
PR
XX
XX 29-MAY-2002; 2002US-0383831P.
XX
XX 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KERODA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2004-213911/20.
DR N-PSDB; ADN62901.
XX
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,

diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
Claim 1; SEQ ID NO 98; 395pp; English.

The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polynucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.

Sequence 181 AA;

Query Match 100.0%; Score 50; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

Db 133 GPLVCRGTL 141

RESULT 5

ID ADA05736 standard; protein; 198 AA.

AC ADA05736;

DT 06-NOV-2003 (first entry)

DE Human NOV18c protein SEQ ID NO:96.

XX human; NOVX; anti-diabetic; anorectic; antibacterial; virucide;

KW immunomodulator; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; antilipaeamic; gene therapy; human disease;

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX WO2003029424-A2.

PD 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328843P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381043P.
PR 17-MAY-2002; 2002US-0381644P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36.

N-PSDB; ADA05735.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have anti-diabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipaeamic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic

CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

XX Sequence 198 AA;

Query Match 100.0%; Score 50; DB 6; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

Db 152 GPLVCRGTL 160

RESULT 6

ADN62900
 ID ADN62900 standard; protein; 198 AA.

XX AC ADN62900;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV18c.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX PD 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 18-OCT-2001; 2001US-0330142P.

XX PR 22-OCT-2001; 2001US-0330309P.

XX PR 24-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 16-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX

PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C B.
 PA (RST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2004-213931/20.

DR N-PSDB; ADN62899.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX Claim 1; SEQ ID NO 96; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient with
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,

CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 50; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 152 GPLVCRGTL 160
|||||||

RESULT 7
ADA05744
ID ADA05744 standard; protein; 224 AA.
XX
AC ADA05744;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18g protein SEQ ID NO:104.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX

PA (CURA-) CURAGEN CORP.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patcurajan M, Szytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerkusen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimketa RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05743.
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 172; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, neuroprotective, antiparkinsonian
CC immunomodulator, cytostatic, nootropic, antibacterial, virucide,
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 50; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 193 GPLVCRGTL 201
|||||||

RESULT 8
ADN62908
ID ADN62908 standard; protein; 224 AA.
XX
AC ADN62908;
XX
DT 01-JUL-2004 (first entry)
XX

DE Human NOV18g.
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX Homo sapiens.
OS US2004038223-A1.
XX 26-FEB-2004.
XX 01-OCT-2002; 2002US-00262511.
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 09-OCT-2001; 2001US-0327499P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383566P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
XX (MILL/) MILLET I.
XX (PEYM/) PEYMAN J A.
XX (KEKU/) KEKUDA R.
XX (JUJJ/) JU J.
XX (LILL/) LI L.
XX (GUOX/) GUO X.
XX (PATI/) PATTURAJAN M.
XX (SPYT/) SPYTEK K A.
XX (EDIN/) EDINGER S R.
XX (ELLE/) ELLERMAN K.
XX (MALY/) MALYANKAR U M.
XX (ORTT/) ORT T.
XX (GORM/) GORMAN L.
XX (ZERH/) ZERHUSEN B D.
XX (ANDE/) ANDERSON D W.
XX (ZHON/) ZHONG M.
XX (CATT/) CATTERTON B.
XX (JIWW/) JI W.
XX (MILL/) MILLER C E.
XX (RAST/) RASTELLI L.
XX (STON/) STONE D J.
XX (PENA/) PENNA C E A.
XX (SHEN/) SHENOY S G.
XX (SHIM/) SHINKETS R A.
XX (ROTH/) ROTHENBERG M E.
XX (LEAC/) LEACH M D.
PA (AGEE/) AGE E M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dippio VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62907.
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX Claim 1; SEQ ID NO 104; 395pp; English.
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX Sequence 224 AA;
Query Match 100.0%; Score 50; DB 8; Length 224;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
Db 193 GPLVCRGTL 201
|||||||
RESULT 9
ADV21100
ID ADV21100 standard; protein; 224 AA.
XX
AC ADV21100;
XX
DT 24-FEB-2005 (first entry)
XX Human stratum corneum chymotrypsin protein.
XX

KW Protein purification; PS133 protein; serine protease; prostate disease;
 KW andrology; genitourinary disease; prostatic cancer; cytostatic;
 KW protein therapy; chymotrypsin; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 26..42
 FT /note = Catalytically functional motif
 FT Domain 83..87
 FT /note = Catalytically functional motif
 FT Domain 174..179
 FT /note = Catalytically functional motif
 XX
 PN US2004241646-A1.
 XX
 XX 02-DEC-2004.
 XX
 PF 20-FEB-2001; 2001US-00789210.
 XX
 PR 06-OCT-1997; 97US-00944483.
 XX
 XX (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GRAN/) GRANADOS E.
 PA (KLAS/) KLAS M R.
 PA (RUS/) RUSSELL J C.
 PA (STEW/) STEWART K D.
 PA (STRO/) STROUPE S D.
 XX
 XX Cohen M, Colpitts TL, Friedman PM, Granados E, Klaas MR;
 PI Russell JC, Stewart KD, Stroupe SD;
 XX WPI; 2005-011614/01.
 DR GENBANK; L33404.
 XX
 XX New isolated polypeptides, useful for detecting, diagnosing, staging,
 PT monitoring, prognosticating, preventing or treating, or determining
 PT predisposition to diseases or conditions of the prostate such as prostate
 PT cancer.
 XX
 PS Example 1; SEQ ID NO 33; 96pp; English.
 XX
 XX The invention relates to PS133 protein, a member of the human serine
 CC protease family and its corresponding nucleic acid sequence. PS133
 CC polypeptide is useful for detecting, diagnosing, staging, monitoring,
 CC prognosticating, preventing or treating or determining predisposition to
 CC diseases or conditions of the prostate such as prostatic cancer. The
 CC present sequence is the human stratum corneum chymotrypsin protein. This
 CC sequence is used to align with PS133 consensus protein.
 XX
 SQ Sequence 224 AA;
 Query Match 100.0%; Score 50; DB 9; Length 224;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPLVCRGTL 9
 Db 178 GPLVCRGTL 186
 RESULT 10
 ID AAB98502 standard; protein; 225 AA.
 XX
 AC AAB98502;
 XX
 DT 03-AUG-2001 (first entry)
 DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
 XX

KW Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
 KW tumour antigen-derived gene 15; serine protease;
 KW Stratum Corneum Chymotryptic Enzyme; SCCE.
 XX
 OS Homo sapiens.
 XX
 PN WO200129056-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-US029095.
 XX
 PR 20-OCT-1999; 99US-00421213.
 XX
 PA (UYAR-) UNIV ARKANSAS.
 XX
 PI O'brien TJ, Tanimoto H;
 XX WPI; 2001-381031/40.
 XX
 DR Novel extracellular serine protease, termed tumor antigen-derived gene 15
 PT protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
 PT treatment, prevention of cancer, particularly breast, ovarian cancer.
 XX
 PS Example 10; Fig 1; 130pp; English.
 XX
 XX The present invention relates to human tumour antigen-derived gene 15
 CC (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-
 CC 15 is an extracellular serine protease. It was found that TADG-15 is over
 CC -expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20
 CC residues that lack TADG-15 protease activity are useful for vaccinating
 CC an individual against TADG-15, having, suspected of having or at risk of
 CC getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic
 CC or therapeutic target in cancer. The present sequence was used in a
 CC sequence homology alignment with the catalytic domain of TADG-15
 XX
 SQ Sequence 225 AA;
 Query Match 100.0%; Score 50; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPLVCRGTL 9
 Db 179 GPLVCRGTL 187
 RESULT 11
 ID ADA05742 standard; protein; 247 AA.
 XX
 AC ADA05742;
 XX
 DT 06-NOV-2003 (first entry)
 DE Human NOV18f protein SEQ ID NO:102.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 XX

05-OCT-2001; 2001US-0327435P.
PR
09-OCT-2001; 2001US-0327449P.
PR
09-OCT-2001; 2001US-0327917P.
PR
09-OCT-2001; 2001US-0328029P.
PR
09-OCT-2001; 2001US-0328044P.
PR
09-OCT-2001; 2001US-0328056P.
PR
12-OCT-2001; 2001US-0328849P.
PR
15-OCT-2001; 2001US-0329414P.
PR
17-OCT-2001; 2001US-0330142P.
PR
18-OCT-2001; 2001US-0330309P.
PR
22-OCT-2001; 2001US-0341058P.
PR
24-OCT-2001; 2001US-0339266P.
PR
24-OCT-2001; 2001US-0343629P.
PR
29-OCT-2001; 2001US-0349575P.
PR
01-NOV-2001; 2001US-0346357P.
PR
17-APR-2002; 2002US-0373260P.
PR
19-APR-2002; 2002US-0373815P.
PR
19-APR-2002; 2002US-0373817P.
PR
19-APR-2002; 2002US-0373826P.
PR
19-APR-2002; 2002US-0373884P.
PR
22-APR-2002; 2002US-0374977P.
PR
16-MAY-2002; 2002US-0381037P.
PR
16-MAY-2002; 2002US-0381038P.
PR
16-MAY-2002; 2002US-0381042P.
PR
17-MAY-2002; 2002US-0381642P.
PR
28-MAY-2002; 2002US-0383656P.
PR
29-MAY-2002; 2002US-0383831P.
PR
25-JUN-2002; 2002US-0391335P.
PR
01-OCT-2002; 2002US-00262511.
XX

(CURA-) CURAGEN CORP.
XX
PA
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DU, Pena CEA, Shenoy SG,
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
WPI: 2003-381626/36.
DR N-PSDB; ADA05741.
XX
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 172; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
CC and anti-lipase activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
XX
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KERU/) KERUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGRE/) AGERS M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62905.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 102; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,

CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 50; DB 8; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
DB 193 GPLVCRGTL 201
|||||||
RESULT 13
ADA05732
ID ADA05732 standard; protein; 250 AA.
XX
AC ADA05732;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18a protein SEQ ID NO:92.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
OS Homo sapiens.
XX
XX WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX (CURA-) CURAGEN CORP.
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spyttek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ott T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CB, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05731.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 169-170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 50; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
|||
Db 204 GPLVCRGTL 212
RESULT 14
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
XX AC ADN62896;

XX 01-JUL-2004 (first entry)
XX Human NOV18a.
XX
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
XX (MILL/) MILLET I.
XX (PEYM/) PEYMAN J A.
XX (KEKU/) KEKUDA R.
XX (JUJU/) JU J.
XX (LILL/) LI L.
XX (GUOX/) GUO X.
XX (PATT/) PATTURAJAN M.
XX (SPYT/) SPYTEK K A.
XX (EDIN/) EDINGER S R.
XX (ELLE/) ELLERMAN K.
XX (MALY/) MALYANKAR U M.
XX (ORTT/) ORT T.
XX (GORM/) GORMAN L.
XX (ZERR/) ZERRHUSEN B D.
XX (ANDE/) ANDERSON D W.
XX (ZHON/) ZHONG M.
XX (CATT/) CATTERTON E.
XX (JIW/) JI W.
XX (MILL/) MILLER C E.
XX (RAST/) RASTELLI L.
XX (STON/) STONE D J.
XX (PENA/) PENA C E A.
XX (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M B.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62895.
DR
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
XX Claim 1; SEQ ID NO 92; 395pp; English.
XX
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 50; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
Db 204 GPLVCRGTL 212
RESULT 15
ADA05734
ID ADA05734 standard; protein; 252 AA.
XX
AC ADA05734;
XX
XX 06-NOV-2003 (first entry)

XX
DE
XX
XX Human NOV18b protein SEQ ID NO:94.
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
XX WO2003029424-A2.
XX
XX 10-APR-2003.
PD
XX
XX 02-OCT-2002; 2002WO-US031373.
PF
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05733.
DR
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector

CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders, such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.

SQ Sequence 252 AA;

Query Match 100.0%; Score 50; DB 6; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPLVCRGTL 9
Db 206 GPLVCRGTL 214
|||||

Search completed: March 11, 2006, 00:24:16
Job time : 86.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------------|
| 1 | 50 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 40 | 80.0 | 261 | 1 A32297 | semenogelase (EC 3 |
| 3 | 40 | 80.0 | 261 | 2 A29586 | tissue kallikrein |
| 4 | 40 | 80.0 | 262 | 2 T35999 | probable aminoglyc |
| 5 | 39 | 78.0 | 155 | 2 G72548 | hypothetical prote |
| 6 | 39 | 78.0 | 265 | 1 KQRTF | tissue kallikrein |
| 7 | 38 | 76.0 | 246 | 1 DBHU | complement factor |
| 8 | 38 | 76.0 | 261 | 1 S35711 | semenogelase (EC 3 |
| 9 | 37 | 74.0 | 46 | 2 I49416 | glandular kallikre |
| 10 | 37 | 74.0 | 96 | 2 A05308 | tissue kallikrein |
| 11 | 37 | 74.0 | 104 | 2 S15395 | tissue kallikrein |
| 12 | 37 | 74.0 | 156 | 2 B23863 | tissue kallikrein |
| 13 | 37 | 74.0 | 188 | 2 B32340 | tissue kallikrein |
| 14 | 37 | 74.0 | 225 | 2 S45356 | probable serine pr |
| 15 | 37 | 74.0 | 239 | 2 A27207 | tissue kallikrein |
| 16 | 37 | 74.0 | 240 | 2 S39047 | trypsin (EC 3.4.21 |
| 17 | 37 | 74.0 | 241 | 2 S39048 | trypsin (EC 3.4.21 |
| 18 | 37 | 74.0 | 244 | 2 A44284 | tissue kallikrein |
| 19 | 37 | 74.0 | 250 | 2 S15685 | tissue kallikrein, glandu |
| 20 | 37 | 74.0 | 254 | 2 S35585 | chymotrypsin-like |
| 21 | 37 | 74.0 | 258 | 2 I56220 | trypsin 2 - rat |
| 22 | 37 | 74.0 | 259 | 1 KQRTIN | tonin (EC 3.4.21.- |
| 23 | 37 | 74.0 | 259 | 2 A29746 | tissue kallikrein |
| 24 | 37 | 74.0 | 259 | 2 D23863 | tissue kallikrein |
| 25 | 37 | 74.0 | 260 | 2 I56559 | neuropsin - mouse |
| 26 | 37 | 74.0 | 261 | 1 KQMS1 | tissue kallikrein |
| 27 | 37 | 74.0 | 261 | 1 NGMSG | 7S nerve growth fa |
| 28 | 37 | 74.0 | 261 | 1 TRMSM5 | tissue kallikrein |
| 29 | 37 | 74.0 | 261 | 2 S45303 | tissue kallikrein |

gamma-renin (EC 3.
tissue kallikrein
tissue kallikrein
tissue kallikrein
tissue kallikrein
tissue kallikrein
tissue kallikrein
granzyme 3 (EC 3.4
riboflavin biosynt
kallikrein - mouse
elastase (EC 3.4.2
tissue kallikrein
tissue kallikrein
duodenase - bovine
trypsin (EC 3.4.21
trypsin (EC 3.4.21
trypsin (EC 3.4.21
snake venom factor

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hanson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:9521214; PIDN:
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 207 GPLVCRGTL 215

RESULT 2

A32297
semenogelase (EC 3.4.21.77) precursor [validated] - human
N;Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A32297; A32423; S03604; S05468; S05467; A32546; S02239; A26757; C31567; A315
R;Riegman, P.H.J.; Vlietstra, R.J.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
Biochem. Biophys. Res. Commun. 159, 95-102, 1989
A;Title: Characterization of the prostate-specific antigen gene: a novel human kallikrein
A;Reference number: A32297; MUID:89165891; PMID:2466464
A;Accession: A32297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <R1E>
A;Cross-references: UNIPROT:P07288; UNIPARC:UPI0000001C9E; GB:M24543
R;Lundwall, A.
Biochem. Biophys. Res. Commun. 161, 1151-1159, 1989
A;Title: Characterization of the gene for prostate-specific antigen, a human glandular ka
A;Reference number: A32423; MUID:89302090; PMID:2472789

A:Accession: A32423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <LUN>
A:Cross-references: UNIPARC:UPI0000001C98; GB:M27274; NID:g190552; PIDN:AAA60192.1; PID: R; Digby, M.; Zhang, X.Y.; Richards, R.I.
A:Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallikrein gene
A:Reference number: S03604; MUID:89183632; PMID:2467258
A:Accession: S03604
A:Molecule type: DNA
A:Residues: 1-261 <DTG>
A:Cross-references: UNIPARC:UPI0000001C98; EMBL:X13940
R; Klobbeck, H.G.; Combiato, G.; Schulz, P.; Arbush, V.; Fittler, F.
submitted to the EMBL Data Library, May 1989
A:Reference number: S05468
A:Accession: S05468
A:Molecule type: DNA
A:Residues: 1-261 <KL1>
A:Cross-references: UNIPARC:UPI0000001C98; EMBL:X14810; NID:g35732; PIDN:CAA32915.1; PID: R; Klobbeck, H.G.; Combiato, G.; Schulz, P.; Arbush, V.; Fittler, F.
Nucleic Acids Res. 17, 1981, 1989
A:Title: Genomic sequence of human prostate specific antigen (PSA)
A:Reference number: S05467; MUID:89282407; PMID:2471958
A:Accession: S05467
A:Molecule type: DNA
A:Residues: 1-29 <KL2>
A:Cross-references: UNIPARC:UPI0000172AC3; EMBL:X14810
R; Henttu, P.; Viikio, P.
Biochem. Biophys. Res. Commun. 160, 903-910, 1989
A:Title: cDNA coding for the entire human prostate specific antigen shows high homology to the rat prostate specific antigen
A:Reference number: A32546; MUID:89246551; PMID:2470373
A:Accession: A32546
A:Molecule type: mRNA
A:Residues: 1-72, 'T', '74-85', 'I', '87-174', 'P', '176-183', 'Q', '185-259', 'D', '261 <HEN>
A:Cross-references: UNIPARC:UPI0000172AC4; GB:M26663
R; Schulz, P.; Stucka, R.; Feldmann, H.; Combiato, G.; Klobbeck, H.G.; Fittler, F.
Nucleic Acids Res. 16, 6226, 1988
A:Title: Sequence of a cDNA clone encompassing the complete mature human prostate specific antigen
A:Reference number: S02239; MUID:88289366; PMID:2456523
A:Accession: S02239
A:Molecule type: mRNA
A:Residues: 1-72, 'T', '74-85', 'I', '87-174', 'P', '176-183', 'Q', '185-259', 'D', '261 <SCH>
A:Cross-references: UNIPARC:UPI0000172AC5; EMBL:X07730
R; Lundwall, A.; Lilja, H.
FEBS Lett. 214, 317-322, 1987
A:Title: Molecular cloning of human prostate specific antigen cDNA.
A:Reference number: A26757; MUID:87190978; PMID:2436946
A:Accession: A26757
A:Molecule type: mRNA
A:Residues: 5-261 <LU2>
A:Cross-references: UNIPARC:UPI000000044B
R; Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
Biochem. Biophys. Res. Commun. 155, 181-188, 1988
A:Title: Molecular cloning and characterization of novel prostate antigen cDNA's.
A:Reference number: A90144; MUID:88326297; PMID:2458104
A:Accession: C31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-164, 'CTPGDGAAGSPDANV' <RL4>
A:Cross-references: UNIPARC:UPI000006F45; GB:M21897; NID:g189529; PIDN:AAAS9997.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
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A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
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Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
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A:Molecule type: mRNA
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Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189529; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Teuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: The authors translated the codon GGC for residue 28 as Arg and TGG for residue 29 as Arg
A:Accession: B31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A

A:Accession: A29586
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: UNIPROT:P20151; UNIPARC:UPI000004CA0C; GB:M18157; NID:g186640; PIDN:
A>Note: the authors translated the codon TAC for residue 43 as Trp
C:Genetics:
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 80.0%; Score 40; DB 2; Length 261;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||: |||
DB 215 GPLVCNGVL 223

RESULT 4
T35999
probable aminoglycoside acetyltransferase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T35999
R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21574
A:Accession: T35999
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-262 <SEE>
A:Cross-references: UNIPROT:O9XAC9; UNIPARC:UPI000000DB235; EMBL:AL096839; PIDN:CAB50752.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SC06DB:SCC22.09
C:Superfamily: Escherichia coli aminoglycoside N3'-acetyltransferase

Query Match 80.0%; Score 40; DB 2; Length 262;
Best Local Similarity 88.9%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||: |||
DB 8 GPLVTRGTL 16

RESULT 5
G72548
hypothetical protein APE1675 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72548
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <KAW>
A:Cross-references: UNIPROT:Q9YBC2; UNIPARC:UPI000005E041; DDBJ:AP000062; NID:G5105244;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1675

Query Match 78.0%; Score 39; DB 2; Length 155;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||: |||
DB 23 GPLITRGTL 31

RESULT 6
KQRTF
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of t
A:Reference number: A00944; MUID:83117659; PMID:6961406
A:Accession: A00944
A:Molecule type: mRNA
A:Residues: 1-265 <SWI>
A:Cross-references: UNIPROT:P00758; UNIPARC:UPI0000167958
A:Experimental source: pancreatic
R:Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: wit
A:Reference number: A41429; MUID:88198057; PMID:3482210
A:Accession: A41429
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-53, 'X', 55-87 <KAT>
A:Cross-references: UNIPARC:UPI0000172ABF
R:Gerald, W.L.; Chao, J.; Chao, L.
Biochim. Biophys. Acta 866, 1-14, 1986
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A:Reference number: A25137; MUID:86131678; PMID:3004582
A:Accession: A25137
A:Molecule type: mRNA
A:Residues: 115-265 <GER>
A:Cross-references: UNIPARC:UPI0000172AC0
R:Inoue, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed i
A:Reference number: JX0073; MUID:89327211; PMID:2753879
A:Accession: JX0073
A:Molecule type: DNA
A:Residues: 1-265 <INO>
A:Cross-references: UNIPARC:UPI0000167958; GB:D00448; NID:g220792; PIDN:BAA00346.1; PID:
A:Experimental source: kidney
R:Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A:Reference number: A23863; MUID:86051477; PMID:2998455
A:Accession: A23863
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <ASH>
A:Cross-references: UNIPARC:UPI0000167958; GB:M11563; NID:g205029; PIDN:AAA41464.1; PID:
A:Experimental source: submaxillary gland
R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A:Title: Organization and expression of the rat kallikrein gene family.
A:Reference number: A33359; MUID:89214217; PMID:2708383
A:Accession: A33359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 5-265 <WIN>
A:Cross-references: UNIPARC:UPI000012DBE1; GB:M23874; GB:J04701; GB:M23875; GB:M23876; N
C:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin
C:Comment: The protein presumably assumes the two-chain form by cleavage between residue
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release l
C:Genetics:
A:Introns: 20/1; 73/2; 169/1; 214/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-28/Domain: activation peptide #status predicted <APT>
F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MPT>
F:29-257/Domain: trypsin homology <TRY>
F:35-177,54-70,156-223,213-238/Disulfide bonds: #status predicted
F:69,124,217/Active site: His, Asp, Ser #status predicted

Query Match 78.0%; Score 39; DB 1; Length 265;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 219 GPLICNGVL 227
|||||

RESULT 7
DBHU
complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N:Alternate names: adipain; C3 convertase activator
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A40197; A00936; A60571; S66645
R:White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.; J. Biol. Chem. 267, 9210-9213, 1992
A:Title: Human adipain is identical to complement factor D and is expressed at high level
A:Reference number: A40197; MUID:92250520; PMID:1374388
A:Accession: A40197
A:Molecule type: mRNA
A:Residues: 1-246 <WHI>
A:Cross-references: UNIPROT:P00746; UNIPARC:UPI0000172AB4; GB:M84526
R:Niemann, M.A.; Bhow, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A:Title: Amino acid sequence of human D of the alternative complement pathway.
A:Reference number: A00936; MUID:85000441; PMID:6383466
A:Accession: A00936
A:Molecule type: protein
A:Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXXITIE',90-172,86-91,185-235,'
A:Cross-references: UNIPARC:UPI0000172AE5
A:Note: a few residues were assigned from the previously published sequence of Reid et al
R:Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya
Mol. Immunol. 27, 637-644, 1990
A:Title: Molecular and functional identification and purification of complement component
A:Reference number: A60571; MUID:90370044; PMID:2395435
A:Accession: A60571
A:Molecule type: protein
A:Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
A:Cross-references: UNIPARC:UPI0000172AE6
R:Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A:Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement
A:Reference number: S66645; MUID:196013156; PMID:7556615
A:Accession: S66645
A>Status: preliminary
A:Molecule type: protein
A:Residues: 19-44,'C',46-48 <BAL>
A:Cross-references: UNIPARC:UPI0000172AE7
C:Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
C:Genetics:
A:Gene: GDB:DF
A:Cross-references: GDB:132645; OMIM:134350
A:Map position: Xpter-Xqter
A:Superfamily: trypsin; trypsin homology
C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-246/Product: complement factor D (fragment) #status experimental <MAT>
F:19-241/Domain: trypsin homology <TRY>
F:44-60,141-207,172-189,197-222/Disulfide bonds: #status predicted
F:59,105,201/Active site: His, Asp, Ser #status predicted

Query Match 76.0%; Score 38; DB 1; Length 246;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 203 GPLVCGGVL 211
|||||

RESULT 8
S35711
semenogelase (EC 3.4.21.77) precursor - rhesus macaque
N:Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: S35711; S34239
R:Gauthier, E.R.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.
Biochim. Biophys. Acta 1174, 207-210, 1993
A:Title: Characterization of rhesus monkey prostate specific antigen cDNA.
A:Reference number: S35711; MUID:93363642; PMID:7689340
A:Accession: S35711
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: UNIPROT:P33619; UNIPARC:UPI000012DEE4; EMBL:X73560; NID:g311843; PID:
C:Comment: This enzyme preferentially cleaves after tyrosine residues.
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; prostate; serine proteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-24/Domain: propeptide #status predicted <PRO>
F:25-261/Product: semenogelase #status predicted <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 76.0%; Score 38; DB 1; Length 261;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 215 GPLVCDGVL 223
|||||

RESULT 9
I49416
glandular kallikrein - western wild mouse (fragment)
C:Species: Mus sputus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A:Accession: I49416
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49416
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-46 <RES>
A:Cross-references: UNIPROT:Q62540; UNIPARC:UPI00000E8743; EMBL:U05716; NID:g497047; PID:
C:Superfamily: trypsin; trypsin homology

Query Match 74.0%; Score 37; DB 2; Length 46;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 1 GPLICDGVL 9
|||||

RESULT 10
A05308
tissue kallikrein (EC 3.4.21.35), submandibular mGK-2 - mouse (fragment)
N:Alternate names: glandular kallikrein
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1997 #text_change 22-Jun-1999
C:Accession: A05308
R:Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.

Nature 303, 300-307, 1983
A;Title: Structure of mouse kallikrein gene family suggests a role in specific processing
A;Reference number: A009411; MUID:83219214; PMID:6602295
A;Accession: A05308
A;Molecule type: DNA
A;Residues: 1-96 <MAS>
A;Cross-references: UNIPARC:UPI000011E01B; GB:V00829; NID:G52775; PIDN:CAA24212.1; PID:9
A;Experimental source: Quakembush inbred strain
A;Note: this sequence has been translated from two exons (11-147 and 522-674) located up
C;Comment: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
C;Genetics:
A;Gene: mGK-2
A;Map position: 7
A;Introns: 45/3
A;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland
F;1-88/Domain: trypsin homology (fragment) <TRY>

Query Match 74.0%; Score 37; DB 2; Length 96;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 50 GPLICDGV 58

RESULT 11
S15395
tissue kallikrein-related proteinase (EC 3.4.21.-) k10 - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 19-Jul-1996 #text_change 17-Oct-1997
C;Accession: S15395; S15448
R;Gutman, N.; Elmoujahed, A.; Brillard, M.; Monegier du Sorbier, B.; Gauthier, F.
Eur. J. Biochem. 197, 425-429, 1991
A;Title: Microheterogeneity of rat submaxillary gland kallikrein k10, a member of the ka
A;Reference number: S15395; MUID:91224135; PMID:2026164
A;Accession: S15395
A;Molecule type: protein
A;Residues: 1-23;24-51;52-104 <GUT>
A;Cross-references: UNIPARC:UPI0000175BB8; UNIPARC:UPI0000175BB9; UNIPARC:UPI0000175BBA
A;Experimental source: submaxillary gland
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-104/Domain: trypsin homology (fragments) <TRY>
F;1-23/Product: tissue kallikrein-related protein k10 light chain (fragment) #status ex
F;24-51/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex
F;52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex

Query Match 74.0%; Score 37; DB 2; Length 104;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 70 GPLICDGV 78

RESULT 12
B23863
tissue kallikrein (EC 3.4.21.35) S1, submaxillary - rat (fragment)
N;Alternate names: glandular kallikrein; kininogenin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
C;Accession: B23863
R;Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A;Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A;Reference number: A23863; MUID:86051477; PMID:2998455
A;Accession: B23863
A;Molecule type: mRNA
A;Residues: 1-156 <ASH>
A;Cross-references: UNIPROT:P15950; UNIPARC:UPI00001709DD; GB:M11564; NID:G205031; PIDN:

C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-148/Domain: trypsin homology (fragment) <TRY>

Query Match 74.0%; Score 37; DB 2; Length 156;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 110 GPLICDGV 118

RESULT 13
B32340
tissue kallikrein (EC 3.4.21.35) 3 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B32340
R;Shai, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
Biochemistry 28, 5334-5343, 1989
A;Title: Characterization of genes encoding rat tonin and a kallikrein-like serine protease
A;Reference number: A32340; MUID:89375248; PMID:2550051
A;Accession: B32340
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <SHA>
A;Cross-references: UNIPROT:P15950; UNIPARC:UPI0000170B08; GB:M26534; NID:G206773; PIDN:
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-180/Domain: trypsin homology (fragment) <TRY>

Query Match 74.0%; Score 37; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 142 GPLICDGV 150

RESULT 14
S45356
probable serine proteinase (EC 3.4.21.-) ACO - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
C;Accession: S45356
R;Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A;Title: A novel serine proteinase-like sequence from human brain.
A;Reference number: S45356; MUID:94289486; PMID:8018728
A;Accession: S45356
A;Molecule type: mRNA
A;Residues: 1-225 <DIH>
A;Cross-references: UNIPARC:UPI000016AFB3; EMBL:X75363; NID:G407137; PIDN:CAA53145.1; PI
A;Experimental source: Alzheimer's disease patient brain cortex
C;Genetics:
A;Gene: ACO
A;Introns: 175/3
A;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase

Query Match 74.0%; Score 37; DB 2; Length 225;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 180 GPLVCGGIL 188

RESULT 15
A27207

tissue kallikrein (EC 3.4.21.35), prostatic - guinea pig
N:Alternate names: glandular kallikrein
C:Species: Cavia porcellus (guinea pig)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27207
R:Dunbar, J.C.; Bradshaw, R.A.
Biochemistry 26, 3471-3478, 1987
A:Title: Amino acid sequence of guinea pig prostatic kallikrein.
A:Reference number: A27207; MUID:88000549; PMID:3307909
A:Accession: A27207
A:Molecule type: protein
A:Residues: 1-239 <DUN>
A:Cross-references: UNIPROT:P12323; UNIPARC:UPI0000012DEE2
A:Note: 50-Trp was also found
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-231/Domain: trypsin homology <TRY>
F:41,96,191/Active site: His, Asp, Ser #status predicted

Query Match 74.0%; Score 37; DB 2; Length 239;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 193 GPLICDGV 201

Search completed: March 11, 2006, 00:40:51
Job time : 14.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 50 | 100.0 | 140 | Q5R567_PONPY | Q5R567 pongo pygma |
| 2 | 50 | 100.0 | 253 | KLK7_HUMAN | P49862 homo sapien |
| 3 | 45 | 90.0 | 250 | KLK9_HUMAN | Q9UKQ9 homo sapien |
| 4 | 45 | 90.0 | 251 | Q9DBQ8_MOUSE | Q9DBQ8 mus musculus |
| 5 | 44 | 88.0 | 210 | Q63211_XENLA | Q63211 xenopus lae |
| 6 | 44 | 88.0 | 251 | KLK14_HUMAN | Q9PQ03 homo sapien |
| 7 | 44 | 88.0 | 251 | Q6B089_HUMAN | Q6B089 homo sapien |
| 8 | 41 | 82.0 | 87 | Q9CQ78_MOUSE | Q9CQ78 m mus muscu |
| 9 | 41 | 82.0 | 249 | Q9QYN4_MOUSE | Q9QYN4 mus musculus |
| 10 | 41 | 82.0 | 253 | Q5QB85_9DIPT | Q5QB85 culicoides |
| 11 | 41 | 82.0 | 276 | Q9QYN3_MOUSE | Q9QYN3 m hippostas |
| 12 | 41 | 82.0 | 612 | Q83WX7_STRBO | Q83WX7 streptomyc |
| 13 | 41 | 82.0 | 621 | Q8G3L1_BIFLO | Q8G3L1 bifidobacte |
| 14 | 41 | 82.0 | 3201 | Q9F828_9ACTO | Q9F828 micromonosp |
| 15 | 41 | 82.0 | 3546 | Q9F830_9ACTO | Q9F830 micromonosp |
| 16 | 40 | 80.0 | 185 | Q7Q831_ANOGA | Q7Q831 anopheles g |
| 17 | 40 | 80.0 | 220 | Q8NCW4_HUMAN | Q8NCW4 homo sapien |
| 18 | 40 | 80.0 | 231 | Q6GYJ5_STRCA | Q6GYJ5 struthio ca |
| 19 | 40 | 80.0 | 248 | Q5M813_XENTR | Q5M813 xenopus tro |
| 20 | 40 | 80.0 | 254 | Q9XSN6_PIG | Q9XSN6 sus scrofa |
| 21 | 40 | 80.0 | 255 | Q7Q235_ANOGA | Q7Q235 anopheles g |
| 22 | 40 | 80.0 | 257 | Q6LDS3_HUMAN | Q6LDS3 homo sapien |
| 23 | 40 | 80.0 | 257 | Q8QG86_BOTIN | Q8QG86 bothrops in |
| 24 | 40 | 80.0 | 258 | VSP3_BOTJA | Q9PTU8 bothrops ja |
| 25 | 40 | 80.0 | 260 | 1_NRPN_RAT | Q8B780 rattus norv |
| 26 | 40 | 80.0 | 260 | Q71QJ2_TRIST | Q71QJ2 trimeresuru |
| 27 | 40 | 80.0 | 260 | Q71QI4_TRIST | Q71QI4 trimeresuru |
| 28 | 40 | 80.0 | 260 | Q71QH9_TRIST | Q71QH9 trimeresuru |
| 29 | 40 | 80.0 | 261 | 1_KLK2_HUMAN | P20151 homo sapien |
| 30 | 40 | 80.0 | 261 | KLK3_HUMAN | P07288 homo sapien |
| 31 | 40 | 80.0 | 261 | Q546G3_HUMAN | Q546G3 homo sapien |

| | | | | | |
|----|----|------|-----|--------------|--------------------|
| 32 | 40 | 80.0 | 262 | Q9YAC9_STRCO | Q9YAC9 streptomyc |
| 33 | 40 | 80.0 | 619 | Q8KEH3_CHLTE | Q8KEH3 chlorobium |
| 34 | 39 | 78.0 | 155 | Q9YBC2_AERPE | Q9YBC2 aeropyrum p |
| 35 | 39 | 78.0 | 161 | Q5TUL3_ANOGA | Q5TUL3 anopheles g |
| 36 | 39 | 78.0 | 176 | Q52Q15_9PERC | Q52Q15 anoplarchus |
| 37 | 39 | 78.0 | 178 | Q52Q14_9PERC | Q52Q14 xiphister m |
| 38 | 39 | 78.0 | 214 | Q4SSW0_TETNG | Q4SSW0 tetraodon n |
| 39 | 39 | 78.0 | 247 | Q9W7Q5_PAROL | Q9W7Q5 paralicthy |
| 40 | 39 | 78.0 | 249 | Q5M910_XENTR | Q5M910 xenopus tro |
| 41 | 39 | 78.0 | 249 | Q5M8T8_XENTR | Q5M8T8 xenopus tro |
| 42 | 39 | 78.0 | 252 | Q5M908_XENTR | Q5M908 xenopus tro |
| 43 | 39 | 78.0 | 254 | Q5XG53_XENLA | Q5XG53 xenopus lae |
| 44 | 39 | 78.0 | 261 | KLK1_RAT | P00758 r nerve gro |
| 45 | 39 | 78.0 | 297 | Q9W174_DROME | Q9W174 drosophila |

ALIGNMENTS

RESULT 1
Q5R567_PONPY
ID Q5R567_PONPY PRELIMINARY; PRT; 140 AA.
AC Q5R567;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKF2p459B0918.
GN Name=DKF2p459B0918;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German CDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR860999; CAH93099.1; -; mRNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50240; TRYPsin DOM; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
SQ SEQUENCE 140 AA; 15127 MW; 8DD6280252A39311 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
Db 94 GPLVCRGTL 102

RESULT 2
KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (SC 3.4.21.-) (hK7) (Stratum corneum
chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

| | |
|----|--|
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. |
| OC | NCBI_TaxID=9606; |
| OC | [1] |
| RP | NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53. |
| RP | TISSUE=Skin; |
| RC | MEDLINE=94308225; PubMed=8034709; |
| RA | Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.; |
| RA | "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; |
| RT | Chymotryptic enzyme. A skin-specific human serine proteinase."; |
| RL | J. Biol. Chem. 269:19420-19426 (1994). |
| RL | [2] |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION. |
| RP | TISSUE=Keratinocyte; |
| RC | PubMed=10574542; DOI=10.1016/S0378-1119(00)00280-8; |
| RA | Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., Diamandis E.P.; |
| RA | "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal regulation."; |
| RT | Characterization, mapping, tissue expression and hormonal regulation."; |
| RL | Gene 254:119-128 (2000). |
| RL | [3] |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. |
| RC | PubMed=10574542; DOI=10.1016/S0378-1119(00)00382-6; |
| RA | Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepel B., Wang K.; |
| RA | "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; |
| RT | Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; |
| RL | Gene 257:119-130 (2000). |
| RL | [4] |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. |
| RC | Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.; |
| RA | "Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic itchy dermatitis."; |
| RT | Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic itchy dermatitis."; |
| RL | Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases. |
| RL | [5] |
| RP | NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY. |
| RC | TISSUE=Ovarian carcinoma; |
| RC | MEDLINE=22623266; PubMed=12738725; |
| RA | Dong Y., Kaushal A., Brattsdorf M., Nicklin J., Clements J.A.; |
| RA | "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers."; |
| RT | Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers."; |
| RL | Clin. Cancer Res. 9:1710-1720 (2003). |
| RL | [6] |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1). |
| RC | TISSUE=Skin; |
| RC | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; |
| RA | Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Distchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; |
| RA | "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; |
| RT | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). |
| RL | [7] |
| RP | CHARACTERIZATION. |
| RP | Medline=95314630; PubMed=7794273; |
| RA | Skytt A., Stroemqvist M., Egelrud T.; |
| RT | "Primary substrate specificity of recombinant human stratum corneum chymotryptic enzyme."; |
| RL | Biochem. Biophys. Res. Commun. 211:586-589 (1995). |
| RL | [1] |
| RP | NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY. |
| RC | TISSUE=Skin; |
| RC | MEDLINE=94308225; PubMed=8034709; |
| RA | Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.; |
| RA | "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; |
| RT | Chymotryptic enzyme. A skin-specific human serine proteinase."; |
| RL | J. Biol. Chem. 269:19420-19426 (1994). |
| RL | [2] |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION. |
| RC | TISSUE=Keratinocyte; |
| RC | PubMed=10574542; DOI=10.1016/S0378-1119(00)00280-8; |
| RA | Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., Diamandis E.P.; |
| RA | "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal regulation."; |
| RT | Characterization, mapping, tissue expression and hormonal regulation."; |
| RL | Gene 254:119-128 (2000). |
| RL | [3] |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. |
| RC | PubMed=10574542; DOI=10.1016/S0378-1119(00)00382-6; |
| RA | Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepel B., Wang K.; |
| RA | "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; |
| RT | Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; |
| RL | Gene 257:119-130 (2000). |
| RL | [4] |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. |
| RC | Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.; |
| RA | "Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic itchy dermatitis."; |
| RT | Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic itchy dermatitis."; |
| RL | Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases. |
| RL | [5] |
| RP | NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY. |
| RC | TISSUE=Ovarian carcinoma; |
| RC | MEDLINE=22623266; PubMed=12738725; |
| RA | Dong Y., Kaushal A., Brattsdorf M., Nicklin J., Clements J.A.; |
| RA | "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers."; |
| RT | Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers."; |
| RL | Clin. Cancer Res. 9:1710-1720 (2003). |
| RL | [6] |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1). |
| RC | TISSUE=Skin; |
| RC | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; |
| RA | Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Distchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P |

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200016C12 product:similar to KALLIKREIN 9 (EC 3.4.21.-)
DE (KALLIKREIN-LIKE PROTEIN 3) (KUK- L3).
GN Name=1200016C12R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P. Hayaahizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynehaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaahizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayaahizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kicsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaahizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384 format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima J., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayaahizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AK004807; BAB23579.1; -, mRNA.
DR HSSP; P00746; IFDP.
DR MEROPS; S01.307; -.
DR Ensembl; ENSMUSG00000047884; Mus musculus.
DR MGI; MGI:1921082; 120016C12R1k.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP SP; 1.
DR PROSITE; PS00240; TRYP SIN DOM; 1.
DR PROSITE; PS00134; TRYP SIN HIS; UNKNOWN 1.
SQ SEQUENCE 251 AA; 28155 MW; F4D667F8C80C4A23 CRC64;

Query Match 90.0%; Score 45; DB 2; Length 251;
Best Local Similarity 88.9%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 206 GPLVCEGTL 214
|||||
|||

RESULT 5
Q63211 XENLA
ID Q63211_XENLA PRELIMINARY; PRT; 210 AA.
AC Q63211;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE LOC494802 protein.
GN Name=LOC494802;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

FT DISULFID 52 68 By similarity.
FT DISULFID 143 210 By similarity.
FT DISULFID 175 189 By similarity.
FT DISULFID 200 225 By similarity.
SQ SEQUENCE 251 AA; 27453 MW; 9087953BAFA7ED25 CRC64;

Query Match 88.0%; Score 44; DB 1; Length 251;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
| | | | | | |
Db 206 GPLVCRGQL 214

RESULT 7
Q6B089 HUMAN
ID Q6B089 HUMAN PRELIMINARY; PRT; 251 AA.
AC Q6B089;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 14, preproprotein.
GN Name=KLK14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebrow B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL EMBL; BC074905; AAH74905.1; -; mRNA.
DR EMBL; BC074904; AAH74904.1; -; mRNA.
DR Ensembl; ENSG00000129437; Homo sapiens.
DR GO; GO:004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 251 AA; 27507 MW; C353A7D8B1960BD2 CRC64;

Query Match 88.0%; Score 44; DB 2; Length 251;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
| | | | | | |
Db 206 GPLVCRGQL 214

RESULT 8
Q9CQ78 MOUSE
ID Q9CQ78 MOUSE PRELIMINARY; PRT; 87 AA.
AC Q9CQ78;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Mus musculus adult male tongue cDNA, RIKEN full-length
DE library, clone:2310081E03 product:protease, serine, 20, full insert
DE sequence (Mus musculus adult male tongue cDNA, RIKEN full-length
DE enriched library, clone:2310021N04 product:protease, serine, 20, full
DE insert sequence) (Fragment).
DE GN Name=2310015I08Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085560; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Clothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., Mckenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Pavlovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RN Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hayama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RN Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanganaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numezaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanganaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK019102; BAB31548.1; -; mRNA.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR MGI; MGI:1929977; 2310015108Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00889; Trypsin; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
FT NON_TER
SQ SEQUENCE 87 AA; 9549 MW; B988D0CD62926EAA CRC64;
Query Match 82.0%; Score 41; DB 2; Length 87;
Best Local Similarity 77.8%; Pred. NO. 5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
DB 42 GPLVCGSL 50
RESULT 9
Q9QYN4 MOUSE
ID Q9QYN4.MOUSE PRELIMINARY; PRT; 249 AA.
AC Q9QYN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hipostasin.
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hipostasin/TLSP (PRSS20).";
RN Biochim. Biophys. Acta 1494:206-210 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016226; BAA88825.1; -; mRNA.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR MGI; MGI:1929977; 2310015108Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00889; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 249;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 GPLVCRGTL 9
||| ||| |||
Db 204 GPLVCNGSL 212

RESULT 10

Q5QBG5 9DIPT
ID Q5QBG5 9DIPT PRELIMINARY; PRT; 253 AA.
AC Q5QBG5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serine protease (Fragment).
OS Culicoides sonorensis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
OX NCBI_TaxID=179676;
RN [1]

NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=15796745;
RA Campbell C.L., Vandyke K.A., Letchworth G.J., Drolet B.S.,
RA Hanekamp T., Wilson W.C.;
RT "Midgut and salivary gland transcriptomes of the arbovirus vector
RT Culicoides sonorensis (Diptera: Ceratopogonidae).";
RL Insect Mol. Biol. 14:121-136 (2005).
DR EMBL; AY752846; AAV84259.1; -; mRNA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0001915; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Protease.
FT NON_TER
SQ SEQUENCE 253 AA; 27254 MW; 1A458EB8B5D32B48 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 253;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
||| ||| |||
Db 210 GPLACNGTL 218

RESULT 11

Q9QYN3_MOUSE
ID Q9QYN3_MOUSE PRELIMINARY; PRT; 276 AA.
AC Q9QYN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hippocampus prostate type (Mus musculus adult male tongue cDNA, RIKEN
DE full-length enriched library, clone:2310015108 product:protease,
DE serine, 20, full insert sequence) (Mus musculus adult male tongue
DE cDNA, RIKEN full-length enriched library, clone:2310040F07
DE product:protease, serine, 20, full insert sequence).
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hippostasin/TLSP (PRSS20).";
RL Biochim. Biophys. Acta 1494:206-210 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RT Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakauchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanaoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016227; BAA36955.1; -; mRNA.
DR EMBL; AK009360; BAB26241.2; -; mRNA.
DR EMBL; AK009720; BAB26461.2; -; mRNA.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257;
DR Ensembl; ENSMUSG0000030893; Mus musculus.
DR MGI; MGI:1929977; 2310015108Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30754 MW; 90BDC03A8AB178D6 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 276;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
||||| |:
Db 231 GPLVCGSL 239

RESULT 12
Q83WX7_STRRO

ID Q83WX7_STRRO PRELIMINARY; PRT; 612 AA.
AC Q83WX7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Streptomyces rochei (Streptomyces parvullus).
OG Plasmid pSLA2-L.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1928;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=7434AN4;
RX MEDLINE=22676866; PubMed=12791134;
DOI=10.1046/j.1365-2958.2003.03523.x;
RA Mochizuki S., Hiratsu K., Suwa M., Ishii T., Sugino F., Yamada K.,
RA Kinaishi H.;
RT "The large linear plasmid pSLA2-L of Streptomyces rochei has an
RT unusually condensed gene organization for secondary metabolism.";
RL Mol. Microbiol. 48:1501-1510 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=7434AN4;
RX MEDLINE=20408175; PubMed=10954087;
RA Hiratsu K., Mochizuki S., Kinaishi H.;
RT "Cloning and analysis of the replication origin and the telomeres of
RT the large linear plasmid pSLA2-L in Streptomyces rochei.";
RL Mol. Genet. 263:1015-1021 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=7434AN4;
RX MEDLINE=20231737; PubMed=10767533; DOI=10.1016/S0378-1119(00)00060-3;
RA Suwa M., Sugino H., Sasaoka A., Mori E., Fujii S., Shinkawa H.,
RA Nimi O., Kinaishi H.;
RT "Identification of two polyketide synthase gene clusters on the linear
RT plasmid pSLA2-L in Streptomyces rochei.";
RL Gene 246:123-131 (2000).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=7434AN4;
RX MEDLINE=99053144; PubMed=9836424;
RA Kinaishi H., Fujii S., Hatanai A., Kurokawa T., Shinkawa H.;
RT "Physical mapping of the linear plasmid pSLA2-L and localization of
RT the eryA and actI homologs.";
RL Biosci. Biotechnol. Biochem. 62:1892-1897 (1998).
DR EMBL; AB088224; BAC76588.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 612 AA; 66525 MW; 9BF0E1EE8D3110FC CRC64;
Query Match 82.0%; Score 41; DB 2; Length 612;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
||||| |:
Db 250 GPLVCACTV 258

RESULT 13
Q8G3L1_BIFLO
ID Q8G3L1_BIFLO PRELIMINARY; PRT; 621 AA.
AC Q8G3L1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable long-chain-fatty-acid--CoA ligase; long-chain acyl-CoA
DE synthetase.
GN Name=fadD4; OrderedLocusNames=BL1748;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216916;

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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL; AE014295; AAN25531.1; -; Genomic_DNA.
DR HSSP; P08659; 1LCI.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; F:aldehyde dehydrog.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR Complete proteome; Ligase.
KW SEQUENCE 621 AA; 67948 MW; 5BCDD84B5BF3083A CRC64;

Query Match 82.0%; Score 41; DB 2; Length 621;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRG 7
Db 436 GPLVCRG 442

RESULT 14
Q9F828_9ACTO
ID Q9F828_9ACTO PRELIMINARY; PRT; 3201 AA.
AC Q9F828_
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Megalomicin 6-deoxyerythronolide B synthase 3.
GN Name=megAIII;
OS Micromonospora megalomicina subsp. nigra.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Micromonospora.
OX NCBI_TaxID=136926;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL3275;
RX MEDLINE=20430101; PubMed=10972798;
RA Volchegursky Y., Hu Z., Katz L., McDaniel R.;
RT "Biosynthesis of the anti-parasitic agent megalomicin: transformation
RT of erythromycin to megalomicin in Saccharopolyspora erythraea.";
RL Mol. Microbiol. 37:752-762(2000).
DR EMBL; AF263245; AAG13919.1; -; Genomic_DNA.
DR HSSP; P72391; 1NM2.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016788; F:hydrolase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0031177; F:phosphotransferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR001227; ACP_transferase.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR006163; Phosphanteth_bind.
DR InterPro; IPR006162; Ppantne_S.
DR Pfam; PF00698; Acyl_transf_1; 3.
DR Pfam; PF00106; adh_short; 2.
DR Pfam; PF00109; ketoacyl-synt_C; 2.
DR Pfam; PF02801; Ketoacyl-synt_C; 2.
DR Pfam; PF00550; PP-binding; 3.
DR PROSITE; PS50075; ACP DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_2.
DR PROSITE; PS00012; PHOSPHOTANTHETINE; 2.
DR SEQUENCE 3546 AA; 371193 MW; 86C6794E95415BBC CRC64;

Query Match 82.0%; Score 41; DB 2; Length 3546;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1877 GPMVCRGGL 1885

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DR Pfam; PF00698; Acyl_transf_1; 2.
DR Pfam; PF00106; adh_short; 2.
DR Pfam; PF00109; ketoacyl-synt_C; 2.
DR Pfam; PF02801; Ketoacyl-synt_C; 2.
DR Pfam; PF00550; PP-binding; 2.
DR Pfam; PF00975; Thioesterase; 1.
DR PROSITE; PS50075; ACP DOMAIN; 2.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR PROSITE; PS00012; PHOSPHOTANTHETINE; 2.
DR PROSITE; PS00626; RCL_2; UNKNOWN_1.
DR SEQUENCE 3201 AA; 343783 MW; 44BDA30E14855650 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 3201;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1877 GPMVCRGGL 1885

RESULT 15
Q9F830_9ACTO
ID Q9F830_9ACTO PRELIMINARY; PRT; 3546 AA.
AC Q9F830_
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Megalomicin 6-deoxyerythronolide B synthase 1.
GN Name=megAI;
OS Micromonospora megalomicina subsp. nigra.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Micromonospora.
OX NCBI_TaxID=136926;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL3275;
RX MEDLINE=20430101; PubMed=10972798;
RA Volchegursky Y., Hu Z., Katz L., McDaniel R.;
RT "Biosynthesis of the anti-parasitic agent megalomicin: transformation
RT of erythromycin to megalomicin in Saccharopolyspora erythraea.";
RL Mol. Microbiol. 37:752-762(2000).
DR EMBL; AF263245; AAG13917.1; -; Genomic_DNA.
DR HSSP; P72391; 1NM2.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0031177; F:phosphotransferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR001227; ACP_transferase.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR006163; Phosphanteth_bind.
DR InterPro; IPR006162; Ppantne_S.
DR Pfam; PF00698; Acyl_transf_1; 3.
DR Pfam; PF00106; adh_short; 2.
DR Pfam; PF00109; ketoacyl-synt_C; 2.
DR Pfam; PF02801; Ketoacyl-synt_C; 2.
DR Pfam; PF00550; PP-binding; 3.
DR PROSITE; PS50075; ACP DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_2.
DR PROSITE; PS00012; PHOSPHOTANTHETINE; 2.
DR SEQUENCE 3546 AA; 371193 MW; 86C6794E95415BBC CRC64;

Query Match 82.0%; Score 41; DB 2; Length 3546;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

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Db 2397 GPWVCRGGL 2405
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Search completed: March 11, 2006, 00:38:52
Job time : 97.3333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 50 | 100.0 | 9 | 2 | US-09-502-600-80 |
| 2 | 50 | 100.0 | 9 | 2 | US-09-918-243-80 |
| 3 | 50 | 100.0 | 224 | 2 | US-08-944-483-33 |
| 4 | 50 | 100.0 | 225 | 1 | US-08-557-146-12 |
| 5 | 50 | 100.0 | 225 | 1 | US-09-027-337-4 |
| 6 | 50 | 100.0 | 225 | 1 | US-09-154-344-12 |
| 7 | 50 | 100.0 | 225 | 2 | US-09-644-600-4 |
| 8 | 50 | 100.0 | 225 | 2 | US-09-654-600A-4 |
| 9 | 50 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 10 | 50 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 11 | 50 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 12 | 50 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 13 | 50 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 14 | 50 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 15 | 50 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 16 | 50 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 17 | 41 | 82.0 | 276 | 2 | US-09-856-320A-4 |
| 18 | 41 | 82.0 | 3201 | 2 | US-09-679-279-15 |
| 19 | 41 | 82.0 | 3546 | 2 | US-09-679-279-13 |
| 20 | 40 | 80.0 | 20 | 1 | US-08-472-228A-19 |
| 21 | 40 | 80.0 | 20 | 2 | PCT-US96-09303-19 |
| 22 | 40 | 80.0 | 20 | 4 | PCT-US96-09303-19 |
| 23 | 40 | 80.0 | 237 | 1 | US-08-096-946-10 |
| 24 | 40 | 80.0 | 237 | 1 | US-08-096-946-11 |
| 25 | 40 | 80.0 | 237 | 1 | US-08-844-024-2 |
| 26 | 40 | 80.0 | 237 | 1 | US-08-718-547-2 |
| 27 | 40 | 80.0 | 237 | 2 | US-08-768-859A-1 |

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|----|----|------|-----|---|-------------------|-------------------|
| 28 | 40 | 80.0 | 237 | 2 | US-08-768-859A-16 | Sequence 16, Appl |
| 29 | 40 | 80.0 | 237 | 2 | US-08-768-859A-21 | Sequence 21, Appl |
| 30 | 40 | 80.0 | 237 | 2 | US-08-767-820A-1 | Sequence 1, Appl |
| 31 | 40 | 80.0 | 237 | 2 | US-08-767-820A-16 | Sequence 16, Appl |
| 32 | 40 | 80.0 | 237 | 2 | US-08-767-820A-21 | Sequence 21, Appl |
| 33 | 40 | 80.0 | 237 | 2 | US-08-622-046B-1 | Sequence 1, Appl |
| 34 | 40 | 80.0 | 237 | 2 | US-08-622-046B-7 | Sequence 7, Appl |
| 35 | 40 | 80.0 | 237 | 2 | US-08-622-046B-12 | Sequence 12, Appl |
| 36 | 40 | 80.0 | 237 | 2 | US-08-944-483-37 | Sequence 37, Appl |
| 37 | 40 | 80.0 | 237 | 2 | US-08-944-483-38 | Sequence 38, Appl |
| 38 | 40 | 80.0 | 237 | 2 | US-09-100-264-3 | Sequence 3, Appl |
| 39 | 40 | 80.0 | 237 | 2 | US-09-100-264-12 | Sequence 12, Appl |
| 40 | 40 | 80.0 | 237 | 2 | US-09-303-339-2 | Sequence 2, Appl |
| 41 | 40 | 80.0 | 237 | 2 | US-08-843-076D-1 | Sequence 1, Appl |
| 42 | 40 | 80.0 | 237 | 2 | US-08-843-076D-7 | Sequence 7, Appl |
| 43 | 40 | 80.0 | 237 | 2 | US-08-843-076D-8 | Sequence 8, Appl |
| 44 | 40 | 80.0 | 237 | 2 | US-09-303-208-1 | Sequence 1, Appl |
| 45 | 40 | 80.0 | 237 | 2 | US-09-303-208-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-502-600-80
; Sequence 80, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-502-600-80

Query Match 100.0%; Score 50; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 1 GPLVCRGTL 9

RESULT 2
US-09-918-243-80
; Sequence 80, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-918-243-80

Query Match 100.0%; Score 50; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 3
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 50; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 187

Db 178 GPLVCRGTL 186
RESULT 4
US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 50; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 179 GPLVCRGTL 187

RESULT 5
US-09-027-337-4
; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: TADG-15: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to

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; OTHER INFORMATION: similar domain in TAGD-15
US-09-027-337-4
Query Match      100.0%; Score 50; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPLVCRGTL 9
Db      179 GPLVCRGTL 187

RESULT 6
US-09-154-344-12
; Sequence 12, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-09-154-344-12
Query Match      100.0%; Score 50; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPLVCRGTL 9
Db      179 GPLVCRGTL 187

RESULT 7
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
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; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4
Query Match      100.0%; Score 50; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPLVCRGTL 9
Db      179 GPLVCRGTL 187

RESULT 8
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4
Query Match      100.0%; Score 50; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPLVCRGTL 9
Db      179 GPLVCRGTL 187

RESULT 9
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 10
US-08-824-874-3
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-08-824-874-3
Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 11
US-09-154-344-2
Sequence 2, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

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RESULT 12
US-08-930-188-2
; Sequence 2, Application US/08930188
; Patent No. 6093397
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,188
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-188-2
Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 13
US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3
Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 14
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
```

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 15
PCT-US96-04294-2
Sequence 2, Application PC/TUS9604294
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
TITLE OF INVENTION: LITTLE, SHEILA P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-04294-2

Query Match 100.0%; Score 50; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

Db 207 GPLVCRGTL 215

Search completed: March 11, 2006, 01:24:27
Job time : 21.2222 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-80

Perfect score: 50

Sequence: 1 GPLVCRGTL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 50 | 100.0 | 9 | 3 | US-09-918-243-80 |
| 2 | 50 | 100.0 | 9 | 3 | US-09-905-083-80 |
| 3 | 50 | 100.0 | 9 | 4 | US-10-372-521-80 |
| 4 | 50 | 100.0 | 9 | 5 | US-10-831-075-80 |
| 5 | 50 | 100.0 | 181 | 4 | US-10-262-511-98 |
| 6 | 50 | 100.0 | 198 | 4 | US-10-262-511-96 |
| 7 | 50 | 100.0 | 224 | 3 | US-09-789-210-33 |
| 8 | 50 | 100.0 | 224 | 4 | US-10-262-511-104 |
| 9 | 50 | 100.0 | 225 | 4 | US-10-600-187-4 |
| 10 | 50 | 100.0 | 247 | 4 | US-10-262-511-102 |
| 11 | 50 | 100.0 | 250 | 4 | US-10-262-511-92 |
| 12 | 50 | 100.0 | 252 | 4 | US-10-262-511-94 |
| 13 | 50 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 14 | 50 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 15 | 50 | 100.0 | 253 | 4 | US-10-071-214-2 |
| 16 | 50 | 100.0 | 253 | 4 | US-10-071-214-48 |
| 17 | 50 | 100.0 | 253 | 4 | US-10-264-283-90 |
| 18 | 50 | 100.0 | 253 | 4 | US-10-295-027-498 |
| 19 | 50 | 100.0 | 253 | 4 | US-10-173-999-48 |
| 20 | 50 | 100.0 | 253 | 4 | US-10-408-765A-639 |
| 21 | 50 | 100.0 | 253 | 5 | US-10-643-795A-95 |
| 22 | 50 | 100.0 | 253 | 5 | US-10-948-518-95 |
| 23 | 50 | 100.0 | 253 | 5 | US-10-868-490A-1 |
| 24 | 50 | 100.0 | 257 | 4 | US-10-344-394-38 |
| 25 | 47 | 94.0 | 249 | 4 | US-10-071-214-47 |
| 26 | 45 | 90.0 | 247 | 3 | US-09-764-898-284 |
| 27 | 45 | 90.0 | 247 | 3 | US-09-764-847-742 |

28 45 90.0 247 4 US-10-092-154-742 Sequence 742, App
29 45 90.0 250 4 US-10-055-569A-69 Sequence 69, Appl
30 45 90.0 250 4 US-10-344-394-29 Sequence 29, Appl
31 45 90.0 250 5 US-10-492-740-3 Sequence 3, Appl
32 45 90.0 251 3 US-09-764-898-212 Sequence 212, App
33 45 90.0 259 4 US-10-072-012-222 Sequence 222, App
34 44 88.0 243 4 US-10-071-214-46 Sequence 46, Appl
35 44 88.0 251 4 US-10-344-394-27 Sequence 27, Appl
36 44 88.0 267 5 US-10-480-988-20 Sequence 20, Appl
37 42 84.0 89 4 US-10-424-599-210636 Sequence 210636,
38 42 84.0 115 5 US-10-450-763-49720 Sequence 49720, A
39 41 82.0 23 4 US-10-071-214-6 Sequence 6, Appl
40 41 82.0 80 4 US-10-425-115-348061 Sequence 348061,
41 41 82.0 249 4 US-10-055-569A-68 Sequence 68, Appl
42 41 82.0 276 4 US-10-055-569A-67 Sequence 67, Appl
43 41 82.0 276 6 US-11-055-989-4 Sequence 4, Appl
44 40 80.0 54 3 US-09-860-739-5 Sequence 5, Appl
45 40 80.0 82 4 US-10-437-963-182803 Sequence 182803,

ALIGNMENTS

RESULT 1

US-09-918-243-80
; Sequence 80, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-918-243-80

Query Match 100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

Db 1 GPLVCRGTL 9

RESULT 2

US-09-905-083-80
; Sequence 80, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-905-083-80
Query Match      100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 3
US-10-372-521-80
; Sequence 80, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-372-521-80
Query Match      100.0%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 4
US-10-831-075-80
; Sequence 80, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-831-075-80
Query Match      100.0%; Score 50; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 5
US-10-262-511-98
; Sequence 98, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-262-511-98

Query Match 100.0%; Score 50; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 133 GPLVCRGTL 141

RESULT 6

US-10-262-511-96

; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Szytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Wei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curasequid version 0.1
; SEQ ID NO 96

; LENGTH: 198

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 50; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 152 GPLVCRGTL 160

RESULT 7

US-09-789-210-33
; Sequence 33, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-789-210-33
; Query Match 100.0%; Score 50; DB 3; Length 224;
; Best Local Similarity 100.0%; Pred. No. 1.3;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9

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Db          178 GPLVCRGTL 186
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RESULT 8
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104
Query Match          100.0%; Score 50; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GPLVCRGTL 9
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Db          193 GPLVCRGTL 201
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RESULT 9
US-10-600-187-4
; Sequence 4, Application US/10600187
; Publication No. US20040086910A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/10/600,187
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/654,600A
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 09/027,337
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-10-600-187-4
Query Match          100.0%; Score 50; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GPLVCRGTL 9
|||||
Db          179 GPLVCRGTL 187
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RESULT 10
US-10-262-511-102
; Sequence 102, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
```

APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 102
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-102

Query Match 100.0%; Score 50; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 193 GPLVCRGTL 201

RESULT 11
US-10-262-511-92
Sequence 92, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.

APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 92
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-92

Query Match 100.0%; Score 50; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 204 GPLVCRGTL 212

RESULT 12
US-10-262-511-94
Sequence 94, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen

```
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Stone, David J.
/ APPLICANT: Pena, Carol E. A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Rothenberg, Mark E.
/ APPLICANT: Leach, Martin D.
/ APPLICANT: Agee, Michele L.
/ APPLICANT: Berghs, Constance
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-462C
/ CURRENT APPLICATION NUMBER: US/10/262,511
/ CURRENT FILING DATE: 2003-05-28
/ PRIOR APPLICATION NUMBER: 60/326,483
/ PRIOR FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: 60/373,815
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/327,917
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/381,642
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/328,029
/ PRIOR FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: 60/381,038
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/328,056
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/373,260
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/373,826
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/327,435
/ PRIOR FILING DATE: 2001-10-05
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 439
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 94
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-262-511-94

Query Match          100.0%; Score 50; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      206  GPLVCRGTL 214

RESULT 13
US-09-888-615-98
/ Sequence 98, Application US/09888615
/ Patent No. US20020064856A1
/ GENERAL INFORMATION:
/ APPLICANT: PLOWMAN, GREGORY
/ APPLICANT: WHYTE, DAVID
/ APPLICANT: CAENEPEEL, SEAN
/ APPLICANT: CHARYDCZAK, GLEN
/ APPLICANT: MANNING, GERARD
/ APPLICANT: SUDARSANAM, SUCHA
/ TITLE OF INVENTION: NOVEL PROTEASES
/ FILE REFERENCE: 038602/1214
/ CURRENT APPLICATION NUMBER: US/09/888,615
/ CURRENT FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/214,047
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 98
/ LENGTH: 253

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match          100.0%; Score 50; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      207  GPLVCRGTL 215

RESULT 14
US-09-764-762-3
/ Sequence 3, Application US/09764762
/ Patent No. US20020068341A1
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ TITLE OF INVENTION: NOVEL KALLIKREIN
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0252 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 532504
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match          100.0%; Score 50; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      207  GPLVCRGTL 215

RESULT 15
US-10-071-214-2
/ Sequence 2, Application US/10071214
/ Publication No. US20030066099A1
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; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match      100.0%; Score 50; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPLVCRGTL 9
Db      207 GPLVCRGTL 215

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Job time : 70.4444 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-80

Perfect score: 50

Sequence: 1 GPLVCRGTL 9

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Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 50 | 100.0 | 181 | 6 | US-10-412-748-19 |
| 2 | 50 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 3 | 50 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 4 | 50 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 5 | 50 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 6 | 44 | 88.0 | 267 | 6 | US-10-395-561-552 |
| 7 | 44 | 88.0 | 267 | 6 | US-10-995-561-553 |
| 8 | 40 | 80.0 | 194 | 6 | US-10-401-386B-12 |
| 9 | 40 | 80.0 | 237 | 6 | US-10-401-386B-24 |
| 10 | 40 | 80.0 | 261 | 7 | US-11-138-242A-8 |
| 11 | 40 | 80.0 | 261 | 7 | US-11-150-066-8 |
| 12 | 40 | 80.0 | 261 | 7 | US-11-033-039-358 |
| 13 | 40 | 80.0 | 261 | 7 | US-11-155-288-10 |
| 14 | 40 | 80.0 | 269 | 6 | US-10-401-386B-2 |
| 15 | 38 | 76.0 | 236 | 6 | US-10-821-234-1274 |
| 16 | 38 | 76.0 | 237 | 6 | US-10-401-386B-6 |
| 17 | 38 | 76.0 | 237 | 7 | US-11-138-242A-5 |
| 18 | 38 | 76.0 | 237 | 7 | US-11-150-066-5 |
| 19 | 38 | 76.0 | 260 | 6 | US-10-131-826A-396 |
| 20 | 38 | 76.0 | 260 | 6 | US-10-510-321-2 |
| 21 | 38 | 76.0 | 260 | 6 | US-10-973-115B-396 |
| 22 | 38 | 76.0 | 260 | 7 | US-11-183-914-7 |
| 23 | 38 | 76.0 | 261 | 7 | US-11-138-242A-3 |
| 24 | 38 | 76.0 | 261 | 7 | US-11-138-242A-10 |
| 25 | 38 | 76.0 | 261 | 7 | US-11-150-066-3 |

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26      38      76.0      261      7      US-11-150-066-10      Sequence 10, Appl
27      38      76.0      293      6      US-10-131-826A-456      Sequence 456, App
28      38      76.0      293      6      US-10-412-748-2      Sequence 2, Appli
29      38      76.0      293      6      US-10-412-748-7      Sequence 7, Appli
30      38      76.0      293      6      US-10-973-115B-456      Sequence 456, App
31      38      76.0      738      7      US-11-087-099-11986      Sequence 11986, A
32      37      74.0      15      7      US-11-234-786-512      Sequence 512, App
33      37      74.0      40      6      US-10-989-226-42      Sequence 42, Appl
34      37      74.0      40      7      US-11-066-967-69      Sequence 69, Appl
35      37      74.0      159      7      US-11-234-786-172      Sequence 172, App
36      37      74.0      205      7      US-11-234-786-176      Sequence 176, App
37      37      74.0      220      7      US-11-234-786-327      Sequence 327, App
38      37      74.0      254      7      US-11-234-786-523      Sequence 523, App
39      37      74.0      254      7      US-11-234-786-525      Sequence 525, App
40      37      74.0      320      7      US-11-037-243-90      Sequence 90, Appl
41      37      74.0      449      7      US-11-234-786-617      Sequence 617, App
42      36      72.0      283      7      US-11-072-512-2687      Sequence 2687, Ap
43      36      72.0      446      6      US-10-527-500-1      Sequence 1, Appli
44      36      72.0      451      7      US-11-087-099-1581      Sequence 1581, Ap
45      36      72.0      557      6      US-10-718-264-8      Sequence 8, Appli

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ALIGNMENTS

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RESULT 1
US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

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Query Match      100.0%; Score 50; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1      GPLVCRGTL 9
Db      135      GPLVCRGTL 143

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RESULT 2
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 5
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 50; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 6
US-10-995-561-552
; Sequence 552, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-552

Query Match      88.0%; Score 44; DB 6; Length 267;
Best Local Similarity 88.9%; Pred. No. 0.49;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 222 GPLVCRGTL 230

RESULT 7
US-10-995-561-553
; Sequence 553, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
```

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; PRIOR FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-553

Query Match 88.0%; Score 44; DB 6; Length 267;
Best Local Similarity 88.8%; Pred. No. 0.49;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 222 GPLVCRGQL 230
|||||

RESULT 8

US-10-401-386B-12
; Sequence 12, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP for Use
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-12

Query Match 80.0%; Score 40; DB 6; Length 194;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 148 GPLVCRGVL 156
|||||

RESULT 9

US-10-401-386B-24
; Sequence 24, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP for Use
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-24

Query Match 80.0%; Score 40; DB 6; Length 237;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 191 GPLVCRGVL 199
|||||

RESULT 10

US-11-138-242A-8
; Sequence 8, Application US/11138242A
; Publication No. US20050266530A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Deborah J.
; APPLICANT: Snyder, Linda A.
; TITLE OF INVENTION: Cynomolgus Prostate Specific Antigen
; FILE REFERENCE: CEN5056 USA NP
; CURRENT APPLICATION NUMBER: US/11/138,242A
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575,079
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-138-242A-8

Query Match 80.0%; Score 40; DB 7; Length 261;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 215 GPLVCRGVL 223
|||||

RESULT 11

US-11-150-066-8
; Sequence 8, Application US/11150066
; Publication No. US20050276758A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Deborah J.
; APPLICANT: Snyder, Linda A.
; TITLE OF INVENTION: Method for Screening Agents Against Human Prostate Disease
; FILE REFERENCE: CEN5067 USA NP
; CURRENT APPLICATION NUMBER: US/11/150,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/579,871
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-150-066-8

Query Match 80.0%; Score 40; DB 7; Length 261;

Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 215 GPLVCNGVL 223

RESULT 12

US-11-033-039-358
; Sequence 358, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 358
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-358

Query Match 80.0%; Score 40; DB 7; Length 261;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 215 GPLVCNGVL 223

RESULT 13

US-11-155-288-10
; Sequence 10, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-10

Query Match 80.0%; Score 40; DB 7; Length 261;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 215 GPLVCNGVL 223

RESULT 14

US-10-401-386B-2
; Sequence 2, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-2

Query Match 80.0%; Score 40; DB 6; Length 269;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 223 GPLVCNGVL 231

RESULT 15

US-10-821-234-1274
; Sequence 1274, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1274
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1274

Query Match 76.0%; Score 38; DB 6; Length 236;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 193 GPLVCNGVL 201

Search completed: March 11, 2006, 01:38:43
Job time : 9 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-86

Perfect score: 41

Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 41 | 100.0 | 9 | 4 AAE08291 | Aae08291 Human str |
| 2 | 41 | 100.0 | 9 | 8 ADR68847 | Adr68847 Human str |
| 3 | 41 | 100.0 | 136 | 4 ABG23378 | Abg23378 Novel hum |
| 4 | 41 | 100.0 | 198 | 6 ADA05736 | Ada05736 Human NOV |
| 5 | 41 | 100.0 | 198 | 8 ADN62900 | Adn62900 Human NOV |
| 6 | 41 | 100.0 | 253 | 2 AAR67888 | Aar67888 Human str |
| 7 | 41 | 100.0 | 253 | 2 AAU05383 | Aau05383 Human amy |
| 8 | 41 | 100.0 | 253 | 5 ABB84421 | Abb84421 Human SCC |
| 9 | 41 | 100.0 | 253 | 5 ABB84406 | Abb84406 Human SCC |
| 10 | 41 | 100.0 | 253 | 5 AAU82740 | Aau82740 Amino aci |
| 11 | 41 | 100.0 | 253 | 6 ABU07440 | Abu07440 Protein d |
| 12 | 41 | 100.0 | 253 | 6 ABU07471 | Abu07471 Protein d |
| 13 | 41 | 100.0 | 253 | 6 ABR58471 | Abr58471 Human str |
| 14 | 41 | 100.0 | 253 | 7 ADB80484 | Adb80484 Ovarian c |
| 15 | 41 | 100.0 | 253 | 7 ADJ68833 | Adj68833 Human hea |
| 16 | 41 | 100.0 | 253 | 7 ADN39180 | Adn39180 Cancer/an |
| 17 | 41 | 100.0 | 253 | 8 ADL06515 | Adl06515 Human tum |
| 18 | 41 | 100.0 | 253 | 8 ADN04182 | Adn04182 Antipeori |
| 19 | 41 | 100.0 | 253 | 8 ADR72880 | Adr72880 Human ova |
| 20 | 41 | 100.0 | 253 | 9 ADY67588 | Ady67588 Human kal |
| 21 | 41 | 100.0 | 253 | 9 AEC00353 | Aec00353 Human kal |
| 22 | 41 | 100.0 | 257 | 3 AAB21326 | Aab21326 Human HSC |
| 23 | 37 | 90.2 | 752 | 8 ADI28864 | Adi28864 Human ser |
| 24 | 36 | 87.8 | 9 | 4 AAE08320 | Aae08320 Human str |

| | | | | | |
|----|----|------|-----|------------|--------------------|
| 25 | 36 | 87.8 | 9 | 8 ADR68877 | Adr68877 Human str |
| 26 | 36 | 87.8 | 210 | 8 ADX88035 | Adx88035 Plant ful |
| 27 | 36 | 87.8 | 567 | 8 ADY10906 | Ady10906 Plant ful |
| 28 | 36 | 87.8 | 818 | 5 ABB98135 | Abb98135 Human PMM |
| 29 | 36 | 87.8 | 818 | 5 AAU82753 | Aau82753 Amino aci |
| 30 | 35 | 85.4 | 346 | 8 ADT79403 | Adt79403 Human BAC |
| 31 | 35 | 85.4 | 475 | 4 AAE10657 | Aae10657 Secreted |
| 32 | 35 | 85.4 | 475 | 4 AAE02609 | Aae02609 Human sec |
| 33 | 35 | 85.4 | 475 | 5 ABB78618 | Abb78618 Secreted |
| 34 | 35 | 85.4 | 518 | 2 AAWE1362 | Aaw61362 Aspartic |
| 35 | 35 | 85.4 | 518 | 2 AAY13799 | Aay13799 Human asp |
| 36 | 35 | 85.4 | 518 | 2 AAY22239 | Aay22239 Human CSP |
| 37 | 35 | 85.4 | 518 | 2 AAY41714 | Aay41714 Human PRO |
| 38 | 35 | 85.4 | 518 | 3 AAY88424 | Aay88424 Human asp |
| 39 | 35 | 85.4 | 518 | 3 AAB44270 | Aab44270 Human PRO |
| 40 | 35 | 85.4 | 518 | 4 AAU07201 | Aau07201 Human asp |
| 41 | 35 | 85.4 | 518 | 4 AAE10628 | Aae10628 Human asp |
| 42 | 35 | 85.4 | 518 | 4 AAE10656 | Aae10656 Human-Asp |
| 43 | 35 | 85.4 | 518 | 4 AAE06858 | Aae06858 Human asp |
| 44 | 35 | 85.4 | 518 | 4 AAE02608 | Aae02608 Human Asp |
| 45 | 35 | 85.4 | 518 | 4 AAE02580 | Aae02580 Human asp |

ALIGNMENTS

RESULT 1
AAE08291
ID AAE08291 standard; peptide; 9 AA.

AC AAE08291;

DT 01-NOV-2001 (first entry)

DE Human stratum corneum chymotrypsin enzyme peptide #56 (residues 1-9).

KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;

KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;

KW antisense therapy; malignant hyperplasia.

OS Homo sapiens.

PN WO200159158-A1.

PD 16-AUG-2001.

PF 07-FEB-2001; 2001WO-US003977.

PR 11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 114; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

```
Query Match      100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 2
ADR68847
ID ADR68847 standard; peptide; 9 AA.
AC ADR68847;
XX
XX
DT 02-DEC-2004 (first entry)
XX
XX Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:86.
XX
XX serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
XX Homo sapiens.
XX
XX WO2004075723-A2.
XX
XX 10-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005134.
XX
XX 21-FEB-2003; 2003US-00372521.
XX
XX (UYAR-) UNIV ARKANSAS.
XX
XX O'brien TJ, Cannon MJ, Santin A;
XX
XX WPI; 2004-653294/63.
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX Claim 5; SEQ ID NO 86; 117pp; English.
XX
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;
XX
XX Query Match      100.0%; Score 41; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 3
ABG23378
ID ADR68847 standard; peptide; 9 AA.
AC ADR68847;
XX
XX
DT 02-DEC-2004 (first entry)
XX
XX Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:86.
XX
XX serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
XX Homo sapiens.
XX
XX WO2004075723-A2.
XX
XX 10-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005134.
XX
XX 21-FEB-2003; 2003US-00372521.
XX
XX (UYAR-) UNIV ARKANSAS.
XX
XX O'brien TJ, Cannon MJ, Santin A;
XX
XX WPI; 2004-653294/63.
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX Claim 5; SEQ ID NO 86; 117pp; English.
XX
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;
XX
XX Query Match      100.0%; Score 41; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX
XX
DT 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #23369.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS87565.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 53737; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 136 AA;
XX
XX Query Match      100.0%; Score 41; DB 4; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 2.2;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 7 MARSLLLPL 15

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX
XX
```

ADA05736;
06-NOV-2003 (first entry)
Human NOV18c protein SEQ ID NO:96.
human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaeamic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
Homo sapiens.
WO2003029424-A2.
10-APR-2003.
02-OCT-2002; 2002WO-US031373.
02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327817P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328056P.
12-OCT-2001; 2001US-0328849P.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-00262511.
(CURA-) CURAGEN CORP.
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorwan L, Zerkow BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
WPI; 2003-381626/36.
N-PSDB; ADA05735.
New NOVX polypeptides and nucleic acids, useful for diagnosing,
preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
cancer or dyslipidemia, and in chromosome mapping, tissue typing or
pharmacogenomics.
Claim 1; Page 170; 586pp; English.
The present invention describes NOVX proteins, where X can be 1 to 55
(e.g. NOV1). Also described: (1) a composition comprising a polypeptide

described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
binds to the polypeptide described above; (6) an antibody that immunospecifically
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of treating
or preventing a pathology associated with the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
and antilipaeamic activities, and can be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
syndrome associated with a human disease. The polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
disorders such as diabetes or obesity, infections, cachexia, cancer,
neurodegenerative disorders such as Alzheimer's disease or Parkinson's
disease, immune disorders, haematopoietic disorders and various
dyslipidaemias. The nucleic acids can also be used as hybridisation
probes, in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. The present sequence represents a human NOVX from the
present invention.

Sequence 198 AA;
Query Match 100.0%; Score 41; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
|||||||
Db 1 MARSLLLPL 9
RESULT 5
ADN62900
ID ADN62900 standard; protein; 198 AA.
XX ADN62900;
AC ADN62900;
XX 01-JUL-2004 (first entry)
XX Human NOV18c.
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
Alzheimer's disease; Parkinson's disease; immune disorder;
XX haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
XX wasting disorder.
XX Homo sapiens.
OS
XX US2004038223-A1.
PN
XX 26-FEB-2004.
PD
XX 01-OCT-2002; 2002US-00262511.
PF
XX 02-OCT-2001; 2001US-0326483P.
PR
XX 05-OCT-2001; 2001US-0327435P.
PR
XX 05-OCT-2001; 2001US-0327449P.
PR
XX 09-OCT-2001; 2001US-0327817P.
PR
XX 09-OCT-2001; 2001US-0328029P.
PR
XX 09-OCT-2001; 2001US-0328044P.
PR
XX 09-OCT-2001; 2001US-0328056P.
PR
XX 12-OCT-2001; 2001US-0328849P.
PR
XX 15-OCT-2001; 2001US-0329414P.
PR
XX 17-OCT-2001; 2001US-0330142P.
PR
XX 18-OCT-2001; 2001US-0330309P.
PR
XX 22-OCT-2001; 2001US-0341058P.
PR
XX 24-OCT-2001; 2001US-0339266P.
PR
XX 24-OCT-2001; 2001US-0343629P.
PR
XX 29-OCT-2001; 2001US-0349575P.
PR
XX 01-NOV-2001; 2001US-0346357P.
PR
XX 17-APR-2002; 2002US-0373260P.
PR
XX 19-APR-2002; 2002US-0373815P.
PR
XX 19-APR-2002; 2002US-0373817P.
PR
XX 19-APR-2002; 2002US-0373826P.
PR
XX 19-APR-2002; 2002US-0373884P.
PR
XX 22-APR-2002; 2002US-0374977P.
PR
XX 16-MAY-2002; 2002US-0381037P.
PR
XX 16-MAY-2002; 2002US-0381038P.
PR
XX 16-MAY-2002; 2002US-0381042P.
PR
XX 17-MAY-2002; 2002US-0381642P.
PR
XX 28-MAY-2002; 2002US-0383656P.
PR
XX 29-MAY-2002; 2002US-0383831P.
PR
XX 25-JUN-2002; 2002US-0391335P.
PR
XX 01-OCT-2002; 2002US-00262511.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
XX Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
XX Or T, Gorwan L, Zerkow BD, Anderson DW, Zhong M, Catterton E;
XX Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
XX Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
XX Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
XX N-PSDB; ADA05735.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
XX preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
XX cancer or dyslipidemia, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX
XX Claim 1; Page 170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
XX (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERRHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIMW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENR/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerrhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2004-213931/20.
 DR N-PSDB; ADN62899.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 41; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARSLLLPL 9
 Db 1 MARSLLLPL 9
 RESULT 6
 AAR67888
 ID AAR67888 standard; protein; 253 AA.
 XX
 AC AAR67888;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-AUG-1995 (first entry)
 XX
 DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
 XX
 KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
 KW callosities; keratosis pilaris; ichthyoses; eczema.
 XX
 OS Homo sapiens.
 XX
 XX WO9500651-A1.
 PN
 XX 05-JAN-1995.
 PD
 XX 20-JUN-1994; 94WO-IB000166.
 PF
 XX 18-JUN-1993; 93DK-00000725.
 PR
 PA (SYMB-) SYMBICOM AB.
 XX
 XX Egelrud T, Hansson L;
 PI
 XX WPI; 1995-052088/07.
 DR
 DR N-PSDB; AAO81203.
 XX

PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
PT related vectors, transformed cells and polypeptides, useful for treating
PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.

XX Disclosure; Page 97; 137pp; English.

XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callosities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammalian, insect, plant, or microorganism
CC transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

RESULT 7
AAW05383
ID AAW05383 standard; protein; 253 AA.

AC AAW05383;

XX 31-DEC-1996 (first entry)

XX Human amyloid precursor protein protease.

XX Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
XX therapy.

OS Homo sapiens.

XX WO9631122-A1.

XX 10-OCT-1996.

XX 02-APR-1996; 96WO-US004294.

XX 04-APR-1995; 95US-00416257.

XX (BLIL) LILLY & CO ELI.

XX Dixon EP, Johnstone EM, Little SP;

XX WPI; 1996-464694/46.

XX N-PSDB; AAT39783.

XX New isolated human amyloid precursor protein protease - used to develop
PT prods. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.

XX Claim 1; Page 44-45; 55pp; English.

XX Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obtd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells. It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

RESULT 8

AB884421

ID AB884421 standard; peptide; 253 AA.

XX AB884421;

XX 08-NOV-2002 (first entry)

XX Human SCCE protein N-terminal fragment SEQ ID 48.

XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

OS Homo sapiens.

XX WO200262135-A2.

XX 15-AUG-2002.

XX 08-FEB-2002; 2002WO-IB001300.

XX 09-FEB-2001; 2001CA-02332655.

XX 09-FEB-2001; 2001DK-00000218.

XX (EGEL/) EGELRUD T.

XX (HANS/) HANSSON L.

XX Egelrud T, Hansson L;

XX WPI; 2002-643380/69.

XX Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.

XX Example 6; Page 37; 74pp; English.

XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the N-terminal
CC fragment of the human stratum corneum chymotryptic enzyme, SCCE
CC synonymous with human kallikrein 7 (KLK7), used in the development of the
CC transgenic mammals described in the invention

XX

SQ Sequence 253 AA;
Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
| | | | | | | | | |
Db 1 MARSLLLPL 9

RESULT 9
ABB84406
ID ABB84406 standard; protein; 253 AA.
XX ABB84406;
XX 08-NOV-2002 (first entry)
XX Human SCCE protein.
DE
XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
XX WO200262135-A2.
FN
PD 15-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-IB001300.
PF
XX 09-FEB-2001; 2001CA-02332655.
PR
XX 09-FEB-2001; 2001DK-00000218.
XX
XX (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
XX Egelrud T, Hansson L;
FI
XX WPI; 2002-643380/69.
DR N-PSDB; ABQ76226.
XX
XX Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
XX Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian
embryo having integrated within its genome, a heterologous nucleotide
sequence comprising at least a significant part of a nucleotide sequence
coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant.
operably linked to a promoter that drives expression of heterologous scce
or its variant in skin. The product of the invention is useful as a model
for the study of disease with the aim of improving treatment, to relieve
or ameliorate a pathogenic condition, for development or testing of a
cosmetic or a pharmaceutical formulation, and for the development of a
diagnostic method. It can also be used as a model for a skin disease or
skin cancer. The invention is also useful for screening or identifying a
compound or composition effective for the prevention or treatment of an
abnormal or unwanted phenotype, and for screening or identifying a
compound or composition effective for the prevention or treatment of
inflammatory skin diseases selected from diseases consisting of epidermal
hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
with epidermal hyperkeratosis. The mammal of the invention is also useful
as a model for further studies of itch mechanisms and the testing of
potential compounds and compositions for relieve of various skin diseases
where itch is a component. This sequence represents the human stratum
corneum chymotryptic enzyme, SCCE which is a serine protease synonymous

CC with human kallikrein 7 (KLK7) and is used in the development of the
CC transgenic mammals described in the invention
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
| | | | | | | | | |
Db 1 MARSLLLPL 9

RESULT 10
AAU82740
ID AAU82740 standard; protein; 253 AA.
XX
XX AAU82740;
XX
XX 23-APR-2002 (first entry)
DT
XX Amino acid sequence of novel human protease #39.
DE
XX Human; protease; cancer; immune-related disorder; cardiovascular disease;
KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
KW nervous system disorder; sexual dysfunction; pain; mood disorder;
KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
KW ocular disease; cytostatic; enzyme.
XX
XX Homo sapiens.
OS
XX WO200200860-A2.
PN
XX 03-JAN-2002.
XX
XX 26-JUN-2001; 2001WO-US020171.
PF
XX 26-JUN-2000; 2000US-0214047P.
PR
XX (SUGS-) SUGEN INC.
XX
XX Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Charyczak G;
XX
XX WPI; 2002-139913/18.
DR N-PSDB; ABK31782.
XX
XX Nucleic acids encoding novel human proteases, useful for useful for
PT treating diseases and disorders such as cancers, immune-related diseases
PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
PT disorders.
XX
XX Claim 6; Fig 2N; 313pp; English.

The present invention relates to the isolation of novel human proteases,
and the nucleic acids encoding them. The sequences of the invention are
useful for treating diseases and disorders such as cancers (e.g. breast,
colon, lung), immune-related diseases and disorders (e.g. inflammatory
diseases and asthma), cardiovascular diseases (e.g. restenosis and
coronary thrombosis), brain or neuronal-associated diseases, metabolic
disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
rheumatoid arthritis and psoriasis), central or peripheral nervous system
diseases, migraines, pain, sexual dysfunction, mood disorders, attention
disorders, cognitive disorders, hypotension, hypertension, psychotic
disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
disease) and dyskinesias. The nucleic acids and polypeptides are also
useful for treating viral infections caused by human immunodeficiency
virus (HIV), and non-viral infections such as ocular disease (e.g.
glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
human proteases of the invention
XX

SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|||||

Db 1 MARSLLLPL 9

RESULT 11

ABU07440

ID ABU07440 standard; protein; 253 AA.

XX AC ABU07440;

XX 28-JAN-2003 (first entry)

XX Protein differentially regulated in prostate cancer #43.

XX Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX Homo sapiens.

OS WO200281638-A2.

PN 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010824.

XX 06-APR-2001; 2001US-0281731P.

PR 06-APR-2001; 2001US-0281732P.

XX (ORIG-) ORIGENE TECHNOLOGIES INC.

PI Sun Z, Jay G;

DR WPI; 2003-058520/05.

DR N-PSDB; ABX10343.

XX Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.

PS Claim 1; Page 293-294; 416pp; English.

XX The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially regulated in
CC prostate cancer, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.

CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|||||

Db 1 MARSLLLPL 9

RESULT 12

ABU07471

ID ABU07471 standard; protein; 253 AA.

XX AC ABU07471;

XX 28-JAN-2003 (first entry)

XX Protein differentially regulated in prostate cancer #74.

XX Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX Homo sapiens.

OS WO200281638-A2.

PN 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010824.

XX 06-APR-2001; 2001US-0281731P.

PR 06-APR-2001; 2001US-0281732P.

XX (ORIG-) ORIGENE TECHNOLOGIES INC.

PI Sun Z, Jay G;

DR WPI; 2003-058520/05.

DR N-PSDB; ABX10375.

XX Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.

PS Claim 1; Page 351; 416pp; English.

XX The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially-regulated in
CC prostate cancer, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.

CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARSLLLLPL 9
Db 1 MARSLLLLPL 9

RESULT 13
ABR58471
ID ABR58471 standard; protein; 253 AA.

AC ABR58471;

XX 07-JUL-2003 (first entry)

XX Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.

XX Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.

XX Homo sapiens.

XX WO2003029469-A1.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031467.

XX 02-OCT-2001; 2001US-0327135P.

XX 30-MAY-2002; 2002US-0384531P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Mannion J;

XX WPI; 2003-372001/35.

XX New polynucleotide and polypeptide useful for diagnosing and/or treating
PT cancer, particularly ovarian cancer, and as a vaccine.

XX Claim 2; Page 157-158; 169pp; English.

XX The invention relates to a novel isolated polynucleotide. The
CC polynucleotides of the invention have cytostatic activity, and may have a
CC use in gene therapy, and in a vaccine. The composition and methods are
CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
CC The composition may also be used as a vaccine to prevent cancer. The
CC present sequence is used in the exemplification of the invention

XX SQ Sequence 253 AA;
Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARSLLLLPL 9
Db 1 MARSLLLLPL 9

RESULT 14
ADB80484
ID ADB80484 standard; protein; 253 AA.

XX ADB80484;

XX 04-DEC-2003 (first entry)

XX Ovarian cancer-associated protein #24.

XX cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW post-operative chemotherapy; radiation therapy; tumour prognosis;
KW pre-cancerous lesion detection.

XX Homo sapiens.

XX WO2002102235-A2.

XX 27-DEC-2002.

XX 18-JUN-2002; 2002WO-US019297.

XX 18-JUN-2001; 2001US-0299234P.

XX 27-AUG-2001; 2001US-0315287P.

XX 05-SEP-2001; 2001US-0317544P.

XX 13-NOV-2001; 2001US-0350666P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Gish KC;

XX WPI; 2003-167431/16.

XX N-PSDB; ADB80483.

XX Detecting an ovarian cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT polynucleotide that hybridizes to an ovarian cancer gene.

XX Claim 13; Page 291; 332pp; English.

XX The invention relates to a method of detecting an ovarian cancer-
CC associated transcript in a cell from a patient, by contacting a
CC biological sample from the patient with a polynucleotide that selectively
CC hybridizes to a sequence at least 80% identical to any of one of 80
CC nucleic acid sequences given in the specification. The method is useful
CC in diagnosing ovarian cancer and in identifying and using agents and/or
CC targets that inhibit ovarian cancer. The nucleic acid molecule,
CC polypeptide and the antibody may also be used in detecting ovarian
CC cancers, monitoring and early detection of relapse following treatment,
CC monitoring response to therapy, selecting patients for post-operative
CC chemotherapy or radiation therapy, in selection of pre-cancerous lesions,
CC and as vaccines. This sequence corresponds to one of the proteins used
CC for the detection method of the invention.

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

Qy 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

Search completed: March 11, 2006, 00:24:18
Job time : 88.6667 secs

RESULT 15
ADJ68833
ID ADJ68833 standard; protein; 253 AA.

XX AC ADJ68833;
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID639.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.

OS Homo sapiens.

XX WO2003087768-A2.

XX 23-OCT-2003.

XX 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

XX 17-JUN-2002; 2002US-0389987P.

XX 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

PS Claim 1; SEQ ID NO 639; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 41 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 34 | 82.9 | 461 | 2 A46394 | suppressor protein |
| 3 | 33 | 80.5 | 397 | 2 B87343 | conserved hypothet |
| 4 | 33 | 80.5 | 571 | 2 E96550 | hypothetical prote |
| 5 | 33 | 80.5 | 582 | 2 I48673 | matrix metalloprot |
| 6 | 33 | 80.5 | 582 | 2 I84471 | hypothetical prote |
| 7 | 32 | 78.0 | 81 | 2 B97856 | DNA-binding protei |
| 8 | 32 | 78.0 | 126 | 2 C82169 | hypothetical prote |
| 9 | 32 | 78.0 | 432 | 2 A83060 | conserved membrane |
| 10 | 32 | 78.0 | 506 | 2 B87102 | ionotropic glutama |
| 11 | 32 | 78.0 | 921 | 2 T51136 | probable ligand-ga |
| 12 | 32 | 78.0 | 923 | 2 F84732 | hypothetical prote |
| 13 | 32 | 78.0 | 1628 | 2 T38055 | sodium channel alp |
| 14 | 31 | 75.6 | 138 | 2 I48107 | hypothetical prote |
| 15 | 31 | 75.6 | 147 | 2 S28698 | cell division inhi |
| 16 | 31 | 75.6 | 169 | 2 AB0627 | cell division inhi |
| 17 | 31 | 75.6 | 169 | 2 B29016 | hypothetical prote |
| 18 | 31 | 75.6 | 294 | 2 B86450 | NADH2 dehydrogenas |
| 19 | 31 | 75.6 | 346 | 2 T11364 | probable transamin |
| 20 | 31 | 75.6 | 375 | 2 C71917 | probable transamin |
| 21 | 31 | 75.6 | 375 | 2 H64597 | PTS system, n-acet |
| 22 | 31 | 75.6 | 452 | 2 A83734 | stromelysin 3 (EC |
| 23 | 31 | 75.6 | 491 | 2 JC6197 | inulinase (EC 3.2. |
| 24 | 31 | 75.6 | 556 | 1 S31330 | cytolysin B transp |
| 25 | 31 | 75.6 | 708 | 2 T43109 | sodium channel pro |
| 26 | 31 | 75.6 | 2005 | 2 B25019 | rifamycin polyketi |
| 27 | 31 | 75.6 | 5069 | 2 T17464 | corazonin precursor |
| 28 | 30 | 73.2 | 72 | 2 JC2384 | hypothetical prote |
| 29 | 30 | 73.2 | 74 | 2 T17834 | |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 30 | 73.2 | 170 | 2 S43476 | histone-like DNA-b |
| 31 | 30 | 73.2 | 216 | 2 JE0297 | DRE/CRT-binding pr |
| 32 | 30 | 73.2 | 216 | 2 T51830 | transcription fact |
| 33 | 30 | 73.2 | 222 | 2 D82132 | hypothetical prote |
| 34 | 30 | 73.2 | 299 | 2 T17832 | hypothetical prote |
| 35 | 30 | 73.2 | 314 | 2 D85294 | transcription acti |
| 36 | 30 | 73.2 | 314 | 2 T05799 | transcription acti |
| 37 | 30 | 73.2 | 323 | 2 S47741 | probable transcrip |
| 38 | 30 | 73.2 | 323 | 2 B86025 | probable transcrip |
| 39 | 30 | 73.2 | 323 | 2 A91179 | protein zC155.4 [i |
| 40 | 30 | 73.2 | 325 | 2 A88452 | hypothetical prote |
| 41 | 30 | 73.2 | 325 | 2 T25122 | hypothetical prote |
| 42 | 30 | 73.2 | 325 | 2 A97482 | conserved hypothet |
| 43 | 30 | 73.2 | 325 | 2 A12699 | hypothetical prote |
| 44 | 30 | 73.2 | 331 | 2 G87494 | transmembrane glyc |
| 45 | 30 | 73.2 | 354 | 2 A48931 | |

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968

R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:1

C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35

C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>
Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 MARSLLLPL 9
| | | | | | | | | |
DB 1 MARSLLLPL 9

RESULT 2

A46394
suppressor protein SSL1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1531; protein YLR005W
C;Species: Saccharomyces cerevisiae

C;Date: 18-May-1994 #sequence_revision 19-Jul-1996 #text_change 31-Dec-2004
C;Accession: A46394; S64827
R;Yoon, H.; Miller, S.P.; Pabich, E.K.; Donahue, T.F.
Genes Dev. 6, 2463-2477, 1992

A;Title: SSL1, a suppressor of a HIS4 5'-UTR stem-loop mutation, is essential for transla
A;Reference number: A46394; MUID:94040711; PMID:1340463
A;Accession: A46394
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-461 <YOO>
A;Cross-references: UNIPROT:Q04673; UNIPARC:UPI0000053049; GB:Z17385; NID:G2695; PID:G2695

R;Vandenbol, M.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64742
A;Accession: S64827

A:Molecule type: DNA
A:Residues: 1-461 <V>N>
A:Cross-references: UNIPARC:UPI0000053049; EMBL:Z73177; NID:gl360293; PID:gl360294; MIPS
A>Note: experimental_source strain S288C
C:Genetics:
A:Gene: SGD:SSL1
A:Cross-references: SGD:S0003995; MIPS:YLR005W
A:Map position: 12R
C:Superfamily: TFIIF basal transcription factor complex, subunit SSL1
C:Keywords: transmembrane protein
F:356-372/Domain: transmembrane #status predicted <TMM>

Query Match 82.9%; Score 34; DB 2; Length 461;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 216 MARGLLLPV 224
|||||

RESULT 3
B87343
Conserved hypothetical protein CC0757 [imported] - Caulobacter crescentus
C:Species: Caulobacter Crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87343
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <STO>
A:Cross-references: UNIPROT:Q9AAM49; UNIPARC:UPI000000C7168; GB:AE005673; NID:gl3421992; E
C:Genetics:
A:Gene: CC0757

Query Match 80.5%; Score 33; DB 2; Length 397;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 285 LARALLPL 293
|||||

RESULT 4
E96550
Hypothetical protein FILM15.13 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96550
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-571 <STO>
A:Cross-references: UNIPROT:Q9SYC9; UNIPARC:UPI000009EC28; GB:AE005173; NID:g4836937; PI
C:Genetics:

A:Gene: FILM15.13
A:Map position: 1

Query Match 80.5%; Score 33; DB 2; Length 571;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 332 MLRSLLVPL 340
|||||

RESULT 5
I48673
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C:Accession: I48673
R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: I48673
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: UNIPARC:UPI0000030971; EMBL:X83536; NID:g804999; PIDN:CAA58520.1; PI
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MMP>
F:313-508/Domain: hemopexin repeat homology <PXN>
F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status I
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match 80.5%; Score 33; DB 2; Length 582;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARSLLLPL 9
Db 8 SRSLLLPL 15
|||||

RESULT 6
I84471
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N:Alternate names: membrane-type metalloproteinase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I84471; I61946
R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: I84471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: UNIPROT:Q10739; UNIPARC:UPI0000030970; EMBL:X83537; NID:g805012; PIDN
A:Accession: I61946
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-67,'M',69-254,'A',256-582 <RE2>
A:Cross-references: UNIPARC:UPI00001679D1; EMBL:X91785; NID:gl001926; PIDN:CAA62897.1; PI
C:Genetics:
A:Gene: mt-mmp
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>

RESULT 9

A83060
hypothetical protein PA4684 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: A83060
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: A83060
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-432 <STO>
A/Cross-references: UNIPROT:O9HVB1; UNIPARC:UPI00000C5DC4; GB:AE004882; GB:AE004091; NID
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA4684

Query Match 78.0%; Score 32; DB 2; Length 432;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARSLLPL 9
|||
Db 245 ARELLPL 252

RESULT 10

B87102
conserved membrane protein ML1544 [imported] - *Mycobacterium leprae*
C/Species: *Mycobacterium leprae*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: B87102
R/Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: B87102
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-506 <STO>
A/Cross-references: UNIPROT:Q9Z5I3; UNIPARC:UPI00000D4376; GB:AL450380; NID:gl3093364; P
C/Genetics:
A/Gene: ML1544
C/Superfamily: *Mycobacterium tuberculosis* hypothetical protein Rv1782

Query Match 78.0%; Score 32; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
|||
Db 223 MNRVLLPL 231

RESULT 11

T51136
ionotropic glutamate receptor glr5 [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C/Accession: T51136
R/Davenport, R.J.; Kiegle, E.A.; Tester, M.
submitted to the EMBL Data Library, December 1999
A/Description: GLR5, an ionotropic glutamate receptor ortholog from *Arabidopsis*.
A/Reference number: Z25309
A/Accession: T51136
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-921 <DAV>
A:Cross-references: UNIPROT:Q9SDQ4; UNIPARC:UPI00000A3CDO; EMBL:AF210701; PIDN:AAF21042.
A:Experimental source: cultivar Columbis
C:Genetics:
A:Gene: glr5
A:Map position: 2

Query Match 78.0%; Score 32; DB 2; Length 921;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|||||:|
Db 705 MARSRLVPL 713

RESULT 12
F84732
probable ligand-gated ion channel subunit [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84732
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84732
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-923 <STO>
A:Cross-references: UNIPROT:Q9SDQ4; UNIPARC:UPI000017A6D8; GB:AE002093; NID:g3831456; PIDN:
C:Genetics:
A:Gene: At2g32400
A:Map position: 2

Query Match 78.0%; Score 32; DB 2; Length 923;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|||||:|
Db 707 MARSRLVPL 715

RESULT 13
T38055
hypothetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T38055; T38177; S62429
R.Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1995
A:Reference number: Z21765
A:Accession: T38055
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-26 <LY1>
A:Cross-references: UNIPROT:Q09779; UNIPARC:UPI0000162020; EMBL:Z69239; PIDN:CAA93223.1;
R.Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21776
A:Accession: T38177
A:Molecule type: DNA
A:Residues: 8-1621 <LY2>
A:Cross-references: UNIPARC:UPI000017B1DE; EMBL:Z54285; NID:g1008429; PIDN:CAA91079.2; C
C:Genetics:
A:Gene: SPAC1D4.14
A:Map position: 1L

Query Match 78.0%; Score 32; DB 2; Length 1628;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RSLLLPL 9
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Db 583 RSLLLPL 589

RESULT 14
I48107
sodium channel alpha subunit - long-tailed hamster (fragment)
C:Species: Cricetulus longicaudatus (long-tailed hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48107
R.Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A:Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A:Reference number: I48107
A:Accession: I48107
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-138 <RES>
A:Cross-references: UNIPROT:Q60463; UNIPARC:UPI00000E7D6C; GB:M87540; NID:g191067; PIDN:
C:Genetics:
A:Gene: chol
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 75.6%; Score 31; DB 2; Length 138;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 8
|||||:|
Db 1 MARSVLVP 8

RESULT 15
S28698
hypothetical protein 16 - Agrobacterium tumefaciens plasmid pTi15955
C:Species: Agrobacterium tumefaciens
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S28698
R.Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo
A:Reference number: S28683
A:Accession: S28698
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-147 <BAR>
A:Cross-references: UNIPROT:Q44395; UNIPARC:UPI00000BE55A; EMBL:X00493; NID:g39062; PIDN:
C:Genetics:
A:Genome: plasmid

Query Match 75.6%; Score 31; DB 2; Length 147;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 8
|||||
Db 1 MARYLLLP 8

Search completed: March 11, 2006, 00:40:53
Job time : 16.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05_80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--------------|
| 1 | 41 | 100.0 | 66 | 2 | Q6DTY1_HUMAN |
| 2 | 41 | 100.0 | 253 | 1 | KLK7_HUMAN |
| 3 | 36 | 87.8 | 855 | 1 | POLS2_HUMAN |
| 4 | 35 | 85.4 | 47 | 2 | Q5DIH8_HUMAN |
| 5 | 35 | 85.4 | 396 | 2 | Q9NZL1_HUMAN |
| 6 | 35 | 85.4 | 468 | 2 | Q9NZL2_HUMAN |
| 7 | 35 | 85.4 | 518 | 1 | BACE2_HUMAN |
| 8 | 35 | 85.4 | 593 | 2 | Q4NGK9_GMCC |
| 9 | 35 | 85.4 | 1135 | 2 | Q84W49_ARATH |
| 10 | 35 | 85.4 | 1192 | 2 | Q9S7T0_ARATH |
| 11 | 34 | 82.9 | 118 | 2 | Q7R254_NEUCR |
| 12 | 34 | 82.9 | 129 | 2 | Q8H584_ORYSA |
| 13 | 34 | 82.9 | 322 | 2 | Q67P07_SYNTH |
| 14 | 34 | 82.9 | 348 | 2 | Q7UAK2_SYNXP |
| 15 | 34 | 82.9 | 439 | 2 | Q6FTA5_CANGA |
| 16 | 34 | 82.9 | 461 | 1 | SSL1_YEAST |
| 17 | 34 | 82.9 | 461 | 2 | Q6B237_YEAST |
| 18 | 33 | 80.5 | 188 | 2 | Q6SSD7_WHEAT |
| 19 | 33 | 80.5 | 272 | 2 | Q8LC74_ARATH |
| 20 | 33 | 80.5 | 272 | 2 | Q9FNC4_ARATH |
| 21 | 33 | 80.5 | 291 | 2 | Q56Y44_ARATH |
| 22 | 33 | 80.5 | 295 | 2 | Q8W2V5_ORYSA |
| 23 | 33 | 80.5 | 297 | 2 | Q7P016_CHRVO |
| 24 | 33 | 80.5 | 323 | 2 | Q5VJ91_9BURK |
| 25 | 33 | 80.5 | 368 | 2 | Q8SAT6_ORYSA |
| 26 | 33 | 80.5 | 397 | 2 | Q9AA49_CAUCR |
| 27 | 33 | 80.5 | 424 | 2 | Q827F2_STRAW |
| 28 | 33 | 80.5 | 464 | 1 | OTSA_RHISN |
| 29 | 33 | 80.5 | 526 | 2 | Q9ZRH9_ORYSA |
| 30 | 33 | 80.5 | 531 | 2 | Q6ZK46_ORYSA |
| 31 | 33 | 80.5 | 571 | 2 | Q9SYC9_ARATH |

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|----|----|------|------|---|--------------|
| 32 | 33 | 80.5 | 582 | 1 | MMP14_MOUSE |
| 33 | 33 | 80.5 | 582 | 1 | MMP14_RAT |
| 34 | 33 | 80.5 | 582 | 2 | Q8BTX2_MOUSE |
| 35 | 33 | 80.5 | 582 | 2 | Q6DFU5_MOUSE |
| 36 | 33 | 80.5 | 582 | 2 | Q6IN06_RAT |
| 37 | 33 | 80.5 | 809 | 2 | Q8S23_ENCCU |
| 38 | 33 | 80.5 | 934 | 2 | Q9DER4_CHICK |
| 39 | 33 | 80.5 | 1048 | 2 | Q6ZJF7_ORYSA |
| 40 | 33 | 80.5 | 1124 | 2 | Q6ZBI6_ORYSA |
| 41 | 32 | 78.0 | 81 | 2 | Q92G73_RICCN |
| 42 | 32 | 78.0 | 126 | 2 | Q9KRE6_VIBCH |
| 43 | 32 | 78.0 | 139 | 2 | Q658A9_ORYSA |
| 44 | 32 | 78.0 | 149 | 2 | Q69YF9_HUMAN |
| 45 | 32 | 78.0 | 149 | 2 | Q8KAK3_CHLTE |

ALIGNMENTS

RESULT 1
Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646152; AAT6047.1; -, mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 41; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.99; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 MARSLLLPL 9
|||||
DB 1 MARSLLLPL 9

RESULT 2
KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

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Query Match 100.0%; Score 41; DB 1; Length 253;
 Best Local Similarity 100.0%; Pred. NO. 3.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
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 Db 1 MARSLLLPL 9

RESULT 3
 ID POLS2 HUMAN STANDARD; PRT; 855 AA.
 AC Q5K4E3; Q8NEY4;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Polypeptide-2 precursor (EC 3.4.21.-) (Polyserine protease-2) (Protease
 DE serine 36).
 GN Name=PRSS36;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], ENZYME ACTIVITY, ENZYME REGULATION,
 RP SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND N-GLYCOSYLATION.
 RC TISSUE=Liver;
 RX PubMed=15536082; DOI=10.1074/jbc.M409139200;
 RA Cal S., Quesada V., Llamazares M., Diaz-Perales A., Garabaya C.,
 RA Lopez-Otin C.;
 RT "Human polypeptide-2, a novel enzyme with three tandem serine protease
 RT domains in a single polypeptide chain."
 RL J. Biol. Chem. 280:1953-1961(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hoshiro T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Iehibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togashi S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oehima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukushima Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs."
 RL Nat. Genet. 36:40-45(2004).
 CC -1- FUNCTION: Serine protease. Hydrolyzes the peptides N-t-Boc-Gln-
 CC Ala-Arg-AMC and N-t-Boc-Gln-Gly-Arg-AMC and, to a lesser extent,
 CC N-t-Boc-Ala-Phe-Lys-AMC and N-t-Boc-Val-Lys-AMC. Has a
 CC preference for substrates with an Arg instead of a Lys residue in

CC position PL.
 CC -1- ENZYME REGULATION: Inhibited by serine proteinase inhibitor 4-(2-
 CC aminoethyl)-benzenesulfonyl fluoride, but not with EDTA or E-64.
 CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix. Not attached
 CC to membranes.
 CC -1- TISSUE SPECIFICITY: Expressed in fetal kidney, skeletal muscle,
 CC liver, placenta and heart. Also expressed in tumor cell lines,
 CC derived from lung and colon adenocarcinomas.
 CC -1- DOMAIN: The first serine protease domain is catalytically active,
 CC whereas the second domain lacks the essential His residue of the
 CC catalytic triad at position 363, and the third domain lacks the
 CC essential Asp residue of the catalytic triad at position 679. The
 CC second and third domains are therefore predicted to be inactive
 CC (by similarity).
 CC -1- PTM: The 3 protease domains are not proteolytically cleaved.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 3 peptidase S1 domains.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 51.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AJ627034; CAF25303.1; -; mRNA.
 CC EMBL; AK075142; BAC11431.1; ALT_FRAME; mRNA.
 CC HSSP; P00750; 1RTP.
 CC MEROPS; S01.414; -.
 CC HGNC; HGNC:26906; PRSS36.
 CC InterPro; IPR001254; Peptidase_S1_S6.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; Trypsin; 3.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 3.
 CC PROSITE; PS02440; TRYPSIN_DOM; 3.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Extracellular matrix; Glycoprotein; Hydrolase; Protease; Repeat;
 CC Serine protease; Signal; Zymogen.
 CC SIGNAL 1 22 Potential.
 CC PROPEP 23 46 Potential.
 CC CHAIN 47 855 Peptidase-2.
 CC DOMAIN 47 291 Peptidase S1 1.
 CC DOMAIN 323 555 Peptidase S1 2.
 CC DOMAIN 590 808 Peptidase S1 3.
 CC ACT_SITE 87 87 Charge relay system (By similarity).
 CC ACT_SITE 139 139 Charge relay system (By similarity).
 CC ACT_SITE 243 243 Charge relay system (By similarity).
 CC CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 217 217 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 317 317 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 402 402 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 407 407 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 421 421 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 508 508 By similarity.
 CC DISULFID 72 88 By similarity.
 CC DISULFID 173 249 By similarity.
 CC DISULFID 206 228 By similarity.
 CC DISULFID 239 267 By similarity.
 CC DISULFID 348 364 By similarity.
 CC DISULFID 444 516 By similarity.
 CC DISULFID 505 534 By similarity.
 CC DISULFID 616 631 By similarity.
 CC DISULFID 711 772 By similarity.
 CC DISULFID 739 751 By similarity.
 CC SEQUENCE 855 AA; 91921 MW; D1AF788019BD3A71 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 855;

Best Local Similarity 88.9%; Pred. No. 1.4e+02; Mismatches 0; Indels 1; Gaps 0;

QY 1 MARSLLLPL 9
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Db 1 MARLLLLPL 9

RESULT 4

QSDIH8_HUMAN
ID QSDIH8_HUMAN PRELIMINARY; PRT; 47 AA.
AC QSDIH8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE BACE2 (Fragment).
GN Name=BACE2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15857888;
RA Sun X., Wang Y., Qing H., Christensen M.A., Liu Y., Zhou W., Tong Y.,
RA Xiao C., Huang Y., Zhang S., Liu X., Song W.;
RT "distinct transcriptional regulation and function of the human BACE2
and BACE1 genes.";
RL FASEB J. 19:739-749 (2005).
DR EMBL; AV769996; AAX14808.1; -; Genomic_DNA.
FT NON TER 47
SQ SEQUENCE 47 AA; 4914 MW; C46FBC50BB70971B CRC64;

Query Match 85.4%; Score 35; DB 2; Length 47;

Best Local Similarity 77.8%; Pred. No. 13; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
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Db 4 LARALLLPL 12

RESULT 5

Q9NZL1_HUMAN
ID Q9NZL1_HUMAN PRELIMINARY; PRT; 396 AA.
AC Q9NZL1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Aspartyl protease.
GN Name=BACE2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de La Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytogenet. Cell Genet. 89:177-184 (2000).
DR EMBL; AF189277; AAF35836.1; -; mRNA.
DR HSSP; P56817; 1FKN.
DR Ensembl; ENSG00000182240; Homo sapiens.
DR GO; GO:0015021; C:integral to membrane; ISS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR GO; GO:0042985; P:negative regulation of amyloid precursor pr. . .; ISS.
DR GO; GO:0016486; P:peptide hormone processing; ISS.
DR InterPro; IPR009121; Pept_A1_BACE2.

Query Match 85.4%; Score 35; DB 2; Length 468;
Best Local Similarity 77.8%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
||| |||||
Db 4 LARALLLPL 12

RESULT 7
BACE2_HUMAN
ID BACE2_HUMAN STANDARD; PRT; 518 AA.

DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR01817; BACE2.
DR PRINTS; PR01815; BACEFAMILY.
DR PRINTS; PR00792; PPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 396;

Best Local Similarity 77.8%; Pred. No. 1.1e+02; Mismatches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
||| |||||
Db 4 LARALLLPL 12

RESULT 6

Q9NZL2_HUMAN
ID Q9NZL2_HUMAN PRELIMINARY; PRT; 468 AA.
AC Q9NZL2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Aspartyl protease.
GN Name=BACE2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de La Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytogenet. Cell Genet. 89:177-184 (2000).
DR EMBL; AF188276; AAF35835.1; -; mRNA.
DR HSSP; P56817; 1FKN.
DR Ensembl; ENSG00000182240; Homo sapiens.
DR GO; GO:0015021; C:integral to membrane; ISS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR GO; GO:0042985; P:negative regulation of amyloid precursor pr. . .; ISS.
DR GO; GO:0016486; P:peptide hormone processing; ISS.
DR InterPro; IPR009119; Pept_A1_BACE.
DR InterPro; IPR009121; Pept_A1_BACE2.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR01817; BACE2.
DR PRINTS; PR01815; BACEFAMILY.
DR PRINTS; PR00792; PPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Protease.
SQ SEQUENCE 468 AA; 50325 MW; 717E0920126A0142 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 468;

Best Local Similarity 77.8%; Pred. No. 1.3e+02; Mismatches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
||| |||||
Db 4 LARALLLPL 12

AC Q9Y5Z0; O9UJ76;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Beta secretase 2 precursor (SC 3.4.23.45) (Beta-site APP-cleaving
 DE enzyme 2) (Aspartyl protease 1) (ASP1) (Membrane-associated
 DE aspartic protease 1) (Memapsin-1) (Down region aspartic protease).
 GN Name=BACE2; Synonym=ASP21; ORFNames=UNQ418/PRO852;
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torg M.C., Pauley A.M.,
 RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomaselli A.G., Parodi L.A., Henrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity.";
 RL Nature 402:533-537 (1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim B., Grieshammer U.,
 RA Giese K.;
 RT "Identification of a novel aspartic-like protease differentially
 RT expressed in human breast cancer cell lines.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
 RT "Cloning of a gene from chromosome 21 Down region encoding a potential
 RT transmembrane aspartyl protease.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Solana A., Estivill X., de la Luna S.;
 RT "Cloning of a novel mammalian aspartyl protease.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427 (1999).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20144060; PubMed=10677483; DOI=10.1073/pnas.97.4.1456;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashi A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460 (2000).
 [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seethagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vanden R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein human secreted and transmembrane proteins: a
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).

[8]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.B.,
 RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.-L.;
 RT "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319 (2000).
 [9]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [10]
 RP CHARACTERIZATION.
 RX MEDLINE=22088158; PubMed=12093293; DOI=10.1021/bi025928t;
 RA Turner R.T. III, Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
 RA Koelsch G., Tang J.;
 RT "Specificity of memapsin 1 and its implications on the design of
 RT memapsin 2 (beta-secretase) inhibitor selectivity.";
 RL Biochemistry 41:8742-8746 (2002).
 CC -|- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- SIMILARITY: Belongs to the peptidase A1 family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
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 CC EMBL; AF200342; AAF17078.1; -; mRNA.
 CC EMBL; AF117892; AAD45240.1; -; mRNA.
 CC EMBL; AF050171; AAD45963.1; -; mRNA.
 CC EMBL; AF178532; AAF29494.1; -; mRNA.
 CC EMBL; AF204944; AAF26368.1; -; mRNA.
 CC EMBL; AF200192; AAF13714.1; -; mRNA.
 CC EMBL; AY358927; AAQ89286.1; -; mRNA.
 CC EMBL; AL163284; CAB90458.1; -; Genomic DNA.
 CC EMBL; AL163285; CAB90554.1; -; Genomic DNA.
 CC EMBL; BC014453; AAH14453.1; -; mRNA.
 CC HSP; P56817; 1M4H.
 CC MEROPS; A01.041; -.

```

DR Ensembl: ENSG00000182240; Homo sapiens.
DR HGNC: HGNC:934; BACE2.
DR MIM: 605668; -- C: integral to membrane; NAS.
DR GO: GO:0016021; C: integral to membrane; NAS.
DR GO: GO:0005624; C: membrane fraction; TAS.
DR GO: GO:0004190; F: aspartic-type endopeptidase activity; IDA.
DR GO: GO:0006509; P: membrane protein ectodomain proteolysis; IDA.
DR GO: GO:0042985; P: negative regulation of amyloid precursor pr. . .; IMP.
DR GO: GO:0016486; P: peptide hormone processing; NAS.
DR GO: GO:0006464; P: protein modification; TAS.
DR GO: GO:0009306; P: protein secretion; TAS.
DR InterPro: IPR009119; Pept Al BACE.
DR InterPro: IPR009121; Pept Al_BACE2.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR009007; Pept_Aspartc_cat.
DR InterPro: IPR001461; Peptidase_Al.
DR PANTHER: PTHR13683:SF15; Pept Al BACE; 1.
DR PANTHER: PTHR13683: Peptidase_Al; 1.
DR Pfam: PF00026; Asp; 1.
DR PRINTS: PR01817; BACE2.
DR PRINTS: PR01815; BACEFAMILY.
DR PRINTS: PR00792; PEPSIN.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
DR KW Aspartyl protease; Glycoprotein; Hydrolase; Protease; Signal;
Transmembrane; Zymogen.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 ? Potential.
FT CHAIN 21 518 Beta secretase 2.
FT TOPO_DOM 21 473 Extracellular (Potential).
FT TRANSMEM 474 494 Potential.
FT TOPO_DOM 495 518 Cytoplasmic (Potential).
FT ACT_SITE 110 110 By similarity.
FT ACT_SITE 303 303 By similarity.
FT CARBOHYD 170 170 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 366 366 N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 36 A -> T (in Ref. 6).
SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 4 LARALLPL 12

RESULT 8
Q4NGK9_9M1CC PRELIMINARY; PRT; 593 AA.
AC Q4NGK9_9M1CC PRELIMINARY; PRT; 593 AA.
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE ATP-binding region, ATPase-like; Histidine kinase A, N-terminal.
GN ORFNames=ArthDRAFT_2772;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococciaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lipidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Iserni S., Pfluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: RAHG01000005; EAL96513.1; -; Genomic_DNA.
KW ATP-binding; Kinase.
SQ SEQUENCE 593 AA; 64710 MW; 2D81CDAA7841B21C CRC64;

Query Match 85.4%; Score 35; DB 2; Length 593;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 199 LARSLLPLV 207

RESULT 9
Q84W49_ARATH PRELIMINARY; PRT; 1135 AA.
AC Q84W49;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein At3g01780 (Fragment).
GN Name=At3g01780;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BT004227; AAO42242.1; -; mRNA.
DR InterPro: IPR002048; EF-hand.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1135 1135
SQ SEQUENCE 1135 AA; 126119 MW; C5FDDC178D1E2D96 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1135;
Best Local Similarity 77.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 237 MARSLLPLV 245

RESULT 10
Q9S7T0_ARATH PRELIMINARY; PRT; 1192 AA.
AC Q9S7T0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE F28J7.11 protein (F4P13.33 protein).
GN Name=F28J7.11; Synonym=F4P13.33;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OX NCBI_TaxID=3702;
RN [1]

```

RP NUCLEOTIDE SEQUENCE
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC010797; AAF03433.1; -; Genomic DNA.
DR EMBL; AC009325; AAF01560.1; -; Genomic DNA.
DR InterPro; IPR002048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
SQ SEQUENCE 1192 AA; 132863 MW; 4F67B124CBAPF154 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1192;
Best Local Similarity 77.8%; Pred. No. 31e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 237 MARSLVLPV 245
|||||:

RESULT 11
Q7RZ54 NEUCR PRELIMINARY; PRT; 118 AA.
ID Q7RZ54;
AC Q7RZ54;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Predicted protein (Hypothetical protein G21B4.400).
GN Names=NCU04420.1; Synonyms=G21B4.400;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR748;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels W., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000720; EAA28261.1; -; Genomic DNA.
DR EMBL; BX908808; CAF06025.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 118 AA; 12596 MW; D1F84E47108B2145 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 118;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARSLLLPL 9
Db 23 ARSLLLPM 30
|||||:

RESULT 12
Q8H584 ORYSA PRELIMINARY; PRT; 129 AA.
ID Q8H584;
AC Q8H584;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Hypothetical protein OJ1656_E11.113 (Hypothetical protein
DE P0496D04.53).
GN Names=OJ1656_E11.113; Synonyms=P0496D04.53;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OJ1656_E11.1";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0496D04.53";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003843; BAC24850.1; -; Genomic DNA.
DR EMBL; AP004670; BAC30793.1; -; Genomic DNA.
DR Gramene; O8H584; -;
KW Hypothetical protein.
SQ SEQUENCE 129 AA; 13891 MW; 6334E639E1A6DEAE CRC64;

Query Match 82.9%; Score 34; DB 2; Length 129;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLP 8
Db 40 LARSLLLP 47
|||||:

RESULT 13
Q67P07 SYMTH PRELIMINARY; PRT; 322 AA.
ID Q67P07;
AC Q67P07;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Ferrichrome ABC transporter permease protein.
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JAM14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD40586.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006610; P:transport; IEA.
DR InterPro; IPR000522; FecD.

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DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 322 AA; 34949 MW; 80157DE1533812D9 CRC64;

Query Match      82.9%; Score 34; DB 2; Length 322;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db |||||:||||
1 MKRSLLIPL 9

RESULT 14
Q7U4K2_SYNXP PRELIMINARY; PRT; 348 AA.
AC Q7U4K2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ldpA protein.
GN OrderedLocuNames=SYNW2065;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahmanha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.B., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
CC -1- SUBUNIT: The cyanobacterial PSI reaction center is composed of one
CC copy each of psaA,B,C,D,E,F,I,J,K,L,M and X, and forms trimeric
CC complexes (By similarity).
CC -1- SUBCELLULAR LOCATION: Tightly associated with stromal side of the
CC thylakoid membrane (By similarity).
DR EMBL; BX569694; CAB08580.1; -; Genomic_DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FE4SFERDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Thylakoid; Transport.
SQ SEQUENCE 348 AA; 37531 MW; 1E1903BE684081A95 CRC64;

Query Match      82.9%; Score 34; DB 2; Length 348;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db |||||:||||
298 MARRLMLPL 306

RESULT 15
Q6FTA5_CANGA PRELIMINARY; PRT; 439 AA.
AC Q6FTA5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|Q04673|Saccharomyces cerevisiae YLR005w SSL1.
GN OrderedLocuNames=CRGJ0G040599;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;

[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaut J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380953; CAG59466.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR004595; Ssl1.
DR InterPro; IPR007198; Ssl1_like.
DR InterPro; IPR012170; TFIIF_SSL1.
DR InterPro; IPR020355; VWF_A.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF04056; Ssl1; 1.
DR PIRSF; PIRSF015919; TFIIF_SSL1; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR00622; Ssl1; 1.
DR PROSITE; PS00234; VWFA; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 439 AA; 49183 MW; 07D1A63D1575D894 CRC64;

Query Match      82.9%; Score 34; DB 2; Length 439;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db |||||:||||
194 MARGLLLPV 202

Search completed: March 11, 2006, 00:38:56
Job time : 99.3333 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
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3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 41 | 100.0 | 9 | 2 | US-09-502-600-86 |
| 2 | 41 | 100.0 | 9 | 2 | US-09-502-600-86 |
| 3 | 41 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 4 | 41 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 5 | 41 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 6 | 41 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 7 | 41 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 8 | 41 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 9 | 41 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 10 | 41 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 11 | 36 | 87.8 | 9 | 2 | US-09-502-600-116 |
| 12 | 36 | 87.8 | 9 | 2 | US-09-918-243-116 |
| 13 | 35 | 85.4 | 475 | 2 | US-09-668-314C-67 |
| 14 | 35 | 85.4 | 518 | 2 | US-08-999-723-2 |
| 15 | 35 | 85.4 | 518 | 2 | US-09-434-427-2 |
| 16 | 35 | 85.4 | 518 | 2 | US-09-548-372D-2 |
| 17 | 35 | 85.4 | 518 | 2 | US-09-548-367D-2 |
| 18 | 35 | 85.4 | 518 | 2 | US-09-551-853D-2 |
| 19 | 35 | 85.4 | 518 | 2 | US-09-215-450-19 |
| 20 | 35 | 85.4 | 518 | 2 | US-09-416-901B-2 |
| 21 | 35 | 85.4 | 518 | 2 | US-09-548-376D-2 |
| 22 | 35 | 85.4 | 518 | 2 | US-09-886-143-2 |
| 23 | 35 | 85.4 | 518 | 2 | US-09-794-927A-2 |
| 24 | 35 | 85.4 | 518 | 2 | US-09-548-373D-2 |
| 25 | 35 | 85.4 | 518 | 2 | US-09-795-847B-2 |
| 26 | 35 | 85.4 | 518 | 2 | US-09-869-414-2 |
| 27 | 35 | 85.4 | 518 | 2 | US-09-548-366F-2 |

28 35 85.4 518 2 US-09-548-368D-2 Sequence 2, Appli
29 35 85.4 518 2 US-09-794-925A-2 Sequence 2, Appli
30 35 85.4 518 2 US-09-806-194A-2 Sequence 2, Appli
31 35 85.4 518 2 US-09-668-314C-2 Sequence 2, Appli
32 35 85.4 518 2 US-09-668-314C-66 Sequence 66, Appli
33 35 85.4 518 2 US-09-548-365-2 Sequence 2, Appli
34 35 85.4 518 2 US-09-794-743-2 Sequence 2, Appli
35 85.4 518 2 US-09-999-833A-196 Sequence 196, App
36 35 85.4 518 2 US-10-020-445A-196 Sequence 196, App
37 35 85.4 541 2 US-09-949-016-11075 Sequence 11075, A
38 32 78.0 43 2 US-09-149-476-355 Sequence 355, App
39 32 78.0 123 2 US-09-270-767-33977 Sequence 33977, A
40 32 78.0 123 2 US-09-270-767-49194 Sequence 49194, A
41 32 78.0 175 2 US-09-869-388-8 Sequence 8, Appli
42 32 78.0 204 2 US-09-134-000C-3659 Sequence 3659, Ap
43 32 78.0 226 2 US-09-869-388-10 Sequence 10, Appli
44 32 78.0 227 2 US-09-869-388-6 Sequence 6, Appli
45 32 78.0 230 2 US-09-869-388-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-502-600-86
; Sequence 86, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-502-600-86

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 2
US-09-918-243-86
; Sequence 86, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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/
;
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-918-243-86

Query Match      100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARLLLLPL 9
Db      1 MARLLLLPL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARLLLLPL 9
Db      1 MARLLLLPL 9

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARLLLLPL 9
Db      1 MARLLLLPL 9

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-154-344-2

Query Match 100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 6
US-08-930-188-2
; Sequence 2, Application US/08930188
; Patent No. 6093397
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; ADDRESSEE: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,188
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-188-2

APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 7
US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; ADDRESSEE: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; US-09-210-084-3

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 8
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; ADDRESSEE: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
```

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/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0252 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: 532504
/ LIBRARY: GenBank
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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/ US-09-764-762-3
/
/ Query Match 100.0%; Score 41; DB 2; Length 253;
/ Best Local Similarity 100.0%; Pred. No. 0.49;
/ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 MARSLLLPL 9
/ Db 1 MARSLLLPL 9
/
/ RESULT 9
/ PCT-US96-04294-2
/ Sequence 2, Application PC/TUS9604294
/ GENERAL INFORMATION:
/ APPLICANT: Dixon, Eric P.
/ APPLICANT: Johnstone, Edward M.
/ APPLICANT: Little, Sheila P.
/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Eli Lilly and Company
/ STREET: Lilly Corporate Center
/ CITY: Indianapolis
/ STATE: Indiana
/ COUNTRY: United States of America
/ ZIP: 46285
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/04294
/ FILING DATE:
/ CLASSIFICATION:
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0252 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: 532504
/ LIBRARY: GenBank
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
/
/ US-09-764-762-3
/
/ Query Match 100.0%; Score 41; DB 2; Length 253;
/ Best Local Similarity 100.0%; Pred. No. 0.49;
/ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 MARSLLLPL 9
/ Db 1 MARSLLLPL 9
/
/ RESULT 10
/ US-09-949-016-7716
/ Sequence 7716, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7716
/ LENGTH: 265
/ TYPE: PRT
/ ORGANISM: Human
/
/ US-09-949-016-7716
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/ Query Match 100.0%; Score 41; DB 2; Length 265;
/ Best Local Similarity 100.0%; Pred. No. 0.51;
/ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 MARSLLLPL 9
/ Db 13 MARSLLLPL 21
/
/ RESULT 11
/ US-09-502-600-116
/ Sequence 116, Application US/09502600A
/ Patent No. 6294344
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
/ TITLE OF INVENTION: Ovarian Cancer
/ FILE REFERENCE: D6223C1P-C
/ CURRENT FILING DATE: 2000-02-11
/ CURRENT APPLICATION NUMBER: US/09/502,600A
/
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; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-502-600-116

Query Match      87.8%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ARSLLLPL 9
Db      1 ARSLLLPL 8

RESULT 12
US-09-918-243-116
; Sequence 116, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-918-243-116

Query Match      87.8%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ARSLLLPL 9
Db      1 ARSLLLPL 8

RESULT 13
US-09-668-314C-67
; Sequence 67, Application US/09668314C
; Patent No. 6844148
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314C
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-668-314C-67

Query Match      85.4%; Score 35; DB 2; Length 475;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      4 LARALLPL 12

RESULT 14
US-08-999-723-2
; Sequence 2, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-999-723-2

Query Match      85.4%; Score 35; DB 2; Length 518;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      4 LARALLPL 12

RESULT 15
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
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US-09-434-427-2

Query Match 85.4%; Score 35; DB 2; Length 518;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
Db :||:|||||
4 LARALLLPL 12

Search completed: March 11, 2006, 01:24:28
Job time : 22.2222 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083a-86

Perfect score: 41

Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 41 | 100.0 | 9 | 3 | US-09-918-243-86 |
| 2 | 41 | 100.0 | 9 | 3 | US-09-905-083-86 |
| 3 | 41 | 100.0 | 9 | 4 | US-10-372-521-86 |
| 4 | 41 | 100.0 | 9 | 5 | US-10-831-075-86 |
| 5 | 41 | 100.0 | 136 | 5 | US-10-450-763-53737 |
| 6 | 41 | 100.0 | 198 | 4 | US-10-262-511-96 |
| 7 | 41 | 100.0 | 253 | 3 | US-09-888-615-98 |
| 8 | 41 | 100.0 | 253 | 3 | US-09-764-762-3 |
| 9 | 41 | 100.0 | 253 | 4 | US-10-071-214-2 |
| 10 | 41 | 100.0 | 253 | 4 | US-10-071-214-48 |
| 11 | 41 | 100.0 | 253 | 4 | US-10-264-283-90 |
| 12 | 41 | 100.0 | 253 | 4 | US-10-295-027-498 |
| 13 | 41 | 100.0 | 253 | 4 | US-10-173-999-48 |
| 14 | 41 | 100.0 | 253 | 4 | US-10-408-765A-639 |
| 15 | 41 | 100.0 | 253 | 5 | US-10-643-795A-95 |
| 16 | 41 | 100.0 | 253 | 5 | US-10-948-518-95 |
| 17 | 41 | 100.0 | 253 | 5 | US-10-868-490A-1 |
| 18 | 41 | 100.0 | 257 | 4 | US-10-344-394-38 |
| 19 | 37 | 90.2 | 752 | 5 | US-10-612-466B-6 |
| 20 | 36 | 87.8 | 9 | 3 | US-09-918-243-116 |
| 21 | 36 | 87.8 | 9 | 3 | US-09-905-083-116 |
| 22 | 36 | 87.8 | 9 | 4 | US-10-372-521-116 |
| 23 | 36 | 87.8 | 9 | 5 | US-10-831-075-116 |
| 24 | 36 | 87.8 | 99 | 4 | US-10-424-599-279409 |
| 25 | 36 | 87.8 | 172 | 4 | US-10-424-599-239079 |
| 26 | 36 | 87.8 | 210 | 4 | US-10-425-114-50699 |
| 27 | 36 | 87.8 | 542 | 4 | US-10-425-115-318442 |

28 36 87.8 567 4 US-10-425-114-66721 Sequence 66721, A
29 36 87.8 818 3 US-09-888-615-111 Sequence 111, App
30 36 87.8 818 5 US-10-433-757-13 Sequence 13, Appl
31 35 85.4 232 4 US-10-424-599-262566 Sequence 262566,
32 35 85.4 346 4 US-10-791-488A-4 Sequence 4, Appli
33 35 85.4 475 5 US-10-817-979-67 Sequence 67, Appli
34 35 85.4 517 5 US-10-749-714-2 Sequence 2, Appli
35 35 85.4 518 3 US-09-794-927-2 Sequence 2, Appli
36 35 85.4 518 3 US-09-795-847-2 Sequence 2, Appli
37 35 85.4 518 3 US-09-794-743-2 Sequence 2, Appli
38 35 85.4 518 3 US-09-794-748-2 Sequence 2, Appli
39 35 85.4 518 3 US-09-794-925-2 Sequence 2, Appli
40 35 85.4 518 3 US-09-215-450-19 Sequence 19, Appli
41 35 85.4 518 3 US-09-681-442-2 Sequence 2, Appli
42 35 85.4 518 3 US-09-978-295A-196 Sequence 196, App
43 35 85.4 518 3 US-09-886-143-2 Sequence 2, Appli
44 35 85.4 518 3 US-09-978-697-196 Sequence 196, App
45 35 85.4 518 3 US-09-978-192A-196 Sequence 196, App

ALIGNMENTS

RESULT 1
US-09-918-243-86
; Sequence 86, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CJP/C/D/CJP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-918-243-86

Query Match 100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 2
US-09-905-083-86
; Sequence 86, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CJP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-905-083-86

Query Match      100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 3
US-10-372-521-86
; Sequence 86, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-10-372-521-86

Query Match      100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 4
US-10-831-075-86
; Sequence 86, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-10-831-075-86

Query Match      100.0%; Score 41; DB 5; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match      100.0%; Score 41; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 7 MARSLLLPL 15

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.

```

```
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuroseqList version 0.1
; SEQ ID NO 96
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 41; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 4.9; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 MARSLPL 9
Db 1 MARSLPL 9

RESULT 7
US-09-888-615-98
; Sequence 98, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 41; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLPL 9
Db 1 MARSLPL 9

RESULT 8
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 41; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLPL 9
Db 1 MARSLPL 9

RESULT 9
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US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 10
US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 11
US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US20030144494A1
; GENERAL INFORMATION:
; APPLICANT: Aigate, Paul A.
; APPLICANT: Mannion, Jane
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 12
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | | | | |
Db 1 MARSLLLPL 9

RESULT 13
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | | | | |
Db 1 MARSLLLPL 9

RESULT 14
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | | | | |
Db 1 MARSLLLPL 9

RESULT 15
US-10-643-795A-95
; Sequence 95, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-643-795A-95

Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | | | | |
Db 1 MARSLLLPL 9

Search completed: March 11, 2006, 01:37:25
Job time : 69.4444 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-86

Perfect score: 41

Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pdb*
- 2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pdb*
- 3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pdb*
- 4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pdb*
- 5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pdb*
- 6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pdb*
- 7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pdb*
- 8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pdb*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 41 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 2 | 41 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 3 | 41 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 4 | 41 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 5 | 36 | 87.8 | 818 | 7 | US-11-037-243-111 |
| 6 | 35 | 85.4 | 138 | 7 | US-11-096-568A-1854 |
| 7 | 32 | 78.0 | 303 | 7 | US-11-198-819-2 |
| 8 | 31 | 75.6 | 23 | 7 | US-11-175-690-33 |
| 9 | 30 | 73.2 | 216 | 6 | US-10-798-579A-2 |
| 10 | 30 | 73.2 | 216 | 6 | US-10-883-512-95 |
| 11 | 30 | 73.2 | 216 | 6 | US-10-883-512-96 |
| 12 | 30 | 73.2 | 216 | 6 | US-10-838-616-59 |
| 13 | 30 | 73.2 | 216 | 6 | US-10-714-887-426 |
| 14 | 30 | 73.2 | 216 | 6 | US-10-887-475B-2 |
| 15 | 30 | 73.2 | 216 | 7 | US-11-114-672-12 |
| 16 | 30 | 73.2 | 219 | 6 | US-10-883-512-92 |
| 17 | 30 | 73.2 | 242 | 7 | US-11-096-568A-20677 |
| 18 | 30 | 73.2 | 354 | 6 | US-10-821-234-1618 |
| 19 | 30 | 73.2 | 561 | 7 | US-11-087-099-10415 |
| 20 | 30 | 73.2 | 577 | 7 | US-11-074-176-184 |
| 21 | 29 | 70.7 | 250 | 7 | US-11-087-099-2477 |
| 22 | 29 | 70.7 | 251 | 6 | US-10-883-512-81 |
| 23 | 29 | 70.7 | 251 | 7 | US-11-087-099-7434 |
| 24 | 29 | 70.7 | 259 | 7 | US-11-096-568A-10450 |
| 25 | 29 | 70.7 | 336 | 7 | US-11-096-568A-5367 |

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| 26 | 29 | 70.7 | 372 | 7 | US-11-096-568A-5366 | Sequence 5366, Ap |
| 27 | 29 | 70.7 | 464 | 7 | US-11-096-568A-16302 | Sequence 16302, A |
| 28 | 29 | 70.7 | 494 | 7 | US-11-096-568A-16301 | Sequence 16301, A |
| 29 | 29 | 70.7 | 514 | 7 | US-11-096-568A-16300 | Sequence 16300, A |
| 30 | 29 | 70.7 | 661 | 7 | US-11-072-512-2645 | Sequence 2645, Ap |
| 31 | 29 | 70.7 | 783 | 7 | US-11-082-389-354 | Sequence 354, App |
| 32 | 28 | 68.3 | 89 | 7 | US-11-096-568A-5658 | Sequence 5658, Ap |
| 33 | 28 | 68.3 | 113 | 7 | US-11-096-568A-5657 | Sequence 5657, Ap |
| 34 | 28 | 68.3 | 142 | 7 | US-11-096-568A-5656 | Sequence 5656, Ap |
| 35 | 28 | 68.3 | 182 | 7 | US-11-096-568A-26809 | Sequence 26809, A |
| 36 | 28 | 68.3 | 214 | 7 | US-11-096-568A-26808 | Sequence 26808, A |
| 37 | 28 | 68.3 | 280 | 7 | US-11-096-568A-23041 | Sequence 23041, A |
| 38 | 28 | 68.3 | 289 | 7 | US-11-096-568A-278 | Sequence 278, App |
| 39 | 28 | 68.3 | 351 | 6 | US-10-467-657-5272 | Sequence 5272, Ap |
| 40 | 28 | 68.3 | 353 | 7 | US-11-096-568A-24235 | Sequence 24235, A |
| 41 | 28 | 68.3 | 367 | 7 | US-11-096-568A-18566 | Sequence 18566, A |
| 42 | 28 | 68.3 | 371 | 7 | US-11-096-568A-29391 | Sequence 29391, A |
| 43 | 28 | 68.3 | 412 | 7 | US-11-096-568A-28435 | Sequence 28435, A |
| 44 | 28 | 68.3 | 426 | 7 | US-11-096-568A-20044 | Sequence 20044, A |
| 45 | 28 | 68.3 | 449 | 7 | US-11-096-568A-28434 | Sequence 28434, A |

ALIGNMENTS

RESULT 1

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

| | | | |
|----|---|-----------|---|
| QY | 1 | MARSLLLPL | 9 |
| | | | |
| DB | 1 | MARSLLLPL | 9 |

RESULT 2

US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARSLLLPL 9
|||||

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARSLLLPL 9
|||||

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MARSLLLPL 9
Db      1 MARSLLLPL 9
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RESULT 5
US-11-037-243-111
; Sequence 111, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-111

Query Match      87.8%; Score 36; DB 7; Length 818;
Best Local Similarity 88.9%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARHLLPL 9
|||||

RESULT 6
US-11-096-568A-1854
; Sequence 1854, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1854
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(138)
; OTHER INFORMATION: Ceres Seq. ID no. 15179472
US-11-096-568A-1854

Query Match      85.4%; Score 35; DB 7; Length 138;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARSLSLPL 9
|||||

RESULT 7
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US-11-198-819-2
; Sequence 2, Application US/11198819
; Publication No. US20050287582A1
; GENERAL INFORMATION:
; APPLICANT: Adema, Gorse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-11-198-819-2
Query Match 78.0%; Score 32; DB 7; Length 303;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 MARLLLLLPL 9
DB 1 MGRPLLLPL 9
RESULT 8
US-11-175-690-33
; Sequence 33, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haeltline et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201

; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-33
Query Match 75.6%; Score 31; DB 7; Length 23;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 MARLLLLLPL 9
DB 3 LAYSLLLPL 11
RESULT 9
US-10-798-579A-2
; Sequence 2, Application US/10798579A
; Publication No. US20060005281A1
; GENERAL INFORMATION:
; APPLICANT: Kirin Beer Kabushiki Kaisha; Japan International Research Center for
; APPLICANT: Agricultural Sciences
; TITLE OF INVENTION: A production of plants having improved rooting efficiency and vase
; TITLE OF INVENTION: using environmental stress-resistant gene
; FILE REFERENCE: PH-2034
; CURRENT APPLICATION NUMBER: US/10/798,579A
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: JP 2003-071082
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-798-579A-2
Query Match 73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 MARLLLLLPL 9
DB 185 MAEGMLLPL 193
RESULT 10
US-10-883-512-95
; Sequence 95, Application US/10883512
; Publication No. US20060005265A1
; GENERAL INFORMATION:
; APPLICANT: Bughara, Suleiman
; APPLICANT: Han, Zhao
; APPLICANT: Wang, Yuexia
; TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation
; FILE REFERENCE: MSU-08807
; CURRENT APPLICATION NUMBER: US/10/883,512
; CURRENT FILING DATE: 2004-07-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95

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; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-883-512-95

Query Match      73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 185 MAEGMLLPL 193

RESULT 11
US-10-883-512-96
; Sequence 96, Application US/10883512
; Publication No. US20060005265A1
; GENERAL INFORMATION:
; APPLICANT: Bughrara, Suleiman
; APPLICANT: Han, Zhou
; APPLICANT: Wang, Yuxia
; TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation
; FILE REFERENCE: MSU-08807
; CURRENT APPLICATION NUMBER: US/10/883,512
; CURRENT FILING DATE: 2004-07-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 96
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-883-512-96

Query Match      73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 185 MAEGMLLPL 193

RESULT 12
US-10-838-616-59
; Sequence 59, Application US/10838616
; Publication No. US2006000874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
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; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: CBF3 G42 polypeptide
US-10-838-616-59

Query Match      73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 185 MAEGMLLPL 193

RESULT 13
US-10-714-887-426
; Sequence 426, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
; FILE REFERENCE: MBI0058-CIP
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 426
; LENGTH: 216
; TYPE: PRT
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; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: CBF3 polypeptide
US-10-714-887-426

Query Match 73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|| :|||
Db 185 MAEGMLLPL 193

RESULT 14
US-10-887-475B-2
; Sequence 2, Application US/10887475B
; Publication No. US20060015973A1
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko;
; APPLICANT: KASUGA, Mie;
; APPLICANT: SAKUMA, Yoh
; TITLE OF INVENTION: Environmental stress-tolerant plants
; FILE REFERENCE: 382.1029CIP
; CURRENT APPLICATION NUMBER: US/10/887,475B
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: US 10/664,771
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 09/301,217
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: JP 10-292348
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-887-475B-2

Query Match 73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|| :|||
Db 185 MAEGMLLPL 193

RESULT 15
US-11-114-672-12
; Sequence 12, Application US/11114672
; Publication No. US20060026716A1
; GENERAL INFORMATION:
; APPLICANT: Sivasankar, Sobhana
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Xu, Deping
; TITLE OF INVENTION: Transcriptional Activators Involved in
; TITLE OF INVENTION: Abiotic Stress Tolerance
; FILE REFERENCE: 1084
; CURRENT APPLICATION NUMBER: US/11/114,672
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US 60/565,430
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-114-672-12

Query Match 73.2%; Score 30; DB 7; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
|| :|||
Db 185 MAEGMLLPL 193
Search completed: March 11, 2006, 01:38:43
Job time : 8 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates

Title: US-09-905-083A-99
Perfect score: 42
Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*
```

SUMMARIES

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|----------|-------------|
| | Score | Match | Length | | | |
| 1 | 42 | 100.0 | 9 | 4 | AAE08334 | Human str |
| 2 | 42 | 100.0 | 9 | 4 | AAE08304 | Human str |
| 3 | 42 | 100.0 | 9 | 8 | ADR68891 | Human str |
| 4 | 42 | 100.0 | 9 | 8 | ADR68860 | Human str |
| 5 | 42 | 100.0 | 97 | 6 | ADAO5740 | Human NOV |
| 6 | 42 | 100.0 | 97 | 8 | ADN62904 | Human NOV |
| 7 | 42 | 100.0 | 144 | 8 | ADI39727 | Stratum c |
| 8 | 42 | 100.0 | 144 | 8 | ADI37151 | Stratum c |
| 9 | 42 | 100.0 | 181 | 6 | ADA05738 | Human NOV |
| 10 | 42 | 100.0 | 181 | 6 | ADN62902 | Human NOV |
| 11 | 42 | 100.0 | 198 | 6 | ADAO5736 | Human NOV |
| 12 | 42 | 100.0 | 198 | 8 | ADN62900 | Human NOV |
| 13 | 42 | 100.0 | 224 | 6 | ADAO5744 | Human NOV |
| 14 | 42 | 100.0 | 224 | 8 | ADN62908 | Human NOV |
| 15 | 42 | 100.0 | 224 | 9 | ADV21100 | Human str |
| 16 | 42 | 100.0 | 225 | 4 | AAB98502 | Human str |
| 17 | 42 | 100.0 | 247 | 6 | ADAO5742 | Human NOV |
| 18 | 42 | 100.0 | 247 | 8 | ADN62906 | Human NOV |
| 19 | 42 | 100.0 | 250 | 6 | ADAO5732 | Human NOV |
| 20 | 42 | 100.0 | 250 | 8 | ADN62896 | Human NOV |
| 21 | 42 | 100.0 | 252 | 6 | ADAO5734 | Human NOV |
| 22 | 42 | 100.0 | 252 | 8 | ADN62898 | Human NOV |
| 23 | 42 | 100.0 | 253 | 2 | ADR67868 | Human str |
| 24 | 42 | 100.0 | 253 | 2 | AAW05383 | Human amy |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAE08334 | |
| ID | AAE08334 standard; peptide; 9 AA. |
| XX | |
| XX | AAE08334; |
| XX | |
| DT | 01-NOV-2001 (first entry) |
| XX | |
| DE | Human stratum corneum chymotrypsin enzyme peptide #99 (residues 91-99). |
| XX | |
| XX | Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; |
| KW | cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; |
| KW | antitense therapy; malignant hyperplasia. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FN | WO200159158-A1. |
| XX | |
| PD | 16-AUG-2001. |
| XX | |
| PF | 07-FEB-2001; 2001WO-US003977. |
| XX | |
| PR | 11-FEB-2000; 2000US-00502600. |
| XX | |
| PA | (UYAR-) UNIV ARKANSAS. |
| XX | |
| PI | O'brien TJ; |
| XX | |
| DR | WPI; 2001-514676/56. |
| XX | |
| PT | Diagnosing cancer comprises detecting stratum corneum chymotrypsin |
| PT | enzyme. |
| XX | |
| PS | Disclosure; Page 124; 127pp; English. |
| XX | |
| CC | The invention relates to diagnosing cancer especially ovarian cancer, by |
| CC | screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are |
| CC | considered to be an integral part of tumour growth and metastasis, and |
| CC | therefore, markers indicative of their presence or absence are useful for |
| CC | the diagnosis of cancer. The method is useful for diagnosing cancer, |
| CC | carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used |
| CC | to treat a cancer selected from ovarian, breast, lung, colon, prostate |
| CC | and other cancers in which SCCE is overexpressed. The present sequence is |
| CC | human SCCE peptide |
| XX | |
| SQ | Sequence 9 AA; |
| SQ | |

Query Match 100.0%; Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 Db 1 QRIKASKSF 9

RESULT 2
 AAE08304
 ID AAE08304 standard; peptide; 9 AA.
 XX
 AC AAE08304;
 DT 01-NOV-2001 (first entry)
 DE Human stratum corneum chymotrypsin enzyme peptide #69 (residues 91-99).
 XX Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
 KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
 KW antitense therapy; malignant hyperplasia.
 XX Homo sapiens.
 OS
 XX WO200159158-A1.
 PN
 XX 16-AUG-2001.
 PD
 XX 07-FEB-2001; 2001WO-US003977.
 PF
 XX 11-FEB-2000; 2000US-00502600.
 PR
 XX (UYAR-) UNIV ARKANSAS.
 PA
 XX O'brien TJ;
 PI
 XX WPI; 2001-514676/56.
 DR
 XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin
 PT enzyme.
 PT
 PS Claim 25; Page 117; 127pp; English.
 XX
 CC The invention relates to diagnosing cancer especially ovarian cancer, by
 CC screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
 CC considered to be an integral part of tumour growth and metastasis, and
 CC therefore, markers indicative of their presence or absence are useful for
 CC the diagnosis of cancer. The method is useful for diagnosing cancer,
 CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
 CC to treat a cancer selected from ovarian, breast, lung, colon, prostate is
 CC and other cancers in which SCCE is overexpressed. The present sequence is
 CC human SCCE peptide
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 Db 1 QRIKASKSF 9

RESULT 3
 ADR68891
 ID ADR68891 standard; peptide; 9 AA.
 XX
 AC ADR68891;
 XX
 DT 02-DEC-2004 (first entry)
 DE Human stratum corneum chymotrypsin enzyme peptide fragment SEQ ID NO:99.
 XX serine protease; stratum corneum chymotrypsin enzyme; SCCE;
 KW immune response; ovarian cancer; lung cancer; prostate cancer;
 KW pancreatic cancer; colon cancer.
 XX Homo sapiens.
 OS
 XX WO2004075723-A2.
 PN
 XX 10-SEP-2004.
 PD

DE Human stratum corneum chymotrypsin enzyme peptide fragment SEQ ID NO:130.
 XX serine protease; stratum corneum chymotrypsin enzyme; SCCE;
 KW immune response; ovarian cancer; lung cancer; prostate cancer;
 KW pancreatic cancer; colon cancer.
 XX Homo sapiens.
 OS
 XX WO2004075723-A2.
 PN
 XX 10-SEP-2004.
 PD
 XX 20-FEB-2004; 2004WO-US005134.
 PF
 XX 21-FEB-2003; 2003US-00372521.
 PR
 XX (UYAR-) UNIV ARKANSAS.
 PA
 XX O'brien TJ, Cannon MJ, Santin A;
 PI
 XX WPI; 2004-653294/63.
 DR
 XX Use of stratum corneum chymotrypsin enzyme (SCCE) peptides, for
 PT vaccinating an individual against SCCE, and in monitoring and developing
 PT immunotherapies for ovarian and other malignancies.
 PT
 XX Disclosure; SEQ ID NO 130; 117pp; English.
 PS
 XX The invention relates to a novel method for vaccinating an individual
 CC against stratum corneum chymotrypsin enzyme (SCCE), comprising inoculating
 CC an individual with a SCCE peptide, which elicits an immune response in
 CC the individual. A peptide of the invention acts as a stratum corneum
 CC chymotrypsin enzyme inhibitor. The SCCE peptide is useful for vaccinating
 CC an individual against SCCE, particularly an individual having, suspected
 CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
 CC cancer. The oligonucleotide is useful for treating a neoplastic state in
 CC an individual, such as ovarian, breast, lung, colon, prostate, or
 CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
 CC peptides are also useful in the monitoring and development of
 CC immunotherapies for ovarian and other malignancies. The present sequence
 CC represents a peptide fragment of serine protease SCCE (stratum corneum
 CC chymotrypsin enzyme).
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 Db 1 QRIKASKSF 9

RESULT 4
 ADR68860
 ID ADR68860 standard; peptide; 9 AA.
 XX
 AC ADR68860;
 XX
 DT 02-DEC-2004 (first entry)
 DE Human stratum corneum chymotrypsin enzyme peptide fragment SEQ ID NO:99.
 XX serine protease; stratum corneum chymotrypsin enzyme; SCCE;
 KW immune response; ovarian cancer; lung cancer; prostate cancer;
 KW pancreatic cancer; colon cancer.
 XX Homo sapiens.
 OS
 XX WO2004075723-A2.
 PN
 XX 10-SEP-2004.
 PD

CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

XX Sequence 97 AA;

Query Match 100.0%; Score 42; DB 6; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORIKASKSF 9
 DB 72 ORIKASKSF 80

RESULT 6
 ADN62904
 ID ADN62904 standard; protein; 97 AA.

XX AC ADN62904;

DT 01-JUL-2004 (first entry)

DE Human NOV18e.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX PD 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349375P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PERN/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (ROTH/) ROTHENBERG R A.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 WIPI; 2004-213931/20.
 N-PSDB; ADN62903.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 Claim 1; SEQ ID NO 100; 395pp; English.
 The invention relates to isolated NOVX polypeptides and polynucleotides.
 NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 treat a medical condition in human related to the aberrant expression and
 activity of NOVX polypeptides. For example, NOVX polypeptides and
 polynucleotides may be used to treat disorders associated with decreased
 expression or activity of NOVX by supplementing the patient our
 production or to rectify mutations. Conversely, antisense NA molecules
 may be administered to down regulate expression of NOVX polypeptides by
 binding with the cells own genes and preventing their expression. NOVX
 polynucleotides and complementary sequences may also be used as DNA
 probes in diagnostic assays to detect and quantitate the presence of
 similar sequences in samples, and so which patients may be in need of
 restorative therapy. NOVX polypeptides may also be used as antigens in
 the production of antibodies and in assays to identify modulators
 (agonists and antagonists) of the expression and activity of NOVX. The
 anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 used to modulate NOVX polynucleotide expression and activity of NOVX
 polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 diagnostic agents for detecting the presence of NOVX in samples. NOVX
 polypeptides and polynucleotides may be used in this way to prevent,
 diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 disorders, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 haematopoietic disorders, and the various dyslipidaemias, metabolic

CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

SQ Sequence 97 AA;

Query Match 100.0%; Score 42; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 QRIKASKSF 9
| | | | | | | |
Db 72 QRIKASKSF 80

RESULT 7
ADI39727
ID ADI39727 standard; protein; 144 AA.
XX AC ADI39727;
XX DT 15-APR-2004 (first entry)
XX DE Stratum corneum chymotryptic enzyme (sccc) catalytic domain.
XX KW Immune T cell; dendritic cell; extracellular serine protease;
XX KW tumour antigen derived gene-14; TADG-14; carcinoma;
XX KW stratum corneum chymotryptic enzyme; sccc.
XX OS Unidentified.
XX PN US6642013-B1.
XX PD 04-NOV-2003.
XX PF 18-JUL-2000; 2000US-00618259.
XX PR 21-AUG-1997; 97US-00915659.
XX PR 21-AUG-1998; 98US-00137944.
XX PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
XX PI O'brien TJ, Underwood LJ;
XX WPI; 2004-118109/12.
XX PT Production of activated immune cells or dendritic cells by exposing
XX PT immune cells to tumor antigen derived gene protein fragment consisting of
XX PT amino acid sequences.
XX PS Example 1; SEQ ID NO 4; 44pp; English.
XX CC The present invention relates to novel activated immune T cells or
XX CC dendritic cells directed toward extracellular serine protease termed
XX CC tumour antigen derived gene-14 (TADG-14). The method of the invention
XX CC involves exposing the immune cells to a TADG-14 protein fragment, where
XX CC exposure to the TADG-14 protein fragment activates the immune cells. The
XX CC invention is used for the production of activated immune T cells or
XX CC dendritic cells. The invention allows screening to identify proteases
XX CC overexpressed in carcinoma. The present sequence is stratum corneum
XX CC chymotryptic enzyme (sccc) catalytic domain. This sequence is used in the
XX CC invention.

SQ Sequence 144 AA;

Query Match 100.0%; Score 42; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 QRIKASKSF 9
| | | | | | | |
Db 28 QRIKASKSF 36

RESULT 8
ADI37151
ID ADI37151 standard; protein; 144 AA.
XX AC ADI37151;
XX DT 06-MAY-2004 (first entry)
XX DE Stratum corneum chymotryptic enzyme (sccc) catalytic domain.
XX KW Serine protease; tumour antigen derived gene-14; TADG-14;
XX KW neoplastic state; cancer; ovary; breast; lung; colon; prostate;
XX KW chymotryptic enzyme; sccc; enzyme.
XX OS Homo sapiens.
XX PN US2003199010-A1.
XX PD 23-OCT-2003.
XX PF 13-JUN-2003; 2003US-00461787.
XX PR 21-AUG-1997; 97US-00915659.
XX PR 21-AUG-1998; 98US-00137944.
XX PR 18-JUL-2000; 2000US-00618259.
XX PA (UYAR-) UNIV ARKANSAS.
XX PI O'brien TJ, Underwood LJ;
XX WPI; 2004-141550/14.
XX PT Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
XX PT for treating neoplastic state (such as ovarian cancer, breast cancer,
XX PT lung cancer, colon cancer, prostate cancer) in an individual.
XX PS Example 1; SEQ ID NO 4; 46pp; English.
XX CC The invention relates to extracellular serine protease termed tumour
XX CC antigen derived gene-14 (TADG-14) and its nucleic acid. Composition
XX CC comprising TADG-14 peptide is useful for treating a neoplastic state in
XX CC an individual. The neoplastic state is chosen from ovarian cancer, breast
XX CC cancer, lung cancer, colon cancer, prostate cancer in which TADG-14 is
XX CC overexpressed. The present sequence is Stratum corneum chymotryptic
XX CC enzyme (sccc) catalytic domain. This sequence is used in the
XX CC exemplification of the invention.

SQ Sequence 144 AA;

Query Match 100.0%; Score 42; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 QRIKASKSF 9
| | | | | | | |
Db 28 QRIKASKSF 36

RESULT 9
ADA05738
ID ADA05738 standard; protein; 181 AA.
XX AC ADA05738;
XX DT 06-NOV-2003 (first entry)
XX DE Human NOV18d protein SEQ ID NO:98.
XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
XX KW immunomodulator; cytostatic; neutropenic; neuroprotective;
XX KW antiparkinsonian; antilipemic; gene therapy; human disease;

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX Homo sapiens.

XX WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 12-OCT-2001; 2001US-0328056P.

XX PR 09-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 29-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 17-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

XX PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dippio VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2003-381626/36.
 DR N-PSDB; ADA05737.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX Claim 1; Page 171; 586pp; English.

CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antilipidemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX SQ Sequence 181 AA;

Query Match 100.0%; Score 42; DB 6; Length 181;

Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 1 QRIKASKSF 9

Db 72 QRIKASKSF 80

|||||||

RESULT 10

ADN62902

ID ADN62902 standard; protein; 181 AA.

XX AC ADN62902;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV18d.

XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX PD 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381039P.
 16-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383656P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 (SMIT// SMITHSON G.
 (MILL// MILLET I.
 (PEYM// PEYMAN J. A.
 (KEKU// KEKUDA R.
 (JUUJ// JU J.
 (LILL// LI L.
 (GUOX// GUO X.
 (PATT// PATTURAJAN M.
 (SPYT// SPYTEK K. A.
 (EDIN// EDINGER S. R.
 (ELLE// ELLERMAN K.
 (MALY// MALYANKAR U. M.
 (ORTT// ORT T.
 (GORM// GORMAN L.
 (ZERH// ZERHUSEN B. D.
 (ANDE// ANDERSON D. W.
 (ZHON// ZHONG M.
 (CATT// CATTERTON E.
 (JIWJ// JI W.
 (MILL// MILLER C. E.
 (RAST// RASTELLI L.
 (STON// STONE D. J.
 (PENA// PENA C. E. A.
 (SHEN// SHENOY S. G.
 (SHIM// SHIMKETS R. A.
 (ROTH// ROTHENBERG M. E.
 (LEAC// LEACH M. D.
 (AGEE// AGEE M. L.
 (BERG// BERGHS C.
 (DIPI// DIPIPPO V. A.
 (EISE// EISEN A.
 (GANG// GANGOLLI E. A.
 (RIEG// RIEGER D. K.
 (SPAD// SPADERNA S. K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI: 2004-213931/20.
 N-PSDB: ADN62901.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 Claim 1; SEQ ID NO 98; 395pp; English.
 The invention relates to isolated NOVX polypeptides and polynucleotides.
 NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 treat a medical condition in human related to the aberrant expression and
 activity of NOVX polypeptides. For example, NOVX polypeptides and
 polynucleotides may be used to treat disorders associated with decreased
 expression or activity of NOVX by supplementing the patient our
 production or to rectify mutations. Conversely, antisense NA molecules

CC may be administered to down regulate expression of NOVX polypeptides by
 binding with the cells own genes and preventing their expression. NOVX
 polynucleotides and complementary sequences may also be used as DNA
 probes in diagnostic assays to detect and quantitate the presence of
 similar sequences in samples, and so which patients may be in need of
 restorative therapy. NOVX polypeptides may also be used as antigens in
 the production of antibodies and in assays to identify modulators
 (agonists and antagonists) of the expression and activity of NOVX. The
 anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 used to modulate NOVX polynucleotide expression and activity of NOVX
 polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 diagnostic agents for detecting the presence of NOVX in samples. NOVX
 polypeptides and polynucleotides may be used in this way to prevent,
 diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 haematopoietic disorders, and the various dyslipidaemias, metabolic
 disturbances associated with obesity, the metabolic syndrome X and
 wasting disorders associated with chronic diseases and various cancers.
 They may also be used as antibacterial agents. The present sequence
 represents the amino acid sequence of a human NOVX protein.

SQ Sequence 181 AA;
 Query Match 100.0%; Score 42; DB 8; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKAKSKF 9
 Db 72 QRIKAKSKF 80

RESULT 11
 ADA05736
 ID ADA05736 standard; protein; 198 AA.
 XX
 AC ADA05736;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18c protein SEQ ID NO:96.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.

PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR WFI; 2004-213931/20.
DR N-PSDB; ADNG2899.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 96; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
XX represents the amino acid sequence of a human NOVX protein.
SQ Sequence 198 AA;

Query Match 100.0%; Score 42; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. NO. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db |||||
91 QRIKASKSF 99
RESULT 13
ADA05744
ID ADA05744 standard; protein; 224 AA.
XX
AC ADA05744;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18g protein SEQ ID NO:104.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytotatic; neurotropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 29-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 15-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WFI; 2003-381626/36.
DR N-PSDB; ADA05743.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 172; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cyostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, hematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 224 AA;
SQ

Query Match 100.0%; Score 42; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 77 QRIKASKSF 85

RESULT 14
ADN62908
ID ADN62908 standard; protein; 224 AA.
XX
XX ADN62908;
XX
XX 01-JUL-2004 (first entry)
XX Human NOV18g.
XX
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
OS
XX US2004038223-A1.
PI

XX PD 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0383656P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUGU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEES M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2004-213931/20.
 DR N-PSDB; ADN62907.
 XX
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 FT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 XX Claim 1; SEQ ID NO 104; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 224 AA;

Query Match 100.0%; Score 42; DB 8; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 |||||
 Db 77 QRIKASKSF 85

RESULT 15

ADV21100
 ID ADV21100 standard; protein; 224 AA.

XX AC ADV21100;

XX DT 24-FEB-2005 (first entry)

XX DE Human stratum corneum chymotrypsin protein.

XX KW Protein purification; PS133 protein; serine protease; prostate disease;
 KW andrology; genitourinary disease; prostatic cancer; cytostatic;
 KW protein therapy; chymotrypsin; enzyme.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 26..42

FT /note = Catalytically functional motif

FT Domain 83..87

FT /note = Catalytically functional motif

FT

FT Domain 174..179
 FT /note = Catalytically functional motif

XX US2004241646-A1.

XX PD 02-DEC-2004.

XX PF 20-FEB-2001; 2001US-00789210.

XX PR 06-OCT-1997; 97US-00944483.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GRAN/) GRANADOS E.

XX (KLAS/) KLAS M R.

XX (RUSS/) RUSSELL J C.

XX (STEM/) STEWART K D.

XX (STRO/) STROUPE S D.

XX Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;
 PI Russell JC, Stewart KD, Stroupe SD;

XX WPI; 2005-011614/01.
 DR GENBANK; L33404.

XX New isolated polypeptides, useful for detecting, diagnosing, staging,
 PT monitoring, prognosticating, preventing or treating, or determining
 PT predisposition to diseases or conditions of the prostate such as prostate
 PT cancer.

XX Example 1; SEQ ID NO 33; 96pp; English.

XX The invention relates to PS133 protein, a member of the human serine
 CC protease family and its corresponding nucleic acid sequence. PS133
 CC polypeptide is useful for detecting, diagnosing, staging, monitoring, to
 CC prognosticating, preventing or treating or determining predisposition to
 CC diseases or conditions of the prostate such as prostatic cancer. The
 CC present sequence is the human stratum corneum chymotrypsin protein. This
 CC sequence is used to align with PS133 consensus protein.

XX Sequence 224 AA;

Query Match 100.0%; Score 42; DB 9; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 |||||
 Db 62 QRIKASKSF 70

Search completed: March 11, 2006, 00:24:19
 Job time : 87.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 42 | 100.0 | 253 | 2 A53968 | serine proteinase |
| 2 | 34 | 81.0 | 373 | 2 D89004 | protein T24A6.11 [|
| 3 | 33 | 78.6 | 427 | 2 A49518 | kallistatin precu |
| 4 | 32 | 76.2 | 895 | 2 D72571 | probable DNA-direc |
| 5 | 31 | 73.8 | 248 | 2 A40625 | tetrachloro-p-hydr |
| 6 | 31 | 73.8 | 298 | 2 S32368 | beta-SNAP protein |
| 7 | 31 | 73.8 | 302 | 2 T50147 | mak16-like protein |
| 8 | 31 | 73.8 | 362 | 2 F81409 | probable phosphate |
| 9 | 30 | 71.4 | 142 | 2 C39610 | BET1 protein - yea |
| 10 | 30 | 71.4 | 321 | 2 C71463 | probable p-loop AT |
| 11 | 30 | 71.4 | 331 | 2 H97051 | probable dehydroge |
| 12 | 30 | 71.4 | 427 | 2 T48159 | hypothetical prote |
| 13 | 30 | 71.4 | 517 | 2 T40129 | hypothetical prote |
| 14 | 30 | 71.4 | 627 | 2 C68850 | neutral endopeptid |
| 15 | 30 | 71.4 | 627 | 2 A47098 | lactococcal enope |
| 16 | 30 | 71.4 | 627 | 2 F53290 | endopeptidase Pepo |
| 17 | 30 | 71.4 | 875 | 2 T19678 | hypothetical prote |
| 18 | 30 | 71.4 | 985 | 2 D82776 | pyruvate dehydroge |
| 19 | 30 | 71.4 | 1102 | 2 H84545 | probable ubiquitin |
| 20 | 30 | 71.4 | 3660 | 1 S02041 | dystrophin, muscle |
| 21 | 29 | 69.0 | 65 | 2 AF2269 | hypothetical prote |
| 22 | 29 | 69.0 | 141 | 1 B46322 | 1eK protein - toba |
| 23 | 29 | 69.0 | 172 | 2 H81251 | NADH2 dehydrogenas |
| 24 | 29 | 69.0 | 182 | 2 C64176 | hypothetical prote |
| 25 | 29 | 69.0 | 203 | 2 C90678 | thiogalactoside ac |
| 26 | 29 | 69.0 | 203 | 2 G85528 | thiogalactoside ac |
| 27 | 29 | 69.0 | 268 | 2 E84339 | quinolinate phosph |
| 28 | 29 | 69.0 | 349 | 2 AE2568 | WD repeat protein |
| 29 | 29 | 69.0 | 368 | 2 T22587 | hypothetical prote |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 29 | 69.0 | 463 | 2 G97300 | aspartyl/asparagin |
| 31 | 29 | 69.0 | 484 | 2 JCS282 | phosphoglucanase d |
| 32 | 29 | 69.0 | 526 | 1 G71081 | probable helicase |
| 33 | 29 | 69.0 | 563 | 2 B82883 | hypothetical prote |
| 34 | 29 | 69.0 | 584 | 2 T48273 | hypothetical prote |
| 35 | 29 | 69.0 | 585 | 2 I37216 | calicin - human (f |
| 36 | 29 | 69.0 | 669 | 2 AB2028 | hypothetical prote |
| 37 | 29 | 69.0 | 691 | 2 T46476 | hypothetical prote |
| 38 | 29 | 69.0 | 717 | 2 AC1419 | DNA topoisomerase |
| 39 | 29 | 69.0 | 738 | 2 E86294 | hypothetical prote |
| 40 | 29 | 69.0 | 743 | 2 C86168 | hypothetical prote |
| 41 | 29 | 69.0 | 759 | 2 S67164 | probable membrane |
| 42 | 29 | 69.0 | 940 | 2 A40985 | projectin - fruit |
| 43 | 29 | 69.0 | 1018 | 2 T15297 | hypothetical prote |
| 44 | 29 | 69.0 | 1742 | 2 S24600 | projectin - fruit |
| 45 | 29 | 69.0 | 6658 | 2 T13931 | projectin - fruit |

ALIGNMENTS

RESULT 1

A53968

N;Alternate names: serine proteinase SCCE precursor - human

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C;Accession: A53968

R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.

J. Biol. Chem. 269, 19420-19426, 1994

A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme

A;Reference number: A53968; MUID:94308225; PMID:8034709

A;Accession: A53968

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-253 <HAN>

A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:

C;Genetics:

A;Gene: GDB:PRSS6; SCCE

A;Cross-references: GDB:377730

A;Map position: 7q35-7q35

C;Superfamily: trypsin; trypsin homology

F;30-245/Domain: trypsin homology <TRI>

Query Match 100.0%; Score 42; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 91 QRIKASKSF 99

RESULT 2

D89004

protein T24A6.11 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: D89004

R;Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: D89004

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-373 <STO>

A;Cross-references: UNIPROT:O61942; UNIPARC:UPI000017A667; GB:chr_V; PIDN:AAC17798.1; PFI

A;Note: contains similarity to C4-type zinc fingers

C;Genetics:

A;Gene: T24A6.11

A;Map position: 5

Query Match 81.0%; Score 34; DB 2; Length 373;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QRIKASKSF 9
| | | | |
Db 9 QEIKSKSP 17

RESULT 3

A49518
Kallistatin precursor - human
N;Alternate names: proteinase inhibitor 4; tissue kallikrein inhibitor
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: A49518; A55560; A45093
R;Chai, K.X.; Chen, L.M.; Chao, J.; Chao, L.
J. Biol. Chem. 268, 24498-24505, 1993
A;Title: Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, tissue culture, and expression of complementary DNA.
A;Reference number: A49518; MUID:94043294; PMID:8227002
A;Accession: A49518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <CHA>
A;Cross-references: UNIPROT:P29622; UNIPARC:UPI000012DC02; GB:L19684; NID:G425145; PIDN:R;Chai, K.X.; Ward, D.C.; Chao, J.; Chao, L.
Genomics 23, 370-378, 1994
A;Title: Molecular cloning, sequence analysis, and chromosomal localization of the human kallistatin gene.
A;Reference number: A55560; MUID:95137583; PMID:7835886
A;Accession: A55560
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-427 <CH2>
A;Cross-references: UNIPARC:UPI000012DC02; GB:L28101; NID:G609489; PIDN:AAC41706.1; PID:R;Zhou, G.X.; Chao, L.; Chao, J.
J. Biol. Chem. 267, 25873-25880, 1992
A;Title: Kallistatin: a novel human tissue kallikrein inhibitor. Purification, characterization, and expression of complementary DNA.
A;Reference number: A45093; MUID:93100304; PMID:1334408
A;Accession: A45093
A;Molecule type: protein
A;Residues: 389-403 <ZHO>
A;Cross-references: UNIPARC:UPI00000353AC; PIDN:AAB24557.1; PID:G261993
A;Note: sequence extracted from NCBI backbone (NCBIP:120847)
C;Genetics:

A;Gene: GDB:PI4; KLST
A;Cross-references: GDB:266537; OMIM:147935
A;Map position: 14q31-14q32.1
C;Superfamily: serpin
C;Keywords: blocked amino end; glycoprotein; pyroglutamic acid; serine proteinase inhibitor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-427/Product: kallistatin #status predicted <WAT>
F;21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;33.108.157.238/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;308/Inhibitory site: Phe (tissue kallikrein) #status experimental

Query Match 78.6%; Score 33; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
| | | | |
Db 355 QKLEASKSF 363

RESULT 4

D72571
Probable DNA-directed RNA polymerase subunit A' APE1853 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72571
R;Kawabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kikuchi, T.
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1.
A;Reference number: A74450; MUID:99310339; PMID:10382966
A;Accession: D72571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-895 <KAW>
A;Cross-references: UNIPROT:Q9YAU1; UNIPARC:UPI000005E0F5; DBJ:AP000062; NID:G5105244; I:1
C;Genetics:
A;Experimental source: strain K1
C;Superfamily: Halobacterium DNA-directed RNA polymerase chain A

Query Match 76.2%; Score 32; DB 2; Length 895;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKS 8
| | | | |
Db 885 QRVKASKA 892

RESULT 5

A40625
tetrahydro-p-hydroquinone reductive dehalogenase (EC 1.-.-.-) - Flavobacterium sp.
N;Alternate names: glutathione S-transferase homolog; Tech reductive dehalogenase
C;Species: Flavobacterium sp.
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A40625
R;Orser, C.S.; Dutton, J.; Lange, C.; Jablonski, P.; Xun, L.; Hargis, M.
J. Bacteriol. 175, 2640-2644, 1993
A;Title: Characterization of a Flavobacterium glutathione S-transferase gene involved in the reduction of tetrahydro-p-hydroquinone.
A;Reference number: A40625; MUID:93239690; PMID:8478329
A;Accession: A40625
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-248 <ORS>
A;Cross-references: UNIPARC:UPI000017A939; GB:M98559; NID:G148689; PIDN:AAA24921.1; PID:R;Orser, C.S.; Dutton, J.; Lange, C.; Jablonski, P.; Xun, L.; Hargis, M.
A;Experimental source: ATCC 39723
A;Note: sequence extracted from NCBI backbone (NCBIN:130432, NCBIP:130433)
C;Keywords: oxidoreductase

Query Match 73.8%; Score 31; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
| | | | |
Db 227 QRMKARRSF 235

RESULT 6

S32368
beta-SNAP protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S32368
R;Whiteheart, S.W.; Griff, I.C.; Brunner, M.; Clary, D.O.; Mayer, T.; Buhrow, S.A.; Rothman, J.
Nature 362, 353-355, 1993
A;Title: SNAP family of NSF attachment proteins includes a brain-specific isoform.
A;Reference number: S32367; MUID:93205122; PMID:8455721
A;Accession: S32368
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <WHI>
A;Cross-references: UNIPROT:P81126; UNIPARC:UPI0000135B11
C;Superfamily: alpha-soluble NSF attachment protein

Query Match 73.8%; Score 31; DB 2; Length 298;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97051
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <KUR>
A;Cross-references: UNIPROT:Q97JP2; UNIPARC:UPI000000CA131; GB:AE001437; PIDN:AAK79203.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1231
C;Superfamily: Escherichia coli yvjR protein

Query Match 71.4%; Score 30; DB 2; Length 331;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKS 8
DB 303 QRLKVS KS 310
||| |||

RESULT 12
T48159
hypothetical protein T1008.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48159
R;Bevan, M.; Pohl, T.; Weizengger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24486
A;Accession: T48159
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <BEV>
A;Cross-references: UNIPROT:Q9M035; UNIPARC:UPI000000A2376; EMBL:AL161746
A;Experimental source: cultivar Columbia; BAC clone T1008
C;Genetics:
A;Map position: 5
A;Introns: 317/1
A;Note: T1008.80

Query Match 71.4%; Score 30; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKS 9
DB 140 RRVKASVS F 148
||| |||

RESULT 13
T40129
hypothetical protein SPBC2F12.12c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40129
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z21907
A;Accession: T40129
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-517 <WOO>
A;Cross-references: UNIPROT:O14342; UNIPARC:UPI0000013A210; EMBL:Z97211; PIDN:CAB10159.1;
A;Experimental source: strain 972H-; cosmid c2F12
C;Genetics:
A;Gene: SPDB:SPBC2F12.12c
A;Map position: 2

A;Introns: 42/3; 126/3; 157/3; 308/3

Query Match 71.4%; Score 30; DB 2; Length 517;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QRIKASKS 9
DB 187 QRIAPKSF 195
||| |||

RESULT 14
C86850
neutral endopeptidase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86850
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <STO>
A;Cross-references: UNIPROT:Q07744; UNIPARC:UPI0000165F0B; GB:AE005176; PID:gl2724829; P;
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: pepO

Query Match 71.4%; Score 30; DB 2; Length 627;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RIKASKS 9
DB 570 RMKASKEF 577
||| |||

RESULT 15
A47098
lactococcal endopeptidase (EC 3.4.-.-) - Lactococcus lactis subsp. cremoris (strain P8-2-
C;Species: Lactococcus lactis subsp. cremoris
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A47098
R;Mierau, I.; Tan, P.S.T.; Haandrikman, A.J.; Kok, J.; Leenhouts, K.J.; Konings, W.N.; Ve
J. Bacteriol. 175, 2087-2096, 1993
A;Title: Cloning and sequencing of the gene for a lactococcal endopeptidase, an enzyme w
A;Reference number: A47098; MUID:93209954; PMID:8458851
A;Accession: A47098
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <MIE>
A;Cross-references: UNIPROT:Q09145; UNIPARC:UPI000016F8B8; GB:L04938; NID:g293013; PIDN:
C;Genetics:
A;Gene: pepO
C;Keywords: hydrolase; oligopeptide transport

Query Match 71.4%; Score 30; DB 2; Length 627;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RIKASKS 9
DB 570 RMKASKEF 577
||| |||

Search completed: March 11, 2006, 00:40:54
Job time: 15.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-99
Perfect score: 42
Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 42 | 100.0 | 253 | 1 KLK7_HUMAN | P49862 homo sapien |
| 2 | 36 | 85.7 | 249 | 1 KLK7_MOUSE | Q91ve3 mus musculus |
| 3 | 34 | 81.0 | 107 | 1 Y1897_PASPU | Q9cju4 pasteurella |
| 4 | 34 | 81.0 | 294 | 2 Q88037_PSEPK | Q88037 pseudomonas |
| 5 | 34 | 81.0 | 296 | 2 Q4K21_PSEPF5 | Q4k21 pseudomonas |
| 6 | 34 | 81.0 | 683 | 2 Q82X80_NITEU | Q82x80 nitrosomonas |
| 7 | 33 | 78.6 | 310 | 2 Q678H2_SVIRU | Q678h2 lymphocysti |
| 8 | 33 | 78.6 | 314 | 1 RLAO_THEAC | P57692 thermoplasm |
| 9 | 33 | 78.6 | 427 | 1 KAIN_HUMAN | P29622 homo sapien |
| 10 | 33 | 78.6 | 427 | 1 KAIN_PONPY | Q5rcr2 pongo pygma |
| 11 | 33 | 78.6 | 445 | 2 Q54TF9_DICDI | Q54tf9 dictyosteli |
| 12 | 33 | 78.6 | 513 | 2 Q54H89_DICDI | Q54h89 dictyosteli |
| 13 | 33 | 78.6 | 671 | 2 Q8EUP9_MYCPE | Q8eup9 mycoplasma |
| 14 | 33 | 78.6 | 1618 | 2 Q4S703_TETNG | Q4s703 tetraodon n |
| 15 | 32 | 76.2 | 161 | 1 RL10_MYCPE | Q8evj0 mycoplasma |
| 16 | 32 | 76.2 | 240 | 2 Q6PDR5_ACTAD | Q6pdr5 acinetobact |
| 17 | 32 | 76.2 | 274 | 2 Q4QB71_LEIMA | Q4qb71 leishmania |
| 18 | 32 | 76.2 | 362 | 2 Q4HKD5_CAMLA | Q4hkds campylobact |
| 19 | 32 | 76.2 | 458 | 2 Q7RKQ8_PLAYO | Q7rkq8 plasmodium |
| 20 | 32 | 76.2 | 467 | 2 Q8IBN4_PLAF7 | Q8ibn4 plasmodium |
| 21 | 32 | 76.2 | 474 | 2 Q7VRX5_CANBF | Q7vrxx5 candidatus |
| 22 | 32 | 76.2 | 490 | 2 Q8SAQ6_CHLRE | Q8saq6 chlamydomon |
| 23 | 32 | 76.2 | 571 | 2 Q5X079_LEGPL | Q5x079 legionella |
| 24 | 32 | 76.2 | 684 | 2 Q18K2_HOLDI | Q8i6k2 holotrichia |
| 25 | 32 | 76.2 | 761 | 2 Q6D7X6_ERWCT | Q6d7x6 erwinia car |
| 26 | 32 | 76.2 | 772 | 2 Q62HP6_BURNA | Q62hp6 burkholderi |
| 27 | 32 | 76.2 | 772 | 2 Q63W23_BURPS | Q63w23 burkholderi |
| 28 | 32 | 76.2 | 793 | 2 Q7QXV1_GIALA | Q7qxv1 giardia lam |
| 29 | 32 | 76.2 | 895 | 2 Q9YAU1_AERPE | Q9yau1 aeropyrum p |
| 30 | 32 | 76.2 | 909 | 2 Q4PQ08_USTWA | Q4peq8 ustilago ma |
| 31 | 32 | 76.2 | 3395 | 2 Q5CW22_CRYPV | Q5cw22 cryptospori |

| | | | | | | |
|----|----|------|-----|---|--------------|--------------------|
| 32 | 31 | 73.8 | 143 | 2 | Q4RUL0_TETNG | Q4rul0 tetraodon n |
| 33 | 31 | 73.8 | 155 | 2 | Q6DGM1_BRAKE | Q6dgm1 brachydanio |
| 34 | 31 | 73.8 | 176 | 2 | Q6AXN0_RAT | Q6axn0 rattus norv |
| 35 | 31 | 73.8 | 176 | 2 | Q6P3B2_MOUSE | Q6p3b2 mus musculu |
| 36 | 31 | 73.8 | 177 | 2 | Q8TB05_HUMAN | Q8tb05 homo sapien |
| 37 | 31 | 73.8 | 200 | 2 | Q4S4E7_TETNG | Q4s4e7 tetraodon n |
| 38 | 31 | 73.8 | 201 | 2 | Q519U9_ENTHI | Q519u9 entamoeba h |
| 39 | 31 | 73.8 | 212 | 2 | Q7IMF6_HUMAN | Q7imf6 homo sapien |
| 40 | 31 | 73.8 | 235 | 2 | Q6PBI0_ACTAD | Q6pbi0 acinetobact |
| 41 | 31 | 73.8 | 247 | 1 | PCPC_SPHCR | Q03520 sphingobium |
| 42 | 31 | 73.8 | 248 | 2 | Q937X0_9SPHN | Q937x0 sphingomona |
| 43 | 31 | 73.8 | 254 | 2 | Q975X7_SULTO | Q975x7 sulfolobus |
| 44 | 31 | 73.8 | 276 | 2 | Q8N8N1_HUMAN | Q8n8n1 homo sapien |
| 45 | 31 | 73.8 | 298 | 1 | SNAB_BOVIN | P81126 bos taurus |

ALIGNMENTS

RESULT 1
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
RT chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
RL [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=Keratinocyte;
RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
RA Diamandis E.P.;
RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
RT enzyme is a new member of the human kallikrein gene family - genomic
RT characterization, mapping, tissue expression and hormonal
RT regulation.";
RL Gene 254:119-128(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Preper B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
RA Wallbrandt P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
RT mice; a model for chronic itchy dermatitis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
RC AND TISSUE SPECIFICITY.
TISSUE=Ovarian carcinoma;

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=C57BL/6J; TISSUE=Tail;
 RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.;
 RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
 RT mice; a model for chronic itchy dermatitis.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nkado I., Osato Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wu L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirokane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Iotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 RN NUCLEOTIDE SEQUENCE OF 1-234, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6; TISSUE=Tail;
 RX MEDLINE=99399282; PubMed=10469296;
 RX DOI=10.1046/j.1523-1747.1999.00662.x;
 RA Baeckman A., Strandén P., Brattand M., Hansson L., Egelrud T.;
 RT "Molecular cloning and tissue expression of the murine analog to human
 RT stratum corneum chymotryptic enzyme."

RL J. Invest. Dermatol. 113:152-155 (1999).
 CC -|- FUNCTION: May catalyze the degradation of intercellular cohesive
 CC structures in the cornified layer of the skin in the continuous
 CC shedding of cells from the skin surface. Specific for amino acid
 CC residues with aromatic side chains in the P1 position. SCCE
 CC cleaves insulin B chain at 6-Leu-Cys-7, 16-Tyr-Leu-17, 25-
 CC Phe-Tyr-26, and 26-Tyr-Thr-27. Could play a role in the
 CC activation of precursors to inflammatory cytokines.
 CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -|- TISSUE SPECIFICITY: Expressed in skin and, at lower levels, in
 CC lung, kidney, brain, heart and spleen. In skin, expressed in high
 CC suprabasal keratinocytes and in the luminal parts of hair
 CC follicles. Not detected in liver and skeletal muscle.
 CC -|- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AB008371; BAB55604.1; -; mRNA
 DR EMBL: AF339930; AAK69652.1; -; Genomic DNA.
 DR EMBL: AK029477; BAC26467.1; -; mRNA.
 DR EMBL: AK077406; BAC36787.1; -; mRNA.
 DR EMBL: BC027823; AAH27823.1; -; mRNA.
 DR EMBL: AF124299; AAF01139.1; -; mRNA.
 DR HSSP: P00760; 1EZX.
 DR MEROPS: S01.300; -;
 DR Ensemble: ENSMUSG00000030713; Mus musculus.
 DR MGI: MGI:1346336; K1k7.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS02040; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 25 Activation peptide (By similarity).
 FT CHAIN 26 249 Kallikrein 7 (By similarity).
 FT REGION 26 246 Serine protease (By similarity).
 FT ACT_SITE 66 66 Charge relay system (By similarity).
 FT ACT_SITE 108 108 Charge relay system (By similarity).
 FT ACT_SITE 201 201 Charge relay system (By similarity).
 FT DISULFID 51 67 By similarity.
 FT DISULFID 140 207 By similarity.
 FT DISULFID 172 186 By similarity.
 FT DISULFID 197 222 By similarity.
 FT CONFLICT 215 217 VSW -> ASR (in Ref. 5).
 SQ SEQUENCE 249 AA; 27257 MW; 0D4E380F12D14F87 CRC64;
 Query Match 85.7%; Score 36; DB 1; Length 249;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QRIKASKSF 9
 Db 87 QKIKATKSF 95
 RESULT 3
 ID Y1897_PASMU STANDARD; PRT; 107 AA.
 AC Q9CJU4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Hypothetical lipoprotein PM1897 precursor.

OrderedLocusNames=PM1897;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.B., Paustian M.L., Whitam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE006227; AK03981.1; -; Genomic DNA.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
KW Palmitate; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 107 Hypothetical protein PM1897.
FT LIPID 18 18 N-palmitoyl cysteine (Potential).
FT LIPID 18 18 S-diacylglycerol cysteine (Potential).
SQ SEQUENCE 107 AA; 12214 MW; 920C61E14A10F405 CRC64;

Query Match 81.0%; Score 34; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 27 QRIEASESF 35
||||:||||

RESULT 4
Q88Q37 PSEPK PRELIMINARY; PRT; 294 AA.
AC Q88Q37;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator AmpR, putative.
GN OrderedLocusNames=PP0661;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfele E.K., Scanlan D., Tran K.,
RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedter H., Lauber J., Stjepandic D., Hohnsels J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoef A., Tuenmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808 (2002).
CC -!- SIMILARITY: Contains 1 HTH_LYR-type DNA-binding domain.
DR EMBL; AE016776; AAN66286.1; -; Genomic DNA.
DR TIGR; PP0661; -;
DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000847; HTH_LYR.
DR InterPro; IPR005119; LysR_subst_bd.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS50931; HTH_LYSR; 1.
KW Activator; Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 294 AA; 32996 MW; 33695F24D26560EF CRC64;

Query Match 81.0%; Score 34; DB 2; Length 294;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 259 QRIEASESF 267
||||:||||

RESULT 5
Q4KA21 PSEF5
ID Q4KA21 PSEF5 PRELIMINARY; PRT; 296 AA.
AC Q4KA21;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Transcriptional regulator, LysR family.
GN ORFNames=PPL3812;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=PF-5;
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Ghinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L., Thomas L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878 (2005).
DR EMBL; CP000076; AAY93076.1; -; Genomic DNA.
SQ SEQUENCE 296 AA; 33530 MW; 3941F0F1EA3E92F0 CRC64;

Query Match 81.0%; Score 34; DB 2; Length 296;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 259 QRIEASESF 267
||||:||||

RESULT 6
Q82XB0 NITEU
ID Q82XB0 NITEU PRELIMINARY; PRT; 683 AA.
AC Q82XB0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sensory transduction histidine kinases.
GN OrderedLocusNames=NE0377;
OS Nitrosomonas europaea
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]

```
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19718 / IF0 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Savavedra-Soto L.A.,
RA Acsiro D.M., Hommes N.G., Whitaker M.M., Alp D.J.;
RA "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321857; CAD84288.1; -; Genomic_DNA.
DR HSP; Q56310; I15D.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000155; P:two-component sensor molecule activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR004358; His_kin_like_C.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HiskA; 1.
DR PRINTS; PR00344; BCTRUSENSOR.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 683 AA; 77013 MW; 6989E595B86543ED4 CRC64;

Query Match 81.0%; Score 34; DB 2; Length 683;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 548 QRIKASKSF 556

RESULT 7
Q678H2_9VIRU PRELIMINARY; PRT; 310 AA.
ID Q678H2_9VIRU PRELIMINARY; PRT; 310 AA.
AC Q678H2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Lymphocystis disease virus - isolate China.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
OX NCBI_TaxID=256729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
RA Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
RT "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
RT China.";
RL J. Virol. 78:6982-6994(2004).
DR EMBL; AY380826; AAU10885.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001545; Gly_hormoneB.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 310 AA; 34349 MW; 714DAC2A33E42C11 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 310;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
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Db 183 QRIKSKNF 191
|:|:|:|:|
|:|:|:|:|

RESULT 8
RLAO THEAC STANDARD; PRT; 314 AA.
ID _RLAO THEAC STANDARD; PRT; 314 AA.
AC P57692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acidic ribosomal protein P0 homolog (L10E).
GN Name=rpP0; OrderedLocNames=Ta0359;
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
CC -!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
CC E.coli protein L10.
CC -!- SIMILARITY: Belongs to the ribosomal protein L10P family.
CC -----
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CC -----
CC EMBL; AL445064; CAC11503.1; -; Genomic_DNA.
DR HAMAP; MF_00280; -; 1.
DR InterPro; IPR001790; Ribosomal_L10.
DR Pfam; PF00466; Ribosomal_L10; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 314 AA; 34583 MW; F40D048680E0B6EB CRC64;

Query Match 78.6%; Score 33; DB 1; Length 314;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKS 8
DB 17 QRIKASRS 24
|:|:|:|:|
|:|:|:|:|

RESULT 9
KAIN HUMAN STANDARD; PRT; 427 AA.
ID _KAIN HUMAN STANDARD; PRT; 427 AA.
AC P29622; Q53XB5; Q86TR9; Q96B25;
DT 01-APR-1993 (Rel. 25, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallistatin precursor (Serpin A4) (Kallikrein inhibitor) (Protease
DE inhibitor 4).
GN Name=SERPIN4; Synonyms=XST, PI4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
RX MEDLINE=94043294; PubMed=8227002;
RA Chai K.X., Chen L.-M., Chao J., Chao L.;
RT "Kallistatin: a novel human serine proteinase inhibitor. Molecular
RT cloning, tissue distribution, and expression in Escherichia coli.";
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DR PANTHER: PTHR11461; Prot_inh_serpin; 1.
DR Pfam: PF00079; Serpin; 1.
DR SMART: SM00093; SERPIN; 1.
DR PROSITE: PS00284; SERPIN; 1.
KW Glycoprotein; Protease inhibitor; Serine protease inhibitor; Serpin;
FT SIGNAL.
FT CHAIN 1 20 Potential.
FT SITE 21 427 Kallistatin.
FT CARBOHYD 388 389 Reactive bond (By similarity).
FT CARBOHYD 33 33 N-linked (GLNac. . .) (Potential).
FT CARBOHYD 108 108 N-linked (GLNac. . .) (Potential).
FT CARBOHYD 157 157 N-linked (GLNac. . .) (Potential).
FT CARBOHYD 238 238 N-linked (GLNac. . .) (Potential).
SQ SEQUENCE 427 AA; 48558 MW; 24E05E0197F27ED CRC64;

Query Match 78.6%; Score 33; DB 1; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 355 OKLEASKSF 363
[::|||||]

RESULT 11
Q54TF9_DICDI
ID Q54TF9_DICDI PRELIMINARY; PRT; 445 AA.
AC Q54TF9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS ORFNames=DD80204663;
GN Dictyostellum discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostellum discoideum."
RL Nature 0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01000075; EAL66649.1; -; Genomic DNA.
DR GO; GO:0031072; F:heat shock protein binding; IEA.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
KW Chaperone; Hypothetical protein.
SQ SEQUENCE 445 AA; 50097 MW; BD1A93FAF109CA13 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 445;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 489 KRKVKSKSF 497
[::|||||]

RESULT 12
Q54H89_DICDI
ID Q54H89_DICDI PRELIMINARY; PRT; 513 AA.
AC Q54H89;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS ORFNames=DD80219472;
GN Dictyostellum discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostellum discoideum."
RL Nature 0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01000218; EAL62638.1; -; Genomic DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 513 AA; 58802 MW; 994053C8156F1DDC CRC64;

Query Match 78.6%; Score 33; DB 2; Length 513;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 489 KRKVKSKSF 497
[::|||||]

RESULT 13
Q8EUP9_MYCPE
ID Q8EUP9_MYCPE PRELIMINARY; PRT; 671 AA.
AC Q8EUP9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heavy-metal transporting P-type ATPase.
GN OrderedLocusNames=MYPE8710;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=1246555; DOI=10.1093/nar/gkf667;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
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RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
RT "The complete genomic sequence of Mycoplasma penetrans, an  
RT intracellular bacterial pathogen in humans.";  
RL Nucleic Acids Res. 30:5293-5300(2002).  
DR EMBL; BA000026; BAC44663.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.  
DR GO; GO:0003624; F:catalytic activity; IEA.  
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0030001; P:metal ion transport; IEA.  
DR InterPro; IPR006416; ATPase-IB_hvy.  
DR InterPro; IPR001757; ATPase_E1-E2.  
DR InterPro; IPR005834; Dehal-like hydro.  
DR InterPro; IPR008250; E1-E2_ATPase-reg.  
DR Pfam; PF00122; E1-E2_ATPase; 1.  
DR Pfam; PF00702; Hydrolase; 1.  
DR PRINTS; PR00119; CATATPASE.  
DR TIGRFAMs; TIGR01525; ATPase-IB_hvy; 1.  
DR TIGRFAMs; TIGR01494; ATPase_P-type; 2.  
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.  
KW Complete proteome.  
SQ SEQUENCE 671 AA; 75854 MW; 8EE005CA3B60671 CRC64;  
  
Query Match 78.6%; Score 33; DB 2; Length 671;  
Best Local Similarity 77.8%; Pred. No. 2.3e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ORIKASKSF 9  
Db 551 KEIKASKSF 559  
  
RESULT 14  
Q4S703 TETNG PRELIMINARY; PRT; 1618 AA.  
AC Q4S703;  
DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
DE Chromosome 14 SCAF14723, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00023047001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segreus B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellino V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn W., Robinson-Rechavi M.,  
RA Laudet V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAE01014723; CAG03579.1; -; Genomic_DNA.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR011511; SH3_2.  
DR Pfam; PF00536; SAM_1; 2.  
DR Pfam; PF07653; SH3_2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00454; SAM; 2.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS0105; SAM_DOMAIN; 1.  
KW SH3 domain.  
FT NON_TER 1618 1618  
SQ SEQUENCE 1618 AA; 177245 MW; C89436939816A448 CRC64;  
  
Query Match 78.6%; Score 33; DB 2; Length 1618;  
Best Local Similarity 77.8%; Pred. No. 5.6e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ORIKASKSF 9  
Db 1192 QRTKGSKSF 1200  
  
RESULT 15  
RL10 MYCPE STANDARD; PRT; 161 AA.  
ID RL10 MYCPE  
AC Q8EVJ0;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE 50S ribosomal protein L10.  
GN Name-rplJ; OrderedLocusNames=MYP5740;  
OS Mycoplasma penetrans.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI_TaxID=28227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=HF-2;  
RX MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;  
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,  
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
RT "The complete genomic sequence of Mycoplasma penetrans, an  
RT intracellular bacterial pathogen in humans.";  
RL Nucleic Acids Res. 30:5293-5300(2002).  
CC -!- SIMILARITY: Belongs to the ribosomal protein L10P family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; BA000026; BAC44364.1; ALT_INIT; Genomic_DNA.  
DR HAMAP; MF 00362; -; 1.  
DR InterPro; IPR001790; Ribosomal_L10.  
DR InterPro; IPR002363; Ribosomal_L10eub.  
DR Pfam; PF00466; Ribosomal_L10; 1.  
DR PROSITE; PS01109; RIBOSOMAL_L10; FALSE_NEG.  
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.  
SQ SEQUENCE 161 AA; 17949 MW; 1D95D1C29B5E87D3 CRC64;  
  
Query Match 76.2%; Score 32; DB 1; Length 161;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ORIKASKSF 9  
Db 17 EQIKSKSF 25  
  
Search completed: March 11, 2006, 00:39:00
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Job time : 99.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgm2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgm2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 42 | 100.0 | 9 | 2 | US-09-502-600-99 |
| 2 | 42 | 100.0 | 9 | 2 | US-09-502-600-130 |
| 3 | 42 | 100.0 | 9 | 2 | US-09-918-243-99 |
| 4 | 42 | 100.0 | 9 | 2 | US-09-918-243-130 |
| 5 | 42 | 100.0 | 144 | 2 | US-09-618-259-4 |
| 6 | 42 | 100.0 | 154 | 2 | US-09-261-416-7 |
| 7 | 42 | 100.0 | 224 | 2 | US-08-944-483-33 |
| 8 | 42 | 100.0 | 225 | 1 | US-08-557-146-12 |
| 9 | 42 | 100.0 | 225 | 1 | US-09-027-337-4 |
| 10 | 42 | 100.0 | 225 | 1 | US-09-154-344-12 |
| 11 | 42 | 100.0 | 225 | 2 | US-09-644-600-4 |
| 12 | 42 | 100.0 | 225 | 2 | US-09-654-600A-4 |
| 13 | 42 | 100.0 | 253 | 1 | US-08-557-146-2 |
| 14 | 42 | 100.0 | 253 | 1 | US-08-824-874-3 |
| 15 | 42 | 100.0 | 253 | 1 | US-09-154-344-2 |
| 16 | 42 | 100.0 | 253 | 2 | US-08-930-188-2 |
| 17 | 42 | 100.0 | 253 | 2 | US-09-210-084-3 |
| 18 | 42 | 100.0 | 253 | 2 | US-09-764-762-3 |
| 19 | 42 | 100.0 | 253 | 4 | PCT-US96-04294-2 |
| 20 | 42 | 100.0 | 265 | 2 | US-09-949-016-7716 |
| 21 | 36 | 85.7 | 9 | 2 | US-09-502-600-97 |
| 22 | 36 | 85.7 | 9 | 2 | US-09-918-243-97 |
| 23 | 31 | 73.8 | 35 | 2 | US-09-149-476-619 |
| 24 | 31 | 73.8 | 132 | 2 | US-09-513-999C-5132 |
| 25 | 31 | 73.8 | 250 | 1 | US-07-914-282D-6 |
| 26 | 31 | 73.8 | 250 | 1 | US-08-276-887A-6 |
| 27 | 31 | 73.8 | 250 | 4 | PCT-US93-02460-6 |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 28 | 31 | 73.8 | 314 | 2 | US-09-248-796A-19386 | Sequence 19386, A |
| 29 | 31 | 73.8 | 2317 | 2 | US-09-949-016-10109 | Sequence 10109, A |
| 30 | 31 | 73.8 | 2860 | 1 | US-08-826-267-2 | Sequence 2, Appli |
| 31 | 30 | 71.4 | 342 | 2 | US-09-252-991A-18101 | Sequence 18101, A |
| 32 | 30 | 71.4 | 666 | 2 | US-08-982-785A-11 | Sequence 11, Appl |
| 33 | 30 | 71.4 | 666 | 2 | US-09-629-498-11 | Sequence 11, Appl |
| 34 | 30 | 71.4 | 726 | 2 | US-09-949-016-5916 | Sequence 5916, Ap |
| 35 | 30 | 71.4 | 737 | 2 | US-09-949-016-11607 | Sequence 11607, A |
| 36 | 29 | 69.0 | 73 | 2 | US-09-248-796A-26710 | Sequence 26710, A |
| 37 | 29 | 69.0 | 203 | 2 | US-09-710-279-2424 | Sequence 2424, A |
| 38 | 29 | 69.0 | 222 | 2 | US-09-134-001C-3400 | Sequence 3400, Ap |
| 39 | 28 | 66.7 | 61 | 1 | US-08-194-211A-3 | Sequence 3, Appli |
| 40 | 28 | 66.7 | 61 | 2 | US-08-456-748B-3 | Sequence 3, Appli |
| 41 | 28 | 66.7 | 61 | 2 | US-09-492-709A-357 | Sequence 357, App |
| 42 | 28 | 66.7 | 67 | 2 | US-09-489-039A-10090 | Sequence 10090, A |
| 43 | 28 | 66.7 | 108 | 2 | US-09-248-796A-17972 | Sequence 17972, A |
| 44 | 28 | 66.7 | 159 | 2 | US-09-134-000C-4565 | Sequence 4565, Ap |
| 45 | 28 | 66.7 | 188 | 2 | US-09-248-796A-27949 | Sequence 27949, A |

ALIGNMENTS

RESULT 1

US-09-502-600-99

; Sequence 99, Application US/09502600A

; Patent No. 6294344

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP-C

; CURRENT FILING DATE: 2000-02-11

; CURRENT APPLICATION NUMBER: US/09/502.600A

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 99

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 91-99 of the SCCE protein

US-09-502-600-99

Query Match 100.0%; Score 42; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 2

US-09-502-600-130

; Sequence 130, Application US/09502600A

; Patent No. 6294344

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP-C

; CURRENT FILING DATE: 2000-02-11

; CURRENT APPLICATION NUMBER: US/09/502.600A

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 130

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 91-99 of the SCE protein
US-09-502-600-130

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 3

US-09-918-243-99
; Sequence 99, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCE protein
US-09-918-243-99

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 4

US-09-918-243-130
; Sequence 130, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCE protein
US-09-918-243-130

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 5

US-09-618-259-4
; Sequence 4, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (sece) catalytic domain
US-09-618-259-4

Query Match 100.0%; Score 42; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 28 QRIKASKSF 36

RESULT 6

US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
; OTHER INFORMATION: domain in TADG-12
US-09-261-416-7

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 37 QRIKASKSF 45

RESULT 7

US-08-944-483-33
; Sequence 33, Application US/08944483

Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183-US.01
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 42; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 62 QRIKASKSF 70

RESULT 8
US-08-557-146-12
Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 9
US-09-027-337-4
Sequence 4, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotooshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of Ssce homologous to
OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Query Match 100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 10
US-09-154-344-12
Sequence 12, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:

; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-09-154-344-12

Query Match 100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 11
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE

US-09-644-600-4

Query Match 100.0%; Score 42; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 12
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
; US-09-654-600A-4

Query Match 100.0%; Score 42; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 13
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.

REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 14
US-08-824-874-3
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0252 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-08-824-874-3

Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 91 QRIKASKSF 99

RESULT 15
US-09-154-344-2
Sequence 2, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

Search completed: March 11, 2006, 01:24:29
Job time : 22.2222 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 42 | 100.0 | 9 | 3 | US-09-918-243-99 |
| 2 | 42 | 100.0 | 9 | 3 | Sequence 99, Appl |
| 3 | 42 | 100.0 | 9 | 3 | Sequence 130, App |
| 4 | 42 | 100.0 | 9 | 3 | Sequence 99, Appl |
| 5 | 42 | 100.0 | 9 | 3 | Sequence 130, App |
| 6 | 42 | 100.0 | 9 | 4 | US-09-905-083-130 |
| 7 | 42 | 100.0 | 9 | 4 | Sequence 99, Appl |
| 8 | 42 | 100.0 | 9 | 5 | US-10-372-521-130 |
| 9 | 42 | 100.0 | 9 | 5 | Sequence 130, App |
| 10 | 42 | 100.0 | 97 | 4 | US-10-831-075-130 |
| 11 | 42 | 100.0 | 144 | 3 | Sequence 100, App |
| 12 | 42 | 100.0 | 144 | 4 | Sequence 4, Appli |
| 13 | 42 | 100.0 | 181 | 4 | Sequence 98, Appl |
| 14 | 42 | 100.0 | 198 | 4 | Sequence 96, Appl |
| 15 | 42 | 100.0 | 224 | 3 | Sequence 33, Appl |
| 16 | 42 | 100.0 | 224 | 4 | Sequence 134, App |
| 17 | 42 | 100.0 | 225 | 4 | Sequence 10, App |
| 18 | 42 | 100.0 | 250 | 4 | Sequence 4, Appli |
| 19 | 42 | 100.0 | 252 | 4 | Sequence 92, Appl |
| 20 | 42 | 100.0 | 253 | 3 | Sequence 94, Appl |
| 21 | 42 | 100.0 | 253 | 3 | Sequence 98, Appl |
| 22 | 42 | 100.0 | 253 | 4 | Sequence 3, Appli |
| 23 | 42 | 100.0 | 253 | 4 | Sequence 2, Appli |
| 24 | 42 | 100.0 | 253 | 4 | Sequence 48, Appl |
| 25 | 42 | 100.0 | 253 | 4 | Sequence 90, Appl |
| 26 | 42 | 100.0 | 253 | 4 | Sequence 498, App |
| 27 | 42 | 100.0 | 253 | 4 | Sequence 639, App |

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28 42 100.0 253 5 US-10-643-795A-95 Sequence 95, Appl
29 42 100.0 253 5 US-10-948-518-95 Sequence 95, Appl
30 42 100.0 253 5 US-10-868-490A-1 Sequence 1, Appl
31 42 100.0 257 4 US-10-344-394-38 Sequence 38, Appl
32 39 92.9 226 4 US-10-071-214-49 Sequence 49, Appl
33 37 88.1 136 5 US-10-450-763-53737 Sequence 53737, A
34 36 85.7 9 3 US-09-918-243-97 Sequence 97, Appl
35 36 85.7 9 3 US-09-905-083-97 Sequence 97, Appl
36 36 85.7 9 4 US-10-372-521-97 Sequence 97, Appl
37 36 85.7 9 5 US-10-831-075-97 Sequence 97, Appl
38 36 85.7 249 4 US-10-071-214-50 Sequence 50, Appl
39 33 78.6 243 4 US-10-071-214-46 Sequence 46, Appl
40 33 78.6 411 4 US-10-210-172-122 Sequence 122, App
41 33 78.6 411 4 US-10-210-172-124 Sequence 124, App
42 33 78.6 411 4 US-10-210-172-126 Sequence 126, App
43 33 78.6 411 4 US-10-210-172-128 Sequence 128, App
44 33 78.6 411 4 US-10-210-172-130 Sequence 130, App
45 33 78.6 411 4 US-10-210-172-132 Sequence 132, App

```

ALIGNMENTS

RESULT 1

US-09-918-243-99

; Sequence 99, Application US/09918243

; Patent No. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 99

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 91-99 of the SCCE protein

US-09-918-243-99

Query Match 100.0%; Score 42; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 QRIKASKSF 9

|||||||

Db 1 QRIKASKSF 9

RESULT 2

US-09-918-243-130

; Sequence 130, Application US/09918243

; Patent No. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 130

; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-130

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 3
US-09-905-083-99
; Sequence 99, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/DiV
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-905-083-99

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 4
US-09-905-083-130
; Sequence 130, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/DiV
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-905-083-130

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 5
US-10-372-521-99
; Sequence 99, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-372-521-99

Query Match      100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 6
US-10-372-521-130
; Sequence 130, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-372-521-130

Query Match      100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9
```

RESULT 7

US-10-831-075-99
; Sequence 99, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-831-075-99

Query Match 100.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 8

US-10-831-075-130
; Sequence 130, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-831-075-130

Query Match 100.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 9

US-10-262-511-100
; Sequence 100, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle

; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSequist version 0.1
; SEQ ID NO 100
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-100

Query Match 100.0%; Score 42; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 72 QRIKASKSF 80

RESULT 10

US-09-796-294-4
; Sequence 4, Application US/09796294
; Patent No. US20020037581A1

```
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4

Query Match          100.0%; Score 42; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 28 QRIKASKSF 36

RESULT 11
US-10-461-787-4
; Sequence 4, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. US20030199010A1e1 Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/618,259
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-10-461-787-4

Query Match          100.0%; Score 42; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 28 QRIKASKSF 36

RESULT 12
US-10-511-98
; Sequence 98, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenna
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
```

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; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fatturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curasequid version 0.1
; SEQ ID NO 98
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-98

Query Match          100.0%; Score 42; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 72 QRIKASKSF 80

RESULT 13
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenna
```

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; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 96
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 42; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 14
US-09-789-210-33
; Sequence 33, Application US/09789210

; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match 100.0%; Score 42; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 62 QRIKASKSF 70

RESULT 15
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
```

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; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104

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```

Query Match      100.0%; Score 42; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 QRIKASKSF 9
Db      77 QRIKASKSF 85

```

Search completed: March 11, 2006, 01:37:26
Job time : 70.4444 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/PTCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US03_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 42 | 100.0 | 181 | 6 | US-10-412-748-19 |
| 2 | 42 | 100.0 | 253 | 6 | US-10-412-748-11 |
| 3 | 42 | 100.0 | 253 | 6 | US-10-412-748-14 |
| 4 | 42 | 100.0 | 253 | 6 | US-10-412-748-17 |
| 5 | 42 | 100.0 | 253 | 7 | US-11-037-243-98 |
| 6 | 31 | 73.8 | 352 | 7 | US-11-036-568A-5482 |
| 7 | 31 | 73.8 | 356 | 7 | US-11-036-568A-5481 |
| 8 | 31 | 73.8 | 386 | 7 | US-11-036-568A-5480 |
| 9 | 30 | 71.4 | 299 | 7 | US-11-087-099-3123 |
| 10 | 30 | 71.4 | 726 | 7 | US-11-051-720-1604 |
| 11 | 30 | 71.4 | 747 | 7 | US-11-051-720-1605 |
| 12 | 29 | 69.0 | 203 | 6 | US-10-793-626-2424 |
| 13 | 29 | 69.0 | 277 | 7 | US-11-036-568A-6766 |
| 14 | 29 | 69.0 | 294 | 7 | US-11-036-568A-20947 |
| 15 | 29 | 69.0 | 296 | 7 | US-11-036-568A-6765 |
| 16 | 29 | 69.0 | 328 | 7 | US-11-036-568A-20946 |
| 17 | 29 | 69.0 | 355 | 7 | US-11-087-099-8470 |
| 18 | 29 | 69.0 | 355 | 7 | US-11-087-099-12111 |
| 19 | 29 | 69.0 | 529 | 7 | US-11-087-099-11190 |
| 20 | 28 | 66.7 | 46 | 6 | US-10-510-959-108 |
| 21 | 28 | 66.7 | 132 | 7 | US-11-036-568A-15475 |
| 22 | 28 | 66.7 | 139 | 7 | US-11-036-568A-15474 |
| 23 | 28 | 66.7 | 182 | 7 | US-11-036-568A-15473 |
| 24 | 28 | 66.7 | 351 | 7 | US-11-087-099-2242 |
| 25 | 28 | 66.7 | 351 | 7 | US-11-087-099-8245 |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 26 | 28 | 66.7 | 384 | 7 | US-11-074-176-78 | Sequence 78, Appl |
| 27 | 28 | 66.7 | 390 | 6 | US-11-096-568A-23573 | Sequence 23573, A |
| 28 | 28 | 66.7 | 469 | 6 | US-10-510-386-14 | Sequence 14, Appl |
| 29 | 28 | 66.7 | 600 | 6 | US-10-131-826A-462 | Sequence 462, App |
| 30 | 28 | 66.7 | 600 | 6 | US-10-973-115B-462 | Sequence 462, App |
| 31 | 27 | 64.3 | 87 | 6 | US-10-667-295-68 | Sequence 68, Appl |
| 32 | 27 | 64.3 | 125 | 6 | US-10-467-557-2128 | Sequence 2128, Ap |
| 33 | 27 | 64.3 | 163 | 7 | US-11-036-568A-25357 | Sequence 25357, A |
| 34 | 27 | 64.3 | 268 | 7 | US-11-096-568A-25355 | Sequence 25355, A |
| 35 | 27 | 64.3 | 318 | 6 | US-10-131-826A-374 | Sequence 374, App |
| 36 | 27 | 64.3 | 318 | 6 | US-10-973-115B-374 | Sequence 374, App |
| 37 | 27 | 64.3 | 343 | 6 | US-10-793-626-1626 | Sequence 1626, Ap |
| 38 | 27 | 64.3 | 343 | 6 | US-10-793-626-1964 | Sequence 1964, Ap |
| 39 | 27 | 64.3 | 744 | 7 | US-11-087-099-3289 | Sequence 3289, Ap |
| 40 | 27 | 64.3 | 838 | 7 | US-11-031-737A-11 | Sequence 11, Appl |
| 41 | 27 | 64.3 | 838 | 7 | US-11-031-482-11 | Sequence 11, Appl |
| 42 | 27 | 64.3 | 1121 | 7 | US-11-113-751-19 | Sequence 19, Appl |
| 43 | 27 | 64.3 | 1248 | 7 | US-11-096-568A-29804 | Sequence 29804, A |
| 44 | 27 | 64.3 | 1295 | 7 | US-11-096-568A-29803 | Sequence 29803, A |
| 45 | 27 | 64.3 | 1305 | 7 | US-11-096-568A-29802 | Sequence 29802, A |

ALIGNMENTS

RESULT 1

US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

Query Match 100.0%; Score 42; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
| | | | | | | | | |
Db 19 QRIKASKSF 27

RESULT 2

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A.
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A.
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 5
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A.
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 6
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 42; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 6
US-11-096-568A-5482
; Sequence 5482, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5482
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(352)
; OTHER INFORMATION: Ceres Seq. ID no. 14310397
US-11-096-568A-5482

Query Match      73.8%; Score 31; DB 7; Length 352;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 176 QRLKASRAY 184

RESULT 7
US-11-096-568A-5481
; Sequence 5481, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

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; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5481
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(356)
; OTHER INFORMATION: Ceres Seq. ID no. 14310396
US-11-096-568A-5481

Query Match      73.8%; Score 31; DB 7; Length 356;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 180 QRLKASRAY 188

RESULT 8
US-11-096-568A-5480
; Sequence 5480, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5480
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(386)
; OTHER INFORMATION: Ceres Seq. ID no. 14310395
US-11-096-568A-5480

Query Match      73.8%; Score 31; DB 7; Length 386;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 210 QRLKASRAY 218

RESULT 9
US-11-087-099-3123
; Sequence 3123, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3123
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-3123

Query Match      71.4%; Score 30; DB 7; Length 299;
Best Local Similarity 55.0%; Pred. No. 29;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 210 QRLKASRAY 218

RESULT 10
US-11-051-720-1604
; Sequence 1604, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1604
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1604

Query Match      71.4%; Score 30; DB 7; Length 726;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 148 QRIKASRS 155

RESULT 11
US-11-051-720-1605
; Sequence 1605, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1605
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1605

Query Match      71.4%; Score 30; DB 7; Length 747;
Best Local Similarity 75.0%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 148 QRIKASRS 155

RESULT 12
US-10-793-626-2424
; Sequence 2424, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
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; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2424
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2424

Query Match 69.0%; Score 29; DB 6; Length 203;
Best Local Similarity 55.6%; Pred. No. 37;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 179 KRLKSDKSF 187
:|:|:|

RESULT 13

US-11-096-568A-6766
; Sequence 6766, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6766
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 14316538
US-11-096-568A-6766

Query Match 69.0%; Score 29; DB 7; Length 277;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IKASKSF 9
Db 69 IRASKSF 75
:|:|:|

RESULT 14

US-11-096-568A-20947
; Sequence 20947, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20947
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 12391401
US-11-096-568A-20947

Query Match 69.0%; Score 29; DB 7; Length 294;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 21 KRLRASESF 29
:|:|:|

RESULT 15

US-11-096-568A-6765
; Sequence 6765, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6765
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(296)
; OTHER INFORMATION: Ceres Seq. ID no. 14316537
US-11-096-568A-6765

Query Match 69.0%; Score 29; DB 7; Length 296;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IKASKSF 9
Db 88 IRASKSF 94
:|:|:|

Search completed: March 11, 2006, 01:38:44
Job time : 9 secs

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